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Listing first 45 summaries
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2: pir2:*
3: pir3:*
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Gapop 10.0 ,
     283308 seqs, 96168682 residues
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Qy 121 GQGTMVTVSS 130 Db 119 GQGTMVTVSS 128	OY 61 AQKFQGRYTMTADGSTSTAYMELNSLRSEDTATYYCARQQNGGWYEGPLLEPRPDALDIW	QY 1 QVQLVQSGAEAKKPGSSYKVSCKASGDTFNSFPISMVRQAPGQGLEMMGGIIPIFGSTKY	Query Match 74.9%; Score 515; DB 2; Li Best Local Similarity 79.2%; Pred. No. 1.4e-39; Matches 103; Conservative 7; Mismatches 18;	A; Modellie (Type: NARA) A;Residuse: 1-128 (MARA) C; Superfamily: immunoglobulin V region; immunoglobulin C; Keywords: heterotetramer; immunoglobulin F; 1-30/Region: framework 1 F; 15-98/Domain: immunoglobulin homology < IMM> F; 15-98/Domain: complementarity-determining 1 F; 36-50/Region: complementarity-determining 2 F; 51-67/Region: complementarity-determining 2 F; 68-98/Region: framework 3 F; 99-116/Region: complementarity-determining 3	;Accession: PH09 ;Status: nucleic	F.; Carson, D.A., Kipps, T.J 91, 1992 omatic selection of natural 952; MUID:92202880; PMID:155	Apr-1993 #sequence_revision 17-Apr-1993	nain V region	ALIGNMENTS	30 446 64.8 118 2 S36265 31 442.5 64.3 122 2 C49590 32 442 64.2 171 2 823623 33 437.5 63.6 160 2 PL0105 34 436.5 63.3 129 2 836260 36 435 63.2 135 2 849530 37 434 63.1 39 2 S46463 38 430.5 62.6 127 2 S34014 39 428.5 62.3 129 2 S46393 40 428 62.2 93 2 S46393 41 426 61.9 97 2 PH0870 42 422.5 61.4 122 2 S36271 43 420.5 61.1 121 2 S20783 45 417 60.6 116 2 S31667
	YCARQQNGGWYBGPLLBPRPDALDIW 120 	SWVRQAPGQGLEWMGGIIPIFGSTKY 60	2; 39; 18	inmunoglobulin homology in <imms 1="" 2="" 3<="" ing="" ning="" td=""><td></td><td>T.J. al autoantibodies. 1552291</td><td>93</td><td>ragment)</td><td></td><td>Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r anti-PR2 erythrocy Ig heavy chain V r Ig heavy chain V r anti-Sm antibody V Ig heavy chain V r Ig heavy chain V r</td></imms>		T.J. al autoantibodies. 1552291	93	ragment)		Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r anti-PR2 erythrocy Ig heavy chain V r Ig heavy chain V r anti-Sm antibody V Ig heavy chain V r

C;Accession: C33548
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R;Kipps, T.J.; Tomhave, B.; Pratt, L.P.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86; 5913-5917, 1989
Proc. Natl. Acad. Sci. U.S.A. 86; 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression of the complex of th

Ig heavy chain V-i region (783) - human C;Species: Homo sapiens (man) C;Sate: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996

RESULT 2 C33548

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R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J. J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural a
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A;Title: Complete nucleotide sequence of the membrane form of A;Reference number: S14683; MUID:90332450; PMID:2115996

A;Accession: S14683
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A; Residues: 1-133 < KIP>
                                                                                                                                                Species: Homo sapiens (man)
10ate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
1Accession: PH0953
                                          Reference number: PH0952; MUID:92202880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; psuperfamily: immunoglobulin C region; immunoglobulin homology
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                                                                                                                                                                                                                                                        heavy chain V region (G6+ CLL-SIC)
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15/Domain: signal sequence #status predicted <SIG>
-627/Product: Ig mu chain #status predicted <NAT>
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72.7%; Pred. No. 4.7e-39;
:ive 10; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 509.5; DB 2; ; Pred. No. 2.5e-38; 10; Mismatches 13;
                                       of natural autoantibodies.
30; PMID:1552291
                                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                                                  (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:g33451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the human IgM heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
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RESULT
PH0962
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F;99-104/Region:
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A;Molecule type:
A;Residues: 1-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F,99-123/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g heavy chain V region
                                                                                                                                                                                                                                                                                                                                ;15-98/Domain: immunoglobulin homology <IMM>;31-35/Region: complementarity-determining 1;36-50/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Molecule type: DNA
;Residues: 1-116 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: PH0959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Homo sapiens (man)
;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
;Accession: PH0959
                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                      51-67/Region:
                                                                                                                                                                                                                                                                                                                                                                                      1-30/Region: framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title: Evidence for somatic selection of Reference number: PH0952, MUID:92202880,
                                                                                                                                                                                                                                                                                                    68-98/Region: framework 3
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68-98/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Martin, T.; Duffy, S.F.; Car
Exp. Med. 175, 983-991, 199
Title: Evidence for somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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 107
                                   121
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                                                                                                      61
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                                                                                                                                                                                                               , 66
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                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-135 <MAR>
                                                                                               AQKFQGRYTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                                                                                         QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
GQGTLVTVSS 116
                                 GQGTMVTVSS 130
                                                                     AQKFQGRVTITADESTSTAYMEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duffy, S.F.; Carson, D.A.; Kipps, T.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNG------GWYEGPLLEPR
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                                                                                                                                                                                                                                                                                                                 complementarity-determining
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framework 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (G6+ T-L26) - human (fragment)
                                                                                                                                                                                                                           72.8%;
76.2%;
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                                                                                                                                    /KVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135
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                                                                                                                                                                                                        Score 501; DB 2;
Pred. No. 2.4e-38;
8; Mismatches 9
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Pred. No. 2e-38;
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                                                                                                                                                                                                                                           Length 116;
                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1933 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0958
                                                                                                                     Query Match
Best Local Similarity 76.9
Conservative
                                                                                                                                                                                                                                                                                                                           Superfamily: immunoglobulin V region; immunoglobulin homology Reywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
Exp. Med. 175, 983-991, 1992
:Title: Evidence for somatic selection of natural autoantibodies.
Reference number: PH0952; MUID:92202880; PMID:1552291
                                                                                                                                                                                                                             68-98/Region:
                                                                                                                                                                                                                                                                                                                                                                                                         Status: nucleic
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Matches 101;
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. Exp. Med. 175, 983-991, 1992
;Title: Evidence for somatic selection of natural autoantibodies;
Reference number: PH0952; MUID:92202880; PMID:1552291
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Best Local Similarity
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8-98/Region:
                                                                                                                                                                                                                                                                              35/Region:
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                                  13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                       1-122 <MAR>
AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGGWYEGELLEEREDALDIW
                                                      QVQLVQSGAEAKKPGSSVKVSCKASGDTENSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-120 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGELLEPRPDALDIW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OVOLVOSGABVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVQLVQSGAEAKKPGSSVKVSCKASGDTENSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
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                                                                                                                                                                                                                                                                      immunoglobulin homology <IMM>
complementarity-determining 1
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                                                                                                                                                                                                    complementarity-determining 3
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                                                                                                                                                                                                                                                                                                                                                                                                     acid sequence
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                                                                                                                                                   72.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.4%; Score 498; DB 2; 77.7%; Pred. No. 4.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                       not shown
                                                                                                                                8; Mismatches
                                                                                                                                             Score 498; DB 2;
Pred. No. 4.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .8; Mismatches
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                                                                                                                                                                Length 122;
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                                                                                                                              Indels
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                    120
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F;99-107/Region:
                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-119 <M
                                                                                                                                                                                                                                                                                                                                                   R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0961
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                                                                                      Query Match
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A;Title: In vitro assembly of repertoires of antibody chains A;Reference number: $46390; MUID:94254092; PMID:8196048
A;Accession: $46394
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C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
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1;Residues: 1-132 <FIG>
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                                                                                                                                                                                                                                             words: heterotetramer;
0/Region: framework 1
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1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
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                                                                                                                                                      complementarity-determining 2 framework 3
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                                                                Conservative
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                                                                             72.3%;
76.2%;
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                                                                                                                                                                                                                                                          immunoglobulin
                                                        Score 497.5; DB pred. No. 5e-38; 9; Mismatches 1
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                                                                        Residues: 1-136 <MAR>
;Superfamily: immunoglobulin V region; immunoglobulin homology;Keywords: heterotetramer; immunoglobulin
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,Title: Evidence for somatic selection of natus; Reference number: PH0952; MUID:92202880; PMID:
                                                                                                                                                                                                                                                                                                  J heavy chain V region (G6+ T-L30) - human (fragment)
iSpecies: Homo sapiens (man)
iDate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
iAccession: PH0960
                                                                                                                                                             Molecule type:
                                                                                                                                                                           Status: nucleic acid sequence
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;Species: Homo saplens (man)
Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
;Accession: PH0954
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Exp. Med. 175, 983-991, 1992
(Itle: Evidence for somatic selection of natural autoantibodies.
(defecence number: PH0952; MUID:92202880; PMID:1552291
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yywords: heterotetramer; immunoglobulin
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PMID:1552291
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F;99-124/Region: complement:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, roc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989; Fitle: Developmentally restricted immunoglobulin heavy (Reference number: A33548; MUID:89345575; PMID:2503826
                                                                                                                                                                                                                                                                                                                                                                                                                                       15-98/Domain:
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                                                                                     PRPDALDIWGOGTMVTVSS 130
                                                                                                                                                         AQKFQGRVTMTADGSTSTAYMBLNSLRSEDTAIYYCARQQNGG------WYEGPLLE 111
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73.4%;
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                                                                                                                                                                                                                                                                                       Score 494.5; DB Pred. No. 1e-37;
                                                                                                                                                                                                                                                                        8; Mismatches
                                                              129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136
                                                                                                                                                                                                                                                                                                      DB 2,
                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                    19,
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                                                                                                                                                                                                                                                                  Gaps
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Ig heavy chain V region C; Species: Homo sapiens

(G6+ CLL-BRA) - (man)

human (fragment)

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C;Accession: PH0957
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0955
R;Martin, T; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0955
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A; Residues: 1-125 < M
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F;36-50/Region:
F;51-67/Region:
                                                                                                                                                                                                                                                                                                                                                                                                      F;1-30/Region: framework
F;15-98/Domain: immunoglo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-127 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Keywords: heterotetramer; immunoglobulin
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Best Local :
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                                                                                                                                                                                                                                                                                                             68-98/Region:
                                                                                                                                                                                        Matches
                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-125 <MAR>
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                                                                                                                                      QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDALDIWGQGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQKFQGRVTITADESTNTAYMELSSLRSEDTAVYYCARDGCSGGSCYFWGWF------
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                                            AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGG------WYEGPLLEP 112
                                                                                            QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARVSIFGVVQHYYYYYY-----
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                                                                                                                                                                                                         71.0%; Score 488.5; DB 2
71.0%; Pred. No. 3.5e-37;
                                                                                                                                                                                     10; Mismatches
                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                  Length 127;
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A;Experimental source: the sequence was determined from the differentiated C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: B33548
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Search completed: December 30, 2003, Job time : 13.4614 secs
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C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
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Best Local Similarity
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                                                                                                                                          114 PDALDIWGQGTMVTVSS 130
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                                                                                                                                                                                                                 61 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGG--------WYEGPLLEPR 113
                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-126 <KIP>
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                                                                                               ---MDVWGLGTTVTVSS 126
                                                                                                                                                                                     AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARVSIFGVVQHYYYYY---
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                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                             70.6%;
                                                                                                                                                                                                                                                                                                                                                                     Score 486; DB 2;
Pred. No. 5.8e-37;
9; Mismatches 12
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                              11:03:13
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R.Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A;Title: Evidence for somatic selection of natural autoantibodies.

A;Reference number: PH0952; MUID:92202880; PMID:1552291

A;Accession: PH0954

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-132 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: framework 1

F;15-98/Domain: immunoglobulin homology <IMM>
F;11-35/Region: complementarity-determining 1

F:12-50/Domain: framework 2
                                                                                                        A; Molecule type: DNA
A; Residues: 1-134
C; Superf-
F;31-35/Region:
F;36-50/Region:
F;51-67/Region:
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                 F;15-98/Domain: immunoglobulin homology <IMM>F;31-35/Region: complementarity-determining 1F;36-50/Region: framework 2
                                                                       C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-30/Region: framework 1
                                                                                                                                                             R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0960
A;Status: nucleic acid sequence not shown
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F;68-98/Region: )
F;99-120/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
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Best Local Sim:
Matches 100;
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                                                                                                                                                                                                                                                                           g heavy chain V region (G6+ T-L30) - human (fragment)
;Species: Homo sapiens (man)
;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
;Accession: PH0960
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                                                                                                                             1-136 <MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                NYYYYGMDVWGQGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                D----ALDIWGQGTMVTVSS 130
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 complementarity-determining
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 496; DB 2;
Pred. No. 7.7e-38;
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C; Superfamil
RESULT 13
PH0957
Ig heavy chain V region
C;Species: Homo sapiens
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F;68-98/Region: framework 3
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Best Local S
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Local Similarity 67.8%;
hes 99; Conservative 10
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                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                 --FDYWGQGTLVTVSS
     (G6+ CLL-BRA) - (man)
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R;Martin, T.; Dufty, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A. Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: A33548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V-1 region (NEI) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: A33548; PH0956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
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                                                                                                                                                61 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGG------WYEGPLLE
                                                                                                                                                                                                                                  1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                    h 71.9%; Score 494.5;
Similarity 73.4%; Pred. No. 1e-
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                                                                                                                                                                                                         QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISMVRQAPGQGLEWMGGIIPIFGTANY 60
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                                              PRPDALDIWGQGTMVTVSS 130
                                                                                                    AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR----GPRLLADVLLWF-GELSE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complementarity-determining
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Pred. No. 7.9e-38;
0; Mismatches 11
129
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human (fragment)

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J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0958
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-122 <MARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0958
                                                                                                                                                                                                                                                                                                                   F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>F;31-35/Region: complementarity-determining 1
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F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Bvidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0962
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A; Residues: 1-120 <MAR>
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                                                                                                                                                                                                                               ;99-110/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                  Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                             68-98/Region:
                                                                                                                                                                                                                                                                              51-67/Region:
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Best Local Similarity
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Species: Homo saptens (man)
JDate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
                                                                                                                                                                                Local
61 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEBRPDALDIW 120
                                                                                                                                                            100;
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                                                                                        1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
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                                                                                                                                                                                                                                                         complementarity-determining 2
framework 3
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                                                                                                                                                        Conservative
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                                                                                                                                                                       72.4%;
76.9%;
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••
                                                                                                                                               Score 498; DB 2;
Pred. No. 4.6e-38;
8; Mismatches 14
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Pred. No. 4.6e-38;
8; Mismatches 11
                                                                                                                                                    14;
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                                                                                                                                                                                      Length 122;
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                                                                                                                                                                                                                                                                                    F;1-30/Region: framework
                                                                                                                                                                                                                                                                                                   C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-119 < MAR>
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J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (G6+ T-L33) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-193 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0961
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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S46394
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A;Molecule type: DNA
A;Residues: 1-132 <FIG>
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A;Title: In vitro assembly of repertoires of antibody chains A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46394
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C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46394
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPD---AL 117
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                                                                                               Similarity
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QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVWGKGTMVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOGTTVTVSS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQGTMVTVSS 130
                                                                                                                                                    complementarity-determining 3
                                                                        Conservative
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                                                                                      72.3%;
76.2%;
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75.9%;
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; Pred. No. 5.1e-38;
11; Mismatches 17
                                                                    Score 497.5; DB
Pred. No. 5e-38;
9; Mismatches
                                                                                                          DB 2;
                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 132;
                                                                    Indels
                                                                                                            Length 119;
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Ig mu chain precursor, membrane-bound (clone 201) - human
C;Species: Homo sapiens (man)
C;Species: J1-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C;Accession: S14683; 808047
R;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A;Title: Complete nucleotide sequence of the membrane form of the human IgM |
A;Reference number: S14683
A;Molecule type: mRNA
A;Residues: 1-627 <FRIDA
A;Coss-references: EMBL:X17115; NID:g33450; PMID:CAA34971.1; PID:g33451
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin; membrane protein
F;1-15/Oomain: signal sequence #status predicted <NAT>
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic A;Molecule type: DNA A;Residues: 1-133 <KIP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Experimental source: the sequence was determined from the differentiated C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
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              R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Bvidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
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A; Accession:
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                                                                                 g heavy chain V region (G6+ CLL-SIC) - human (fragment) Species: Homo sapiens (man) .Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #cext;Accession: PH0953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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PH0953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ALDIWGOGTMVTVSS 130
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                                                                                                                                                                                                                                                                                                                                                                        QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YYYYGMDVWGQGTTVTVSS 133
                                                                                                                                                                                                                               YYYYGMDWWGQGTTVTVSS
                                                                                                                                                                                                                                                               ----ALDIWGQGTMVTVSS 130
                                                                                                                                                                                                                                                                                                  AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAKTGILGPYSSGWY-----PNSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.1%; Score 509.5; DB 2 72.7%; Pred. No. 2.5e-38;
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                                                                                                 17-Apr-1993 #text_change
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A;Molecule type: DNA
A;Residues: 1-135 <MAR>
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R; Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A; Title: Evidence for somatic selection of natural autoantibodies.

A; Reference number: PH0952; MUID:92202880; PMID:1552291

A; Accession: PH0959

A; Status: nucleic acid sequence not shown

A; Molecule type: DNA

A; Residues: 1-116 <MAR>
C; Keywords: heterotetramer; immunoglobulin

C; Keywords: heterotetramer; immunoglobulin

F; 1-30/Region: framework 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region (G6+ T-L26) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0959
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F:51-67/Region: complementarity-determining F:68-98/Region: framework 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-30/Region: framework 1 F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                        F;51-67/Region: complementarity-determining F;68-98/Region: framework 3 F;99-104/Region: complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                                               F;15-98/Domain: immunoglobulin homology <IMM>F;31-35/Region: complementarity-determining 1F;36-50/Region: framework 2
121 GOGTMVTVSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                            AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGFLLEPRPDALDIW 120
                                                                                                                                            QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
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                                              AQKFQGRVTITADES'
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ilarity 75.2%;
Conservative
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                                                                                                                                                                                                                                              Score 501; DB 2;
Pred. No. 2.4e-38;
8; Mismatches 9
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Pred. No. 2e-38;
8; Mismatches
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Post-processing: Minimum Match 0%
Maximum Match 10
Listing first 45
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length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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1 QVQLVQSGAEAKKP
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   QVQLVQSGAEAKKPGSSVKV...
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                  GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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heavy chain V r
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A; Residues: 1-128 < MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 103;
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Result

515 509.5 509.5 502.5 501 498 498

score q Pred. No.

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481 456.5 452.5 452 452

450 447.5

498 497.5 496 496 494.5 490.5 488.5

Minimum Maximum

80 80

seq

Database

Searched:

Scoring table: Sequence: Title: Perfect score: OM protein -

on:

446 64.8 118 2 S36265 Ig heavy chain V r 442 64.3 122 2 C49590 Ig heavy chain V r 442 64.2 171 2 S23623 Ig heavy chain V r 437.5 63.6 160 2 PHO105 Ig heavy chain V r 436.5 63.3 129 2 S36260 Ig heavy chain V r 435.5 63.3 129 2 S36260 Ig heavy chain V r 435.6 63.2 135 2 S49530 Ig heavy chain V r 436.5 63.2 135 2 S49530 Ig heavy chain V r 428.5 62.3 129 2 S46393 Ig heavy chain V r 428.5 62.3 129 2 S46393 Ig heavy chain V r 428.5 62.3 129 2 S46393 Ig heavy chain V r 428.5 61.4 122 2 S36271 Ig heavy chain V r 420.5 61.1 121 2 S36271 Ig heavy chain V r 420.5 61.1 121 2 S30783 Ig heavy chain V r 420.5 61.1 121 2 S30783 Ig heavy chain V r 420.5 61.1 121 2 S30783 Ig heavy chain V r 420.5 61.1 121 2 S36271 Ig heavy chain V r 420.5 61.1 121 2 S30783 Ig heavy chain V r 420.5 61.1 121 2 S30783 Ig heavy chain V r	45	44	43	42	41	40	39	38	37	36	35	34	υ U	32	31	30
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	S31667	S20783	GIHUEU	S36271	PH0870	A30523	S46393	S34014	S46463	S49530	S36260	PH1671	S0101	S23623	C49590	S36265
							heavy	heavy	heavy	anti-Sm an	Ig heavy c		ti-PR2	heavy		

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RESULT 2
C33548
Ig heavy chain V-1 region (783) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: C33548
C;Accession: C33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A;Reference number: A33548; MUID:89345575; PMID:2503826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: PH0952
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0952
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C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-30/Region: framework 1
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framework 3
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Pred. No. 1.4e-39;
7; Mismatches 18
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APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
ITTLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
ITTLE OF INVENTION: THEREOF
ITTLE OF INVENTION: THEREOF
ILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION OUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 127
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-31
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CCURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR PRIOR DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PALENTIN Ver. 2.0
1500 ID NO 1190
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
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Query Match
Best Local Similarity
Matches 105; Conservat
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
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ORGANISM: Homo sapiens
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  Conservative
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78.0%;
73.8%; Score 524.5; DB 12; 78.9%; Pred. No. 1.4e-42; tive 6; Mismatches 15;
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                                                 Length 127;
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APPLICANT: Gazit, Gadi
APPLICANT: Waber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DI
TITLE OF INVENTION: THEREOF
FILE REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT; ORGANISM: homo sapiens US-10-041-860-243
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US-10-041-860-243
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 243
LENGTH: 127
                                                                                                                                                                      Sequence 325, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.8%;
Best Local Similarity 78.9%;
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TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
                                                                                                        APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
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                                                                                                                                                                                                                                                                                                                                                                                 120 DVWGQGTTVTVSS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
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Yang, Xiao-Dong
Chen, Francine
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                                                                                                                                                                                                                                                                                                                                          DVWGQGTTVTVSS
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Weber, Richard
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                                                                                                                                                                                                                                                                                                                                              127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 524.5; DB 12;
Pred. No. 1.4e-42;
6; Mismatches 15;
                                              DIRECTED TO PDGFD AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 127;
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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711
             Maximum Match 100%
Listing first 45 sv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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US-09-880-748-1190
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US-10-041-860-325
US-10-041-860-325
US-09-880-748-1971
US-09-880-748-1777
US-09-880-748-1610
US-09-880-748-1610
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927.994 Million cell updates/sec
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Sequence 31, Appl
Sequence 243, App
Sequence 325, App
Sequence 1674, Ap
Sequence 1921, Ap
Sequence 1777, Ap
Sequence 1777, Ap
Sequence 1610, Ap
Sequence 1610, Ap
Sequence 1562, Ap
Sequence 1576, Ap
Sequence 1576, Ap
Sequence 1572, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 45, Appl
Sequence 1190, Ap
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6 508.5 71.5 125 12 US-10-041-860-42 7 508.5 71.5 125 12 US-10-041-860-42 7 508.5 71.5 125 12 US-10-041-860-207 8 508.5 71.5 257 11 US-09-880-748-1354 9 508 71.4 126 12 US-10-041-860-354 10 US-09-880-748-1405 10 US-09-880-748-1595 12 US-10-041-860-200 12 US-10-041-860-200 12 US-10-041-860-200 12 US-10-041-860-200 12 US-10-041-860-372 12 US-10-269-880-748-1579 12 US-09-880-748-1579 12 US-09-880-748-1116 12 US-09-880-748-1116 12 US-09-880-748-1116 12 US-10-330-633-21 12 US-10-330-633-21 12 US-10-330-633-21 12 US-10-330-633-21 12 US-09-880-748-11872 12 US-10-348-11872 12 US-10-41-860-201 12 US	Sequence Sequence
508.5 71.5 125 12 US- 508.5 71.5 257 11 US- 508.5 71.5 257 11 US- 508.6 71.4 126 12 US- 508.7 71.4 254 11 US- 506.5 71.2 125 12 US- 506.5 71.2 257 11 US- 506.5 71.0 248 11 US- 504.5 71.0 248 11 US- 504.5 71.0 248 11 US- 504.5 70.8 123 12 US- 503.5 70.8 123 12 US- 503.5 70.8 123 12 US- 500.5 70.4 251 11 US- 500.5 70.4 251 11 US- 500.5 70.4 251 11 US- 500.5 70.3 126 12 US- 500 70.3 126 12 US- 499.5 70.3 253 11 US- 499.5 70.1 259 11 US- 499.5 70.1 259 11 US- 499.5 70.1 259 11 US-	
508.5 71.5 125 12 US- 508.5 71.5 257 11 US- 508.5 71.5 257 11 US- 508.6 71.4 126 12 US- 508.6 71.4 254 11 US- 506.5 71.2 125 12 US- 506.5 71.2 257 11 US- 506.5 71.0 248 11 US- 504.5 71.0 248 11 US- 504.5 71.0 248 11 US- 504.5 70.8 123 12 US- 503.5 70.8 123 12 US- 503.5 70.8 248 11 US- 500.5 70.4 251 11 US- 500.5 70.3 126 12 US- 500 70.3 126 12 US- 498.5 70.1 259 11 US- 198.5 70.1 259 11 US- 198.5 70.1 259 11 US-	
508.5 71.5 125 12 US- 508.5 71.5 257 11 US- 508.5 71.5 257 11 US- 508.6 71.4 126 12 US- 508.7 71.3 250 11 US- 506.5 71.2 125 12 US- 506.5 71.2 257 11 US- 506.5 71.0 247 11 US- 504.5 71.0 248 11 US- 504.5 70.8 123 12 US- 503.5 70.8 123 12 US- 503.5 70.8 248 11 US- 503.5 70.3 126 12 US- 500.5 70.3 126 12 US- 500.5 70.3 126 12 US- 500.5 70.3 126 12 US-	
508.5 71.5 125 12 US- 508.5 71.5 257 11 US- 508.5 71.5 257 11 US- 508.6 71.4 126 12 US- 508.7 71.3 250 11 US- 506.5 71.2 125 12 US- 506.5 71.2 257 11 US- 506.5 71.0 247 11 US- 504.5 71.0 248 11 US- 504.5 70.8 123 12 US- 503.5 70.8 123 12 US- 503.5 70.8 248 11 US- 500.5 70.4 251 11 US- 500.7 70.3 126 12 US- 500.7 70.3 126 12 US-	
508.5 71.5 125 12 US- 508.5 71.5 257 11 US- 508.5 71.5 257 11 US- 508.6 71.4 126 12 US- 508.7 71.3 250 11 US- 506.5 71.2 125 12 US- 506.5 71.2 225 11 US- 506.5 71.0 247 11 US- 504.5 71.0 247 11 US- 504.5 71.0 248 11 US- 503.5 70.8 123 12 US- 503.5 70.8 123 12 US- 503.5 70.8 248 11 US- 500.5 70.4 251 11 US-	
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508.5 71.5 125 12 US-10-041-860	

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 45
LENGTH: 125
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Sequence 45, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
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US-10-269-805-45
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                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING
FILE REFERENCE: A-722
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                            Local
                 118 AMDVWGQGTTVTVSS 132
111 GMDVWGQGTTVTVSS 125
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                                                                      61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDRGIAARSAY------YY 110
                                                                                             61 AQKPQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGG----GGAYEDVWSGEYPEYY 117
                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60
                                                                                                                                                                    1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                    74.6%; Score 530.5; DB 1
77.8%; Pred. No. 3.7e-43;
tive 4; Mismatches 13
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                                                                                                                                                                                                                        13; Indels 13;
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RESULT 2

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ARESULT 15
ABP45394
ID ABP45
AC ABP45
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Best Local Similarity 73.7%; Pred. No. 2.1e-39;
Matches 98; Conservative 13; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunosdulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-2773799P.
25-MAY-2001; 2001US-293499P.
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                                                                                                                                                           HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                               Barash SC,
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                                                                               Choi GH,
                                                                           Vaughan T,
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                                                                               Hilbert D;
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNF) super family and induces B cell cumour necrosis factor (TNF) super family and induces B cell correct of the correct of the invention and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAlDS activity and can be used in vaccines to cinhibit the expression and activity of BLyS. The antibodies bind to BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be conditionable and may be used in this way to diagnose disease cand activity such as cancer, immune, and autoimmune disorders and conditionable immunodeficiency (cytD) and conditionable immunodeficiency (cytD) and conditionable immunodeficiency (cytD) and conditionable inventionable inventionable inventionable inventionable inventionable in the method conditionable inventionable inventionable in the method conditionable invention and tragments of the antibodies described in the method conditionable inventionable inventionable in the method conditionable inventionable inventionable in the method conditionable in the method conditionabl
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                                                                                          invention.
254 AA;
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Ş 묽 δ 문 밁 र् Matches 100; Best Local Query Match 115 119 61 61 -Similarity MDVWGQGTTVTVSS 132 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYE--DVWSGEYPEYYA 118 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY FDIWGKGTTVTVSS AQKLQGRVIMITDISMSTAYMELRSLRSDDTAVYYCAR----AFEDYDILTGYY-HHDA Conservative 71.4%; Score 508; DB 23; 74.6%; Pred. No. 2.3e-39; 12; Mismatches 14; Length 254; Indels 8; Gaps 114 60 60

Sequence

Search completed: December 30, Job time : 43.5464 secs 2003, 10:54:30

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RESULT 13
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This invention describes novel antibodies that immunospecifically bind B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in
                                                                                                                                                                                                                                                                     16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; entiAIDS; vaccine; cancer; immune; autoimmune disorder; immunoseficiency; systemic lupus erythematosus; rheumatoid arrhritis; CVID; AIDS;
                                                                                                                                         Antibodies against B Lymphocyte Stimula the diagnosis and treatment of cancers
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114 YMGQGTTVTVSS 125
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CAMBRIDGE ANTIBODY TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVW8GEYPEYYAMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                                                           Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                     2135-2136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                immunodeficiency; acquired immunodeficiency syndrome
                                                                                                                                                                                                          SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCFV SEQ ID 1452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fragments
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76.5%;
                                                                                                                                                                                                          Choi
                                                                                                                 3148pp;
                                                                                                                                                                                                                                  TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 510.5;
Pred. No. 1.3e
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the antibodies described in the method
                                                                                                                                        Stimulating polypeptides, useful for cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                 English.
                                                                                                                                                                                                        Vaughan
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No. 1.3e-39;
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H
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             BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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RESULT 14
ABP45343
ID ABP45343
AC ABP45
AC ABP46
AC ACAMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ś
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-2000;
17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                     (CAMB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200202641-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP45343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP45343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                             ibodies against B Lymphocyte Stimulating polypeptides, undiagnosis and treatment of cancers and immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens.
                                                                                                                                                                                                                                SM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99;
                                                                                                                                                                                                                                                                               HUMAN GENOME SCI INC
CAMBRIDGE ANTIBODY TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FDIWGRGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEY--PEYYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDVWGQGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDRGASNY-DILTGYYAPAQGVA
                                                                                                                                                                                                                                Barash
                                                                                                                                                                                                                                                                                                                                                      ; 2000US-212210P.
; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunodeficiency; acquired immunodeficiency syndrome
                                                                                                                                                                                                                              sc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
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73.9%;
                                                                                                                                                                                                                              Choi GH,
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                                                                                                                                                                                                                                                                            TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 510.5; 1
Pred. No. 1.4e
12; Mismatches
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                                                                                                                                                                                                                           Vaughan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB
                                                                                                                                                                                                                           Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                  useful
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Claim 1;

Page 2018-2019; 3148pp;

English.

novel

antibodies that immunospecifically bind

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RESULT 11
ABP45565
      Query Match
Best Local Similarity
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                                                                                                                                                    B Lymphocyte Stimulator (BHyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in associated with aberrant expression of BLyS. They are also be and may be used to detect and function the complex of BLyS and secondary to diagnose disease administered to treat diseases associated with aberrant ELyS expression diseases. e.g. systemic limits apythematical expression diseases associated with aberrant BLyS expression diseases. e.g. systemic limits apythematical expression diseases as a systemic limits apythematical expression of BLyS. They may also be and activity such as cancer, immune, and autoimmune disorders and diseases. e.g. systemic limits apythematical expression.
                                                                                       diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                       Sequence
                                                                                                                                                                                                                                                                                                                                    This invention describes novel antibodies that immunospecifically bind to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-114799/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-UUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240815P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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17-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP45565 standard;
                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis and tre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN GENOME
CAMBRIDGE ANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FDIWGOGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MDVWGQGTTVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQXLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barash SC,
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                                                                                                                                                                                                                                                                                                                                                                          2283-2284; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         ainst B Lymphocyte Stimulating polypeptides, useful and treatment of cancers and immune disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEC SEQ
     72.1%;
75.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choi GH, Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132
     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257
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     512.5;
No. 9e
DB
-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hilbert
               23;
               Length
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RESULT 12
ABP4551
ID ABP45
AC ABP45
XX ABP45
XX ABP45
XX IS-AU
DE Human
XX Endou
DE Homo
DE
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                                                                               B Lymphocyte Stimulator (BLyS) polypeptides. BlyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in associated with aberrant expression of BLyS. The antipode disease administered to treat disease associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and alloys expression diseases. A carternic limine approximate the procession of BLyS and activity such as cancer, immune, and autoimmune disorders and diseases.
                            diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and
                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel antibodies that immunospecifically B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 2267-2268; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUN-2000; 2000US-212210P
17-0CT-2000; 2000US-240816P,
16-MAR-2001; 2001US-276248P
21-MAR-2001; 2001US-277379P,
25-MAY-2001; 2001US-293499P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLys; B lymphocyte stimulator; tumour necrosis factor; B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human BLyS binding scrv SEQ ID 1562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101; Conservative
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CAMBRIDGE ANTIBODY TECHNOLOGY.
               immunodeficiency syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ጅ
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ABP43990-ABP47228 represent
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19-AUG-2002

(first

entry)

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This invention describes novel antibodies that immunospecifically bind to C BLymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNF) super family and induces B cell crown for the conversation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, contribution and antiALDS activity and can be used in vaccines to contribute the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in a conversate sypression of BLyS. They may also be conditionable and may be used in this way to diagnose disease campoistated with aberrant expression of BLyS. They may also be conditivity such as cancer, immune, and autoimmune disorders and conversated with aberrant BLyS expression conditionable immunodeficiency (e.g. systemic lupus erythematosus, rheumatoid arthritis, conditionable immunodeficiency (c.g. common variable immunodeficiency (c.g. systemic syndrome (AIDS)). ABP43990-ABP47228 represent the invention
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 104
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16-MAR-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 2324-2325; 3148pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-2000;
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                                                                                                                                                                                                                             QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
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DMDVWGRGTLVTVSS 131
                                                 AMDVWGQGTTVTVSS 132
                                                                                           AQELQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDTLG---YDILTG-YPPPYYYY
                                                                                                                                  AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPE---YY 117
                                                                                                                                                                                                             QVQLQQSGAEVKKPGASVKVSCKASGYTFTS:
                                                                                                                                                                                                                                                                                                                                                                                                                          257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
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IDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunodeficiency; acquired immunodeficiency syndrome
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                                                                                                                                                                                                                                                                                                                                       72.4%;
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                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                               Score 514.5; DB 2
Pred. No. 5.9e-40;
                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                  YGISWVRQAPGQGLEWMGWISAYNGNTKY
                                                                                                                                                                                                                                                                                                           18;
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                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                          Length
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S 밁 Ś

61 Ь

QVQLVESGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYY--A 118

QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY

Matches Query Match

103;

Conservative

8

Score 513; DB 23; Pred. No. 7.8e-40; 8; Mismatches 13

Length Indels

249; 10;

Gaps

60 60

Local

Similarity

72.2%; 76.9%;

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This invention describes novel antibodies that immunospecifically bind to CB Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNF) super family and induces B cell CC proliferation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC antirheumatic and antiALDS activity and can be used in vaccines to cinhibit the expression and activity of BLyS. The antibodies bind to BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC alsociated with aberrant expression of BLyS. They may also be associated with aberrant expression of BLyS. They may also be cadministered to treat diseases associated with aberrant BLyS expression CC and activity such as cancer, immune, and autoimmune disorders and CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP4728 represent CC the antibodies and fragments of the antibodies described in the method of the antibodies and fragments of the antibodies described in the method of the antibodies and fragments of the antibodies described in the method of the antibodies.
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
Sequence
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                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-114799/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN GENOME SCI INC
CAMBRIDGE ANTIBODY TO
                                                                                                                                                                                                                                                                                                                                                 Page 2103-2104; 3148pp; English.
 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-240816P.
2001US-276248P.
2001US-277379P.
2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-212210P
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A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stimulator;
ctor; B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCFV SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hilbert
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RESULT 8
ABP45767
ID ABP4
XX ABP4
AC ABP4
XX DP 19-A
XX DE Huma
XX DE Huma
XX Eumc
KW tumc
KW tumc
KW immu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel antibodies that immunospecifically bind to CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNP) super family and induces B cell crown in the control of the invention have control of the control of the control of the invention have control of the control 
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Best Local S
Matches 100
BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; mmunomodulatory; antirheumatic;
                                                                                                                                           19-AUG-2002
                                                                                                                                                                                  ABP45767
                                                                                                                                                                                                                      ABP45767 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
(CAMB-) CAMBRIDGE ANTIBODY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2001; 2001WO-US19110
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                                                                                                BLyS
                                                                                                                                                                                                                                                                                                                           119
                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                   VWGOGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                          AQELQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR-GDFGDY-DILTGYYPVYYGMD
                                                                                                                                                                                                                                                                                                                                                                                                               AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPBYYAMD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OVOLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                            binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.1%;
ilarity 75.8%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barash SC,
                                                                                                                                       (first
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                                                                                              BCFV
                                                                                                                                                                                                                  Protein;
                                                                                                                                     entry)
                                                                                            SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                                                                                                                                                  248
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Pred. No. 1.8e-40;
2; Mismatches 18;
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                                                                                            1778.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 253;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D
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                                                                                                                                                                                                                                                                                                                                                                                          118
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RESULT 9
ABP45599
ID ABP4
XX
AC ABP4
XX

ABP45599 standard;

Protein;

257

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ABP45599

5 밁 Ś 밁 Ś

В

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This invention describes novel antibodies that immunospecifically bind to CC Brymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNP) super family and induces B cell cct tumour necrosis factor (TNP) super family and induces B cell cc proliferation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, can the antial can and antial DS activity and can be used in vaccines to compare the compare to th
                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                         Sequence
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibodies against B Lymphocyte Stimulating the diagnosis and treatment of cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CAMB-)
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                                                                                                                                                                                                                                                                              Local
114
                                      121
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                                                                                                                                                                                                                                                                         Similarity
                        VWGQGTTVTVSS 132
                                                                                               AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD
                                                                                                                                                   OVOLLOSATEVKKPGASMKVSCMASGYPPTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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                                                                    AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR----SYYDILTGYYP--FGMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                           248
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                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
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                                                                                                                                                                                                                                                                                                                                       ΑĄ;
                                                                                                                                                                                                                                                                     72.4%;
75.8%;
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                                                                                                                                                                                                                                                   9,
                                                                                                                                                                                                                                                                       Score 514.5;
Pred. No. 5.
                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaughan
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                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                       23;
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                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                       248;
                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                       Gaps
                                                                    113
                                                                                                             120
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RESULT 6
ABP44
ABP44
AR
AC ABP4
XX
AC ABP4
XX
AC ABP4
XX
BU
DT 19-A
DT 19-A
DT Huma
XX
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                                                                                                                                                                                                                                                                              BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
                                                                    15-JUN-2001; 2001WO-US19110
                                                                                                                      10-JAN-2002
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                             common variable
                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                             BLyS binding scrv SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARVTSLYSSSSGGYY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                          immunodeficiency; acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
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74.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128
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                                                                                                                                                                                                                                                                                                                                                                                                                             973.
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                                                                                                                                                                                                                                                             immunodeficiency syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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RESULT 7
ABP45P6
IID ABP4
XX ABP4
AC ABP4
XX IIP-A
XX Huma
XX Huma
XX BLys
XX Lumo
XX immu
XX immu
XX anti
XW aonti
XW systt
XW systt
XW systt
XW systt
XW Syst Homo
XX Homo
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency yndrome (BryS). ABP43990-ABP47228 represent the artificial of the a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1562-1563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                          ABP45766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP45766 standard; Protein;
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                                                                                                                                                                                                                                                                                                 Human BLyS binding
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                                                                                                               immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                        systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention.
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CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                         variable
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74.5%;
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Pred. No. 1.3e-40;
8; Mismatches 18
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2

Homo sapiens

WO200202641-A1

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RESULT 4
ABP4 5663
ID ABP4
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XX ABP4
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Best Local S
Matches 103
                                                                                                                                                                                                                                                                                  16-JUN-2000; 2000US-212210P.
17-0CT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency;
           Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200202641-A1
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                                                                                                                                                                                                           HUMAN GENOME
CAMBRIDGE ANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein; 252
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                                                                                                                                                           Barash
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                                                                                                                                                                                                              ANTIBODY
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78.0%;
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                                                                                                                                                        Choi GH,
                                                                                                                                                                                                           TECHNOLOGY
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Pred. No. 5.5e-41
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                                                                                                                                                   Vaughan T,
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ABP45910
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AC ABP
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                                                                                                                   16-JUN-2000;
17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomoulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                (HUMA-)
                                                                                                                                                                                                                                                                                                       15-JUN-2001;
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; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
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78.0%;
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Pred. No. 7.5e-41;
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RESULT 2
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Best Local S
Matches 132
This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The
                                                                                                                                                                                                     New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; hear
hemophilia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000
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ilarity 100.0%;
Conservative (
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; VH gene.
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Pred. No. 1.6e-58;
; Mismatches 0;
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RESULT 3
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17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                    BLys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                   Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                common variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human BLyS
                                                                                                                                                                                                         (HUMA-)
                                                                                                                                                                                                                                                                                                                                    10-JAN-2002.
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                                                                                                                                                                                           (CAMB-)
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                                                                                             polypeptides, useful immune disorders -
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tumour necrosis fa proliferation and cytostatic, immuno B Lymphocyte This invention

on describes novel antibodies that immunospecifically Stimulator (BLyS) polypeptides. BLyS is a member of tsis factor (TNF) super family and induces B cell n and differentiation. The antibodies of the invention

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Result
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ALIGNMENTS

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RESULT 1
AAY50953
ID AAY50953
AC AAY5
XX AAY5
XX AAY5
XX Huma
XX Huma
XX Homc

New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
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hemophilia A; VH protein.
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CS Mus n
OC Eukar
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090XE9
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Matches 73
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Q924Q1;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
V23-D-J-C mu protein (Fragment).
V23-D-J-C MU.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Immunoglobulin heavy chain V-D-J region (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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117 AA; 13000 MW; CDDE2AF84D499734 CRC64;
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Best Local S
Matches 75
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Türrect Estimation of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

THydroxy-3-Mitrophenyl)Acetyl (MP).";

Lubmitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB069913; BAB63929.1; -.

RINterPro; IPR0070710; Ig-like.

RINterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

RINterPro; IPR003596; Ig_v.

RINterPro; IPR003596; Ig_v.

REFAME, PF00047; ig; 1.

REFAME, PF00047; ig; 1.

REFAME, PF00047; ig; 1.

REFAME, PF000406; IGv; 1.

REFAME, P
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                121 VWGQGTTVTVSS 132
                                                                                                 61
                                                                                                                                      61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                                                                                                                                                                                                                                                                                                                                           75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                     NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRG-----
                                                                                                                                                                                                                                    QVQLQQPGTELVKPGASVKLSCKASGYTFTSYMMHWVKQRPGQGLEWIGNINPSNGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                       52.8%; Score 375.5; DB 11; Length 142; 56.8%; Pred. No. 1.3e-30; tive 17; Mismatches 25; Indels 15;
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                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Search completed: December 30, 2003, 11:01:02 Job time : 32.169 secs

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Q9Y298
ID Q9Y29
AC Q9Y29
DT 01-NO
DT 01-NO
DT 01-MA
DE 1GG V
GN 1G
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SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 481 AA; 52105 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91WT1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 23, Last annotation updat
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical 52.1 kDa protein.
Mus musculus (Mouse).
Mus musculus (Mouse).
SEQUENCE FROM N.A.

MEDLINE=98322155; PubMed=9657749;

MEDLINE=98322155; PubMed=9657749;

Jacquemin M.G., Vander Elst L.P.L.;

"Mechanism and kinetics of factor VIII inactivation: study with an igg4 monclonal antibody derived from a hemophilia A patient with
                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
19G VH protein precursor (Fragment).
IGG VH.
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                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9Y298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIMT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VWGQGTTVTVSS
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                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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PESULT 13
Q925SZ
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D7 Q925S
D7 Q1-DE
RN RI H
RN SEQUE
RX WCBI
RX PUBME
RX PUBME
RX PUBME
RX WC11d
RX PC1d
RX G1/D
RX SEQUE
RX G1/D

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the same strain.";

The same strain.";

Int. J. Radiat. Biol. Relat. Stu
EMBL; AF240167; AAK43732.1;

InterPro; IPR007110; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG_LIKE; 1.
SEQUENCE 170 AA; 17978 MW; 5
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InterPro; IPRO03006; Ig_MIC.
InterPro; IPRO03006; Ig_v.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGV; 1.
SIGNAL.
SIGNAL.
1 19 P0
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Q925S2;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2003
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SEQUENCE
                                                                                                                                                                                                                    Cui D., Zeng G., Yan X., Li X., Su C.; "Cloning of mouse genes related to repairing of the irradiated mice by treatment with the
                                                                                                                                                                                                                                                                                                                                                 "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice."; World J. Gastroenterol. 6:709-717(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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HSSP; P01772; 2FB4
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Blood 92:496-506(1998)
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     Su C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                  STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Cui D., Zeng
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Query Match Best Local S Matches 74

Similarity

53.1%; Score 377.5; DB 56.1%; Pred. No. 1e-30; tive 14; Mismatches

DB 11;

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RESULT 9
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OBWY24;
OL-MAR-2002 (TrEMBLrel. 2
OL-MAR-2002 (TrEMBLrel. 2
OL-MAR-2003 (TrEMBLrel. 2
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O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
O1-MAR-2003 (Tremblrel. 23, Last annotation update)
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SEQUENCE FROM N.A.

Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Inderpro; Inframe Inframe
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MEDLINE=98277139; PubMed=9614934;
Yan der Merwe P.L.,
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Clin. Immunol. Immunopathol. EMBL; AF035025; AAD56261.1; HSSP; P01810; 2FBJ.
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Mammalia; Eutheria;
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Primates;
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Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2003
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SEQUENCE
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                   the same strain.";
Int. J. Radiat. Biol. Relat. Stud. Phys.
EMBL; AP240166; AAK43731.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                      Pfam; PF00047; ig; 1. —
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 147 AA; 16274 MW;
                                                                                                                                                                                                                                                                                                                                                                                        Cui D., Zeng G., Yan X., Li X., Su C.; "Cloning of mouse genes related to repairing of the irradiated mice by treatment with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mechanism of exogenous nucleic acids and the repair of intestinal epithelium after World J. Gastroenterol. 6:709-717(2000). [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11819679;
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QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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QVKLHQSGPEVVKPGASVKLSCKASGYIFTSYDIDWVRQTPEQGLEWIGWIFPGEGSTEY
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IPR003006;
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116 AA;
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ilarity 62.5%;
Conservative 1
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12605 MW;
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Ig_MHC.
Ig_v.
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                                                                                       55.1%; Score 391.5; DB 11; 59.1%; Pred. No. 3.2e-32; tive 15; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang
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Last annotation updat
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Pred. No. 1.7e-32;
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Sciurognathi; Muridae; Murinae; Mus.
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irradiation in mice.";
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                                                                                          Indels
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Best Local
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Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBar Submitted (JUL-2001) to the EMBL/GenBar Submitted (JUL-2001);
InterPro; IPR003005; HTHARAC.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003306; Ig MHC.
InterPro; IPR003596; Ig v.
Pfam; PF00047; Ig; 5.
SMART; SM00406; IGT; 1.
PROSITE; PS00041; HTH ARAC FAMILY_1; 1
PROSITE; PS00041; HTH ARAC FAMILY_1; 1
PROSITE; PS00041; HTH ARAC FAMILY_1; 1
PROSITE; PS00040; IG MHC; 3.
Hypothetical profein—
                                                                       SEQUENCE FROM N.A.

MEDLINE=98277139; PubMed=9614934;

Wu X., Liu B., Van der Merwe P.L.,

Young D.C.;
                                                                                                                                                                                                    Homo Bapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                O9UL92;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
(Fragment).
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Q96GA6;
01-DEC-2001
01-DEC-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UL92
                                       Myosin-reactive autoantibodies in rheumatic
                                                                                                                                                                                     NCBI_TaxID=9606;
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Homo sapiens (Human)
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614 AA; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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87:184-192 (1998)
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Last annotation
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Best Local
                                                                                                                                                                                                                                                                                                             InterPro; iPR007110; Ig-like.
InterPro; iPR003006; Ig_MHC.
InterPro; iPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Amplification, cloning and sequence analysis of the heavy variable region gene of monoclonal anti-idiotypic antibody Schistosoma japonicum.", Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF282622; AAG01452.1; -. HSSP; P01772; 2FB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9GYZ2
Q9GYZ2;
                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6182;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
01-MAR-2003 anti-idiotypic antibody NP30 heav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Fragment)
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                                                                                                     QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
NOKEKDRVTMTTDKSFSTAYMDLRSLRSADSAVYYCAR--
                                                                            QVQLVESGAEVRKPGASVRVSCKASGYTFTGYYMNWVRQAPGHGLEWIGYINPSRGYTNY
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119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 :
124 AA;
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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13567 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
13580 MW;
                                                                                                                                                                  58.7%; Score 417.5; DB 5; 61.4%; Pred. No. 5.5e-35; tive 17; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124
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Pred. No. 1.6e-35;
1; Mismatches 26
                                                                                                                                                                                                                                                       BA893873FD5FA6AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1BAAACBD96ACD2A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
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heavy chain
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YYDDHYCLD
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                                                                                                                                                               Gaps
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RESULT OPERVOOR OPERV
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Q9U1-99U1
AC Q9U1-M
DT 01-M
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DT 01-M
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Best Local S
Matches 90
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
Pfam; PP00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS050835; IG_LIKE; 4.
PROSITE; PS050835; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 500 AA; 54154 MW; OA
                                                                                                                 Myosin-reactive immunoglobulin (Fragment).
(Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; C.
Mammalia, Eutheria; Primates, C.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                          Q9UL94;
Q9UL94;
01-MAY-2000
01-MAY-2000
01-MAR-2003
    SEQUENCE FROM N.A. MEDLINE=98277139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
Homo Bapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE=Prostate;
Strausberg R.;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AOKFOGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
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                                                                                                                                                                                                                                                                                               (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
ive immunoglobulin heavy chain variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.9%; Score 447; DB 4; 68.2%; Pred. No. 3.1e-37; tive 10; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                        Craniata; Vertebrata; I
Catarrhini; Hominidae;
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             SQKFQGRLTMTRDTSTSTVYMDLSSLRSDDTAVYFCAREMEITFGGA--
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"Homo sapiens putative microfibrillar protein with Ig-like mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).", Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY039025; AAK82649.1; - InterPro; IPR0037110; Ig-like. InterPro; IPR00306; Ig-MHC. InterPro; IPR00306; Ig-MHC. InterPro; IPR003556; Ig-V. SMART; SM00406; IGV; 1. SMART; SM00406; IGV; 1. SMART; SM00406; IGV; 1. SMART; SM00406; IGV; 1. PR05ITE; PS50835; IG_LIKE; 1. SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative matrix cell adhesion molecule-3.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clin. Immunol. Immu
EMBL; AF035020; AAD
HSSP; P01810; 2FBJ.
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SMART; SM00406; IGv; 1. EPROSITE; PS50835; IG_LIKE; 1.
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InterPro; IPR003596; Ig_v.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Q9UL95;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunol. Immunopathol. 87:184-192(1998).
1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                                                                      Similarity 68.2
90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD56255.1; -.
                                                                                                                                                                                                                                                   125
13516 MW; 0D3CD5C232488EAC CRC64;
                                                                                                              63.6%; Score 452.5; DB 4; 68.2%; Pred. No. 1.6e-38; ative 11; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalis N.N., Berney S.M.,
                                                                                                                                                                                 Length
                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region
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                                                                                                           Gaps
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Job time : 7.07717 secs

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Best Local S
Matches 66
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NON TER
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1. ~~
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J00522; AAD15
PIR; E90809; G1MS21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-77100368; PubMed=401950;
Adetugbo K., Milstein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
Nature 265:299-304(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV16_MOUSE STANDARD; PRT; 136 AA. P01783; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 15 heavy chain V region MOPC 21 precursor (Fragment). Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110;
InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDB; 1IGC; 03-JUN-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibodies: somatic mutation Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 17-136.
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Bothwell A.L.M., Paskind M., Reth M.,
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  126
                                             122
                                                                                           78
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                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                              VQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDYA 61
                                                                               DTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCAR--
                                                                                                       QKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMDV 121
                                                                                                                                                               VQLVESGGGLVQÞGGSRKLSCAASGFTFSSFGMHWVRQAÞEKGLEWVAYÍSSGSSTLHÝA
WGQGTSVTVSS 136
                                      WGQGTTVTVSS 132
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119
136
112
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115
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; Ig_MHC.
; Ig_v.
                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                           Score 338; DB 1; Le
Pred. No. 1.5e-28;
Migmatches 30;
                                                                                                                                                                                                                                                                                                                                                                                               HYAD -> DYAH (IN REF. 2)
DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V REGION MOPC 21.
D SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JH4 SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contribution to the NPb family of evident in a gamma 2a variable re
                                                                                                                                                                                                                                                                                                                                                      2276A98DBDBF7016 CRC64;
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                                                                                                                                                                                                                                                                                                        Length 136;
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                                                                          W-GNYP-YYAMDY 125
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                                                                                                                                                                                                                                                           12;
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RESULT 15
HV11 MOUSES
HV11 MOUSES
HV11 MOUSES
HV11 MOUSES
HV12 MOUSES
HV17 MOUSES
HV17 13-JU
DT 21-JU
DT 21-JU
DT 21-JU
DT 15-JU
DT 15-JU
DT 15-JU
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DT 15-JU
DT 15-JU
DT 16-JU

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Matches 71
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21-UUL-1986 (Rel. 01, Last sequence upda
15-UUL-1999 (Rel. 38, Last annotation up
Ig heavy chain V region S43 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Rodentia; Sciurognat
                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DISULFID
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                 SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P01810; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A02038; G2MS43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J00539; AAA38172.1; -.
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Cell 24:625-637(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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P01755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
    126
                                           121
                                                                                      80
                                                                                                                               13
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                                                                                                                                                                                        1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEMWGWISIYSGNTDY
                                    VWGQGTTVTVSS
                                                                                                                                                                                                                                                                                 Similarity
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                                                                        NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCAR-----YR---LGRY-----FD
                                                                                                                 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD
                                                                                                                                                          QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY
  YWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                              137
137 AA;
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V region;
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49
54
68
85
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122
137
137
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                                                                                                                                                                                                                                                                                            47.48;
                                                                                                                                                                                                                                                                          53.8%;
137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                     Score 337; DB
Pred. No. 1.9e
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                D SEGMENT.
JH2 SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION S43.
FRAMEWORK.1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK.2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                       ADD5881BF44B8EC9 CRC64;
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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                                                                                                                                                                                                                                                                          DB 1;
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RESULT 12
HV00, MOUSE
ID HV00
AC P0174
DT 21-JU
DT 21-JU
DT 21-JU
DT 21-JU
DT 21-JU
DT 31-JU
DT 31-JU
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Best Local S
Matches 71
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Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                          PIR; A02022; GIMSAA.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                            NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capra J.D., Nisonoff A.;

"Structural studies on induced antibodies with defined idiotypic specificities. VII. The complete amino acid sequence of the heavy chain variable region of anti-p-azophenylarsenate antibodies from mice bearing a cross-reactive idiotype.";

J. Immunol. 123:279-2841979).
                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V region (Anti-arsonate antibody).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=79195438; PubMed=109536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV00 MOI
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NON TER
SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISCELLANEOUS: ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGION SEQUENCE
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                                 61
                                                                                                                                                      71;
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AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                   OVOLLOSATEVKKPGASMKVSCMASGYPFTSYDISWVROAPGOGLEWMGWISIYSGNTDY
                                                             EVOLOOSGAELVKAGSSVKMSCKATGYTFSSYELYMVRQAPGQSLEDLGYISSSSAYPNY
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114 AA;
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ilarity 55.5%;
Conservative 1
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                                                                                                                                                      16;
                                                                                                                                                 Score 341; DB
Pred. No. 6e-2
16; Mismatches
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D SEGMENT.
JH2 SEGMENT.
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 354;
Pred. No. 3
                                                                                                                                                                                                                                 99DD8F0B6A69F4BE CRC64;
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RESULT 14
HV16_MOUSE
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HV15_MOUSE
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Best Local (
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J00494; AAA38130.1; -. PIR; A02042; HVMSB1. HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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P01759;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V region BCL1 precursor.
Mus musculus (Mouse).
Mus musculus (Mouse).
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SMART; SM00406; IGv;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by a cloned B-cell lymphoma
by two adjacent CH genes.",
Proc. Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Knapp M.R., Liu C.-P., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lattner F.R.;
Simultaneous expression of immunoglobulin מיים וויים וויי
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                              125
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                                                                                                                                                                                                                                                                                                                                   61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVMSGEYPEYYAMD 120
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136
136 AA;
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135
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"A V region determinant (idiotope) exp
lymphocytes is encoded by a large set c
EMBO J. 3:517-523(1984).
PIR: A02040; MHMS38.
HSSP: P01789; IMCD.
InterPro: IPR0037110; Ig-like.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003906; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE: PS50835; IG LIKE; 1.
Immunoglobulin V region.
V CECAPATE

DOMATN
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                      HV51 MOUSE STANDARD; PRT; 118 AA.

P06330;

01-JAN-1988 (Rel. 06, Created)

01-JAN-1988 (Rel. 06, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

1g heavy chain V region AC38 205.12.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; irac.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGV; 1.
PROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
Immunoglobulin V region; PyrroLiDone CarboxyLIC
   Immunoglobulin
DOMAIN
                                                                                                                                                                      SEQUENCE.
MEDLINE=84182519; PubMed=6201362;
                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD RES
DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:amtigen binding activity; !
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gall W.E., Edelman G.M.;

"The covalent structure of a human gamma G-immunoglobuli Thrachain disulfide bonds.",

Biochemistry 9:3188-3196(1970).

-1- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.

-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=71064027; PubMed=4923144;
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                                                                                                                                                                                                                                                                                                                                                                                           ---NGGLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                   VWGQGTTVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPBYYAMD
                                                                                                                                                                                                                                                                                                                                                                                                                                   AQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA--GGYGIYS-----PEEY---
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SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99D60ADAEBD52818 CRC64;
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                                                                                                                              M., Beyreuther K., Rajewsky K.;
) expressed at high frequency i
set of antibody structural gen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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RESULT 11
HV07_MOUSE
ID HV07_MOUSE
ID HV07_MOUSE
AC P01751
DT 21-JUL
DT 15-SEP
DE Mammal
OC Mammal
OC Mammal
OC WOBLIT
RN SEQUEN
RN WEDLIN
RN MEDLIN
CC This S
CC This
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSTITE; PS50835; IG LIKE; 1.
Immunoglobulin v rejTon; Signal SIGNAL
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CCHAIN 20 139
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Best Local S
Matches 71
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P01751: P01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last amotation update)
-- heavy chain V region B1-8/186-2 precursor.
                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                    PDB; 1A6U; 27-MAY-98.
PDB; 1A6W; 15-JUL-98.
                                                                                                                                                                                                                                                                                                                            EMBL; J00529; AAA38170.1; -. PIR; A90809; MHMS18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Heavy chain variable region contribution to antibodies: somatic mutation evident in a gar Cell 24.625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region B1-8/186-2 precursor.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bothwell A.L.M.,
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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DOMAIN
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NPB
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                                                                                                                                  Signal;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                     IG HEAVY CHA
FRAMEWORK-1
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BY SIMILARITY.
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                                                                                   CHAIN V REGION B1-8/186-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of region.";
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음 성

VWGQGTTVTVSS

132 120

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RESULT 8
HV12_MOUSE
ID HV12_MOUSE
AC P01756;
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HV02_MC
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Best Local :
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P01746;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatice Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region 93G7 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                        CHAIN
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sims J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J00493; AAA38128.1; -. PIR; A94264; HVMSG7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capra J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=82152818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Somatic mutation in genes for the immunoglobulin heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ence 216:309-311(1982).
SIMILARITY: Contains 1 immunoglobulin-like
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                                                                                                                                                           YWGQGTPLTVSS 140
                                                                                          VWGOGTTVTVSS 132
                                                                                                                 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCAR---
                                                                                                                                     AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD
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           STANDARD;
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T.H., Estess P.,
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                                                                                                                                                                                                                   50.7%;
                                                                                                                                                                                                                                                      15514 MW;
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Pred. No. 6.8e
22; Mismatches
                                                                                                                                                                                                                                                                            IG HEAVY CHAIN V
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           PRT;
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                                                                                                                 SHYYGGSYDFD
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RESULT 9
HV1A HA H
ID HV1A C P01742
AC P01742
DT 21-UTL
DT 15-SEP
DE IG hea
OS HOMO 8
OC EUKATY
OC Mammal
OX NCBI T
RN [1]
RA CUNDIN
RA GUNG
RT Gacid 8
RT Gacid 80
RT 
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InterPro: IPAv.
InterPro: IPAv.
Pfam; PF00047; ig; 1.
R SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
IG_LIKE.
I
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Best Local
MEDLINE-71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII.
acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
Biochemistry 9:3161-3170(1970).
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PIR; A02039; MMNS4E.
HSSP; P01789; 1MCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_V.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region MOPC 104E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HVIA HUMAN STANDARD; PRT; 17 AA
P01742;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat.
Ig heavy chain V-I region EU.
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Kehry M.R., Fuhrman J.S., Schilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN HAS ALSO BEEN DETERMINED.
-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hood L.E.;
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VWGQGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106
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; Pred. No. 7.1e
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DB 1,
7.1e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .) (COMPLEX)
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HV13 MOUSE STANDARD; PRT; 117 AA.

P01757;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 02, Last annotation update)
3 Ig heavy chain V region J558.
3 Mus musculus (Mouse).
5 Eukaryota; Metazoa; Chordata; Craniata; Vertebre Mammalia; Eutheria; Rodentia; Sciurognathi; Muri
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Matches
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                                                                                                                                                MEDLINE-80078170; PubMed=6765983;
Schilling J., Clevinger B., Davie J.M., Hood L.;

"Amino acid sequence of homogeneous antibodies to dextran rearrangements in heavy chain V-region gene segments.";

Nature 283:35-40(1980).

-i- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS,

-i- MISCELLANEOUS: THE D AND J SEGMENTS.

-i- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.

-i- SIMILBARTY: COntains 1 immunoglobulin-like domain.
                                                                                                                        PIR; ;
HSSP;
                                                                               interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
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Eur. J. Immunol. 12:1023-1032(1982).
-!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL
DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE
CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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-!- SIMILARITY: COI
HSSP; P01789; IMCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genetic basis of antibody production: the dominant idiotype response of the strain A mouse.";
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Siekevitz M., Gefter M.L., Brodeur P.,
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MART; SM00406; IGv; 1
MRSITE; PS50835; IG LIKE; 1
MRDITE; IG LIKE; 1
MRDITE; IG LIKE; 1
MRDITE; IG LIKE; 1
MRDITE; 1
MRDI
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NCBI_TaxID=10090;
[1]
{; A26242; MHMSJ5.
3P; P01789; 1MCP.
LEERETO; IPR007110; Ig-like.
LerPTO; IPR003006; Ig_MHC.
LerPTO; IPR003596; Ig_v.
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72; Conserv
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120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.7%; Score 367.5; DB 1; 55.0%; Pred. No. 1.1e-31; tive 20; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG-LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riblet
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DOMAIN
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PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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P06329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
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InterPro; IPR007110; I
InterPro; IPR003006; I
InterPro; IPR003596; I
InterPro; IPR003596; I
Pfam; PF00047; ig; 1
SMART; SM00406; IGV; 1
                                                                                                                                                                                                                                                                                                                                                                                              MEDITINE-84182519; PubMed=6201362; Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.; "A V region determinant (idiotope) expressed at high frequency ir lymphocytes is encoded by a large set of antibody structural generals J. 17-523(1984).

EMBO J. 3:517-523(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1988 (Rel. 06, Cr
01-JAN-1988 (Rel. 06, La
15-JUL-1999 (Rel. 38, La
Ig heavy chain V region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin V
DOMAIN 1
DISULFID 22
NON_TER 117
                                                                                                                                                                                                                                                                                 [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                         SSP; P01810; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; P850835; IG LIKE;
Immunoqlobulin V region.
                         61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 VWGQGTTVTVSS
                                                                                                                                                           PS50835; IG_LIKE; 1

110bulin V region.

1 99 105 L

106 120 J

120 120 120 B1

120 AA; 13311 MW; 1
                                                                                                                              l Similarity 71; Conserv
 NEKFKSKATLTVDKSSSATYMQLSTPTSEDSAVYYCAR--
                                                                        OVOLLOSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGOGLEWMGWISIYSGNTDY
                                                        QVQLLQPGTELVKÞGASVNLSCKASGYTFTSYWMHWIRQRÞGQGLEWIGGINPSNGGTNY
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22 96 BY
117 117
117 AA; 13024 MW; ;
                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06, Createa;
06, Last sequence update;
38, Last annotation updat
region AC38 15.3.
                                                                                                                                      50.8%;
                                                                                                                                                                                                                                                                                                                                     ; Ig-like.
; Ig_MHC.
; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.1%; Score 363.5; DB 1
53.8%; Pred. No. 2.7e-31;
tive 18; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132
                                                                                                                         18;
                                                                                                                                      Score 361; DB 1;
Pred. No. 5.1e-31;
                                                                                                                                                                                                                    BY O V
                                                                                                                                                                                                                V SEGMENT.
D SEGMENT.
J SEGMENT.
SY SIMILARITY.
                                                                                                                                                                                  914453F426F09834 CRC64;
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                           Mismatches
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                                                                                                                                                   Length 120;
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                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
; Murinae; Mus.
WDYEGDRYF--D
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                                                                                                                  Gaps
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108
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HV1B_HUMAN
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                                                                                                  Query Match
Best Local S
Matches 75
                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sisb-sib.ch).
                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P01743;
21-JUL-1986 (Rel. 01, Created,
21-JUL-1986 (Rel. 01, Last sequence upday
15-SEP-2003 (Rel. 42, Last annotation up
"- heavy chain V-I region HG3 precursor.
                                                                                                                                                                                                                                                                                                                                                       PIR; A02024; HVHUHG.
                                                                                                                                                    SEQÜENCE
                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00240; AAA52988.1;
                                                                                                                                                                 YON_TER
                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=83144028; PubMed=6298778;
Rechavi G., Ram D., Glazer L., Zakut R., Givol
"Evolutionary aspects of immunoglobulin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HV18_HUMAN
P01743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (VH) gene subgroups."
Proc. Natl. Acad. Sci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 1 immunoglobulin-like domain.
80
                       19
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                                                                                                                                                                                                                                                                                                                                           P01772; 2FB4.
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                                                                                                             Similarity
                                                           QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                 AOKFOGRVIMITDISRRIAYMELRSLRSDDIAVYYCAR 98
                                         QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWVRQAPGQGLEWMGIINPSGGSTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVMSGEYP-EY-YA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY
                                                                                                                                                   117 AA;
                                                                                                                                                              1
20
20
117
                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sci. U.S.A. 80:855-859(1983)
                                                                                                                                                  12946 MW;
                                                                                                                                                                                                    19
                                                                                                          54.3%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
                                                                                              6
                                                                                                          Score 386;
Pred. No. 1
                                                                                                                                                                          IG HEAVY CHAIN V-I REGION HG3 IG-LIKE.
                                                                                                                                               2D3F92FC60CD1FE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                             Mismatches
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                                                                                                                     DB 1;
                                                                                                          .2e-33;
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                                                                                                                   Length 117;
                                                                                                                                                CRC64;
                                                                                            Indels
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                                                                                          Gaps
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RESULT 3

HV1G HUMA

ID HV1G PUM

AC P230

DT 01-W

DT 01
RESULT
HV03_MO
ID HV
AC P0
DT 21
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OS Mai
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Best Local
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InterPro; IPRO0306; Ig_MHC.
InterPro; IPRO03596; Ig_v.
InterPro; IPRO03596; Ig_v.
If an; Pr00047; Ig; 1.
IMMART; SM00406; IGv; 1.
IMMART; ES0835; IG_LIKE; 1.
IMMARTGIODULIN V region; Signal.
SIGNAL 1 19
                3_MOUSE STANDA
HY03_MOUSE STANDA
P01747;
21-JUL-1986 (Rel. 01,
21-JUL-1986 (Rel. 01,
15-SEP-2003 (Rel. 42,
15 heavy chain v regi
Mus musculus (Mouse).
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X07448; -; NOT_ANNOTATED_CDS
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P23083;
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Matsuda F., Lee K.H., Nakai S., Sato T.,
Chno H., Fukuhara S., Honjo T.;
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01-NOV-1991 (Rel. 20, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
15 heavy chain V-I region V35 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
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1 Similarity 76.5%;
75; Conservation
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20 117 IG
20 >117 IG
117 117 IG
117 AA; 13009 MW;
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Pred. No. 3.1e-33;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

(Rel. 01, Created)
(Rel. 01, Last sequence up
(Rel. 42, Last annotation
ain V region 36-65.

update)

update)

STANDARD;

120

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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    Score
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.
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   SwissProt_41:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
   GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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HV18 HUMAN
HV16 HUMAN
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ery Match st Local Simi	SEQUENCE	ET CI	FLICT	FLICT	FLICT	RES	AIN	IN	unoglobu NAL	SITE; PS	RT: SMOO	erPro; I	erPro; I	GO: 0006	GO: 000	P; P0178	PROTEIN	MISCELL	ediate h	nich H.H) Bach M	UENCE OF	c. Natl.	oning an unoglobu	1 1.0.,	LINE=830	UENCE FR	Mammalia; Eutheria; P NCBI_TaxID=9606;	o sapien aryota;	heavy ch	OCT-2001 SEP-2003	744; JUL-1986	C_HUMAN	Ž		290.5 290		295	ຸດ	96	297.5	982	299	
ilarity	7	147	ð	53	21 21	20	20	20	ilin V re	50835;	14/; 19; 1406; 1G:	PR003596	PR00300	955; P:	823; F:	9, IMCP	ITY: Cor	ANEOUS:	ypersens	l., Johan	20-147	Acad. 8	d sequer lin epsi	Gould H	65234; I	OM N.A.	otheria, 9606;	Metazoa,	lain V-I	(Rel.	(Rel. (STAI			40.9		<u></u>	٠.		٠,.	2 2	2	
60.1 % 62.7 %	491	147	. 68	54	21	120	131	147	egion; S	IG_LIKE;	7; . 1.	5; 1g_v.	HW BI 'S	immune r	antigen :		ntains 1	THIS EP	sitivity	nsson S.		Sci. U.S	RT "Cloning and sequence determinate RT immunoglobulin epsilon chain exp	.J.;	PubMed=6		; Primat	n). ; Chorda	region	10, Last 12, Last	01, Crea	ANDARD;			123 1 114 1	20	22	17	17	17	24 19	17	
; Score 427; DB ; Pred. No. 7.7e-	MW; 948F9F72A5366	STNG (IN KE	VG -> GV (IN RE	-> HI (IN R	-> V (IN REF	KROLIDONE	LIKE.	HEAVY CHAIN	ignal; Pyrrolidone					se; NAS.	ng activity;		noglobulin-l	CHAIN WAS I	ern concepts	3.0., Von Bant-Lind		9:6661-666	ressed in	gircon m., be	shton M. De		atarrhini;	raniata; Ve	ecursor (ence updat		PRT; 147 AA.		ALIGNMENTS	HV24 MOUSE	HV3U_HUMAN	HV3A HUMAN	HV10_MOUSE	HV43 MOUSE	HV02_CANFA	HV1D_HUMAN	HV05_MOUSE	
1; Length 147; 38; 36. Indela 8. Gana 3	C20 CRC64;		٦,	F. 2)	2	CARBOXYLIC ACID.	i	V-I REGION ND.	carboxylic acid.						NAS.		ike domain.	SOLATED FROM A MYELOMA	and developments, pp.1-36,	IGBE FOM H.;		·	<pre>e gene for the human a myeloma cell line.";</pre>	ite K. W. , Time	Viney J		ПO.	t a	ments).						0178	1782 hom	01762 hom	01754 mus	01812 mus	01785 can	01760 hom 01770 hom	01749 mus	

Matches

84;

Conservative

16;

Mismatches

26;

Indels

8

Gaps

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Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #8equence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36255
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36256; MUID:93178448; PMID:7679990
A;Status: preliminary; nucleic acid sequence not shown
A;Residues: 1-118 cGRIs
A;Cross-references: EMBL:Z18846; NID:933121; PIDN:CAA79298.1; PID:g939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
Search completed: December 30, 2003, 11:03:14 Job time: 13.6531 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-125 <BOE>
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                                                                                                              121 VWGQGTTVTVSS 132
                                                                                107
                                                                                                                                                61 AQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDFLSG----
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                                                                                                                                                                        AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                             YWGQGTLVTVSS 118
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Ig mu chain precursor, membrane-bound (clone 201) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C;Accession: $14683; $808047
R;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A;Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
A;Reference number: $14683; MUID:90332450; PMID:2115996
A;Accession: $14683
A;Molecule type: mRNA
A;Residues: 1-627 <FRI>A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin; membrane protein
F;1-15/Domain: signal sequence #status predicted <SIG>F;16-627/Product: Ig mu chain #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate A;Reference number: S31585
A;Grafuro: S31600
A;Grafuro: S31600
RESULT 12
PH1667
                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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A; Residues: 1-136 <CUI>
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Best Local Similarity
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 79
                                                                                                                                                          AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAKTGILGPYSSGW---YPNSDYYY 136
                                                                                                                                                                                                              QVQLVQSGAEVKKPGASVKVSCRASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY 79
                                                                                                                                                                                                                                QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                                                        VWGQGTTVTVSS 132
                                                                                                                                          AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR-----
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                                                                                                                                                                                                                                                                                Score 460; DB 2;
Pred. No. 2.2e-35;
8; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 462.5; DB 2; Pred. No. 7e-35;
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                                                                                                                                                                                                                                                                                                                 Length 136;
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A; Residues: 1-114 <HIL>
 Ig heavy chain V region - human (fragment) N;Alternate names: anti-cytomegalovirus gl C;Species: Homo sapiens (man)
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A; Residues: 1-118 <HIL>
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Best Local :
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Ig heavy chain V region (clone 2H7) - human (fragment)
(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
(;Accession: PH1667
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
30. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1667
A;Accession: PH1667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (clone 6C9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: PH1666
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1666
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                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental Bource: B cell C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;7-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGNTKYAQKFQGRVT
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                                                                                                                              MTTDTSRRTAYMELRSLRSDDTAVYYCAR---DGGGGAYEDVWSGEYPEYYAMDVWGQGT 126
TVTVSS 118
                                                TVTVSS 132
                                                                                                 ITRDTSASTAYMELSSLRSEDTAVYYCARVTLDGGIKFY-----YYYGMDVWGQGT
                                                                                                                                                                                                     EVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGNTKYAQKFQGRVT 61
                                                                                                                                                                                                                                  EVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDYAQKFQGRVT 69
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Pred. No. 6.4e-35;
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Pred. No. 8.2e-35;
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
                                                                                                                                                                                                                                                                                                                                                   F;51-67/Region: complementa
F;68-98/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                F;31-35/Region: complementarity-determining
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F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-132 < MAR>
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A;Molecule type: mRNA
A;Residues: 1-131 <MOR>
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Bur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene A;Reference number: S26786; MUID:92111632; PMID:1730251
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89;
                                                                                                                                                                                                                                                                                      Similarity
                                                                MDVWGQGTTVTVSS
                                                                                      MDVWGQGTTVTVSS 132
                                                                                                                      AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARP--HASIDDFWSGYYPNYYYYG
                                                                                                                                             AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPE--YYA 118
                                                                                                                                                                                     QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
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                                                                                                                                                                                                                                                                               66.5%;
70.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%; Score 474.5; DB 2; 67.4%; Pred. No. 9.7e-37; tive 17; Mismatches 25;
                                                                132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ic selection of MUID:92202880;
                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                             Score 473; DB 2;
Pred. No. 1.4e-36;
9; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       natural autoantibodies PMID:1552291
                                                                                                                                                                                                                                                             26; Indels
                                                                                                                                                                                                                                                                                             Length 132,
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RESULT
S14683
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S34014

Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 0.2-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S34014; S30535
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidic sequence analysis of the variable domains of four huma
a-Reference number: S34001; MUID:93209281; PMID:7681398
                                                                                                                                                                                                                                                                                                       F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                 A/Experimental source: the sequence was determined from the differentiated C/Superfamily: immunoglobulin V region; immunoglobulin homology C/Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A. Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: C33548
                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-133 < KIP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V-1 region (783) - human
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C:Superfamily: immunoglobulin V region; immunoglobulin homology C:Keywords: heterotetramer; immunoglobulin C:Keywords: immunoglobulin homology </MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-127 < MAR>
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94;
YGMDVWGQGTTVTVSS
                                                                                               AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGBYPE----Y 116
                                     YAMDVWGQGTTVTVSS 132
                                                                                                                                                                       QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                  AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAKTGILGPYSSGW--
                                                                                                                                            QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VWGQGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQKFKGRVTMTRNTSISTAYMELSSLRSEDTAVYFCARALSIGV--AVIRG---YYYALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VWGQGTTVSVSS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AOKFOGRVIMITDISRRIAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
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                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                 65.0%;
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71.2%;
133
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                                                                                                                                                                                                                           Score 462.5; DB 2;
Pred. No. 1.3e-35;
8; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 463.5; DB 2;
Pred. No. 9.7e-36;
2; Mismatches 21;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                Length 133;
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anti-PR2 erythrocyte autoantibody heavy chain precursor - C:Species: Homo sapiens (man) C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_C:Accession: PL0105
                                                                       R;Silberstein,
J. Exp. Med. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; RCCEBBACH.

A; RCEBBACH.

A; ROBCULE type: mRNA
A; Residues: 1-40, 'GLSGWDGSALTMYTQSILDK', 61-118, 'T', 120-124 <JON>
A; RCSGWDGSALTMYTQSILDK', 61-118, 'T', 120-124 <JON>
A; CTOSB--references: EMBL; X61647; NID:937667; PIDN:CAA43828.1; PID:91335368
A; Note: the difference for residues 41-60 results from misplacement of 10 }
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
                                A;Reference
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S19665
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A;Reference number: $24442
A;Accession: $24442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: By-passing immunization. Human antibodies from A;Reference number: S19663; MUID:92085276; PMID:1748994 A;Accession: S19865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (alpha-phOx15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence revision 28-Oct-1994 #text_change 20-Jun-2000
C;Accession: S19665; S24442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Jones,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter J. Mol. Biol. 222, 581-597, 1991
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A;Residues: 1-124 <MAR>
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                     Silberstein, L.E.; Litwin, S.; Carmack, C.E.
Exp. Med. 169, 1631-1643, 1989
Title: Relationship of variable region genes expressed
Reference number: PL0106; MUID:89235583; PMID:2541221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local :
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Best Local
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                                                                                                                                                                                                                                                                               116 YYAMDVWGQGTTVTVSS 132
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                                                                                                                                                                                                                                                                                                                                 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPE-----
                                                                                                                                                                                                                                              HYYIDVWGKGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTKY
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99; Conservative
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76.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.4%;
70.8%;
                                                                                                                                                                                                                                              124
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 486; DB 2; Length 124;
Pred. No. 8e-38;
7; Mismatches 15; Indels
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Pred. No. 8.3e-40;
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                                                                                                         #text_change
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                                      by a
                                                                                                                                                human
                                  human B cell lymphoma secı
                                                                                                         26-Apr-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                            (fragment)
                                                                                                                                                                                                                                                                                                            -- LLPKRTATL 107
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                                                                   RESULT 6
S26792
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains alignment of the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:231680; NID:g509786; PIDN:CAA83485.1; PID:g1335146 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology < IMM>
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S46393
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A;Note: the authors translated the codon GAC for residues 108 and 109 as Glu C;Comment: The antibody is one of the cold agglutinins that preferentially bind C;Superfanily: immunoglobulin v region; immunoglobulin homology

C;Keywords: autoantibody: hemagglutinin

F;1-19/Domain: signal sequence #status predicted «SIG»

F;34-117/Domain: immunoglobulin homology «IMM»

F;49-54/Region: complementarity-determining 1

F;69-84/Region: complementarity-determining 2

F;118-131/Domain: D region «DRG»

F;112-144/Domain: J4-segment «JSG»

F;1145-160/Domain: C region «CRG»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
(;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000 C;Accession: S46393
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local :
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                                                                 121 VWGQGTTVTVSS 132
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97; Conservative
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                                                                                                                                                                         AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                                                                                                                                                                                                      ÓVOLVÓSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRÓAPGOGLEWMGWINPNSGGTNY
                                                                                                                                                                                                                                                                                                             QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEMMGWISIYSGNTDY 60
                                                                                                                               AQKFQGWVTMTRDTSISTAYMELSRLRSDDTAVYYCARD---SAYYYDSSGYYSANYYMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---DYWGOGTLVTVSS 144
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73.5%;
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129
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Pred. No. 4.1e-37;
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Pred. No. 2.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Result
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Maximum DB
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711
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         QVQLLQSATEVKKPGASMKV......YPEYYAMDVWGQGTTVTVSS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003, 10:47:09; Search time 12.6531 Seconds (without alignments) 1003.251 Million cell updates/sec
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Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
anti-PR2 erythrocy
Ig heavy chain V r
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5	44	43	42	41	40	39	38	37	36	ω 5	ω 4	ω ω	32	31	
407.5	411.5	412	413	414	416	417.5	418.5	419	419	419.5	425.5	426	426	427	
57.3	57.9	57.9	58.1	58.2	58.5	58.7	58.9	58.9	58.9	59.0	59.8	59.9	59.9	60.1	
122	109	116	98	111	120	126	148	120	110	142	135	132	122	143	
N	N	ນ	N	N	N	N	N	N	2	N	N	N	N	۳	1
B49590	PH1668	PH0959	S26918	\$21925	S31999	144151	S29257	PH0962	PH1669	A32483	PH0953	S46394	PH0958	E1HUND	
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heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	_	heavy	heavy	heavy	heavy	heavy	

ALIGNMENTS

RESULT S36260

Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
c;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36260
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries
A;Reference number: S36256; MUID:93178448; PMID:7679990

from phage display libraries

A; Accession: S36260

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Ig heavy chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36271
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, EMBO J. 12, 725-734, 193
A;Title: Human anti-self antibodies with high specificity from phage display libraries A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-129 <GRI>
A;Cross-references: EMBL: Z18851; NID:g33124; PIDN:CAA79303.1; PID:g939903
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                          A;Status: preliminary; nucleic acid
A;Molecule type: mRNA
A;Residues: 1-122 <GRI>
                                                                                                                                                                                                                                                                                                                       RESULT
S36271
A;Cross-references: EMBL:Z18832; NID:g33115; PIDN:CAA79284.1; PID:g939895
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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Best Local
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79.5%;
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Pred. No. 5.6e
4; Mismatches
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                                                                                       sequence not
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RESULT 15
US-08-217-918-4
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                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, willaim M
REGISTRATION NUMBER: 30,23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,918
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= HUMAN_I
US-08-964-690-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LAKE, PHILIP
APPLICANT: LAKE, PHILIP
APPLICANT: CSTBERG, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 68.5%; Score 471; DB 3; Length 128; Best Local Similarity 72.6%; Pred. No. 2e-41; Matches 98; Conservative 6; Mismatches 19; Indels 12;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
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NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 1413

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
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LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDMESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: (
ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 YFDYWGQGTLVTVSS 128
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-217-918-4

Ouery Match
Best Local Similarity 70.7%; Pred. No. 2.4e-41;
Matches 94; Conservative 13; Mismatches 18; Indels 8; Gaps 2

Oy
1 OVOLVOSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY 60
Db 20 QVOLVOSGAEVKKPGSSVKVSCKASGGTFSNFAISWVRQAPGQGLEWMGRIMPLFVTSTY 79

Oy
61 AQKFOGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRP---DAL 117
Db 80 AQKFOGRVTISADASTSTAYMELNSLRSEDTAMYYCARD-----ITAPGAAPTPLNFYGM 134

Oy
118 DIWGGGTTVTVSS 147
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Search completed: December 30, 2003, 11:05:31 Job time: 14.284 secs

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US-08-202-047-22
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ZIP: 94105

ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPETWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
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TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 9;
                                                                                                                                                                                                                                                                                                                                                                                             tent No. Saute
THERAL INFORMATION:
                                                                                                                                                                                                                                                      APPLICANT: CHESNUT, Robert W.
APPLICANT: POLLEY, Margaret J.
APPLICANT: PAULSON, James C.
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, Jose W.
APPLICANT: BENDIG, Mary M.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
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APPLICATION NUMBER: GI
FILING DATE: 24-MAR-1:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GI
FILING DATE: 23-SEP-1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
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APPLICATION NUMBER: GB 9525004.9

FILING DATE: 07-DEC-1995

PRIOR APPLICATION DATA;

APPLICATION NUMBER: GB 9610824.6

FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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93; Conservative
                                                                                                                                                                     San Francisco
California
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24-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.5%; Score 471.5; DB 2; 71.5%; Pred. No. 1.7e-41; ative 13; Mismatches 17;
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US-08-964-690-22
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION UNMBER: US/08/964,690
FILING DATE:
CLASSIFICATION UNMBER: US/08/202,047
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                    APPLICANT: SALDANHA, JOSE N.
APPLICANT: BENDIG, Mary M.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: CHESNUT, Robert W.
APPLICANT: POLLEY, Margaret J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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TELEPHONE: 415-326-2400
                                                                                                                                                                                                                    ZIP:
                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein
LOCATION: 1.128
OTHER INFORMATION: /label= HUMAN_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 ALDIWGQGTMVTVSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÖVQLVQSGAEVKKPGASVKVSCKASGYTFTSYALSWVRQAPGQGLEWMGWINPYGNGDTN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 128 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08964690
                                                                                                                                                                                                                                                                                                                                                                               PAULSON, James C.
JONES, S. Tarran
SALDANHA, Jose W.
                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 471; DB 1
Pred. No. 2e-41;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14137-77
                                                                                                                      Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Indels
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RESULT 11
US-08-652-816A-1
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SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.7%;
Best Local Similarity 70.1%;
Matches 94; Conservative 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                squence 1, Application US/08652816A
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APPLICATION NUMBER: PCT/GE
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
**PROTICE OF THE PROTICE OF TH
                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: MCCafferty, JG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Specific methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/01
FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 (
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Illinois
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                                                                         24-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                         GB 9206318.9
                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/652,816A
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Pred. No. 2.6e-42;
3; Mismatches 12
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South Wacker Drive
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RESULT 12
US-08-652-816A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Best Local :
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                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION NUMBER: GB 9125579.4
APPLICATION NUMBER: GB 9125579.4
                           APPLICATION NUMBER: GB 9
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                COUNTRY: United States of America COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Osbour
APPLICANT: Allen,
APPLICANT: McCaff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 28 TELECOMMUNICATION INFORMATION:
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NAME: David W. Clough
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APPLICATION NUMBER: GB 9:
FILING DATE: 07-DEC-1995
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                          CITY: Chicago
                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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5. 5872215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNSPINWLRQAPGQGLEWMGSIIPSFGTANY 60
                                                                                                                                                                                                                                                             Illinois
                                                                                                                                                                                                                                                                                        E: Marshall, O'Too
                                                                                                                                                                                                                                                                                                                                                                                             McCafferty, JG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 amino acids
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02-DEC-1991
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                GB 9125579.8
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ower, 233 South Wacker Drive
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; NAME/KEY: Peptide
; LOCATION: 1..120
US-08-428-197-13
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Best Local Similarity 73.6
Matches 95; Conservative
                         CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: FD-2
REFERENCE/DOCKET NUMBER: FD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO:
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version
APPLICATION UNUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
                                                                                                                                                                                                                                                                                                                            STREET: 1000
CITY: LOS Angeles
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH VICTUAL OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (619) 455-5110
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
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LENGTH: 120 amino acid
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 QKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIWG 121
                                                                                                                                                                                                                                                                                                                  90067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OGTMVIVSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application PC/TUS9310555
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1880 Century Park East - Suite 500
                   (619)
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             455-5110
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                                                                 FD-2630
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RESULT 10
US-08-652-816A-8
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                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/652,816A FILING DATE: 23-MAY-1996 PRIOR APPLICATION DATA: APPLICATION DATA: GB 9125579.4 FILING DATE: 02-DEC-1991 PRIOR APPLICATION UNMBER: GB 9125579.8 APPLICATION UNMBER: GB 9125579.8 FILING DATE: 02-DEC-1991 PRIOR APPLICATION DATA: APP
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                                               APPLICATION NUMBER: GB 920
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 952
FILING DATE: 07-DEC-1995
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FILING DATE: 07-DEC-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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IMMEDIATE SOURCE:
CLONE: KAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Peptide LOCATION: 1..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 QGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 OKFOGRVTITADESTNTAYMELRSLRSDDTAMYYCAKEGYGDY-----GRP--FDFWG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 QKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGFLLERRPDALDIWG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VHĽVOSGAEVKKÞGSSVKVSCKASGGTFSSYAISWVRQAÞGOGLEWNGGIIÐIFGQANYA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VQLVQSGAEAKKPGSSVKVSCKASGDTFNSFDISWVRQAPGQGLEWMGGIIPIFGSTKVA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08652816A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QCTLVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
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73.6%;
                                                                                                                                                                                                   GB 9206372.6
                                                                                              GB 9525004.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
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US-08-983-607-50
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-232-081B-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50
Patent No.
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               APPLICATION NUMBER: US/08/983
PILING DATE: April 27, 1998
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/1B96/
FILING DATE: June 28, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
                                                                                                                                      SOFTWARE: Word Processing CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                      STREET: 266 Whit
CITY: New Haven
STATE: Connection
                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Department of Molecular Biophysics ADDRESSEE: and Biochemistry, Yale University STREET: 266 Whitney Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
COMPUTER: II
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45 6140470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVHLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGQANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQKFQGRVTITADESTNTAYMELRSLRSDDTAMYYCAKEGYGDY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OVOLVOSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                     Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08983607
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                                                                                                                                                                                                                                                                  United States of America
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INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      not relevant
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                                                                                                                                                                                                              1.44 Mb diskette
                                                 PCT/IB96/01032
                                                                                                                       US/08/983,607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 121;
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RESULT 8
US-08-428-197-13
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Patent No. 5891438
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: SILVER
                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MET
TITLE OF INVENTION: VAR
TITLE OF INVENTION: VAC
TITLE OF INVENTION: THE
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: VH antibodies obtained from fUSE5
LIBRARY: fusion phage construct
CLONE: 2-71
FEATURE:
NAME/KEY: heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: OC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                      CLASSIFICATION:
                                                                                                                                                                                                                                STREET: 1880 Centu
CITY: Los Angeles
STATE: California
                                                         FILING DATE:
                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens (melanoma patient ORGANISM: immunized with autologous tumor cells) INDIVIDUAL ISOLATE: peripheral blood lympho-INDIVIDUAL ISOLATE: cytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 VSS 130
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                                                                                                                                                                                                                                                                     E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08428197
                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                   METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.0%;
77.2%;
                                                                                                                                                                                                                                                                                                                                             THEREOF
PCT/US93/10555
                                                                        US/08/428,197
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Pred. No. 1.5e-42;
7; Mismatches 10
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; FEATURE:
; NAME/KEY: I
; LOCATION: 1
US-08-428-197-12
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                                                                                                                                                                                             RESULT 5
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5110
TELEPAX: (619) 455-5110
TELEPAX: (619) 455-5110
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
             SEQUENCE 12, Application PC/TUS9310555

GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROTTLE OF INVENTION: VACCIMATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDENNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: pept:
IMMEDIATE SOURCE:
CLONE: BOR
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/428,197 FILING DATE:
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CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                          112
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  ဝ္ဂ
                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VQLVQSGAEAKKPGSSVKVSCKASGDTENSFPISWVRQAPGQGLEWMGGIIPIFGSTKVA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o 70.4%;
Similarity 75.2%;
                                                                                                                                                                                                                                                                                                                            OKFOGRVTITTDESTSTÄYMEVSSLÄSEDTÄLYYCAR-----EGRRMAINP--FDYMG 111
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                                                                                                                                                                                                                                                                                              QGTMVTVSS 130
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SEQUENCES:
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Pred. No. 7.7e-43;
9; Mismatches 14; Indels 9
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US-08-232-081B-41
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; LOCATION: 1..120
PCT-US93-10555-12
                                                                                                                                                                                                                                                 Sequence 41,
Patent No. 5
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/ACEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1
                                                                                                                        APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
COMPUTER READABLE FORM
                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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LENGTH: 120 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: HOWELS, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD
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            STATE: VA
COUNTRY: USA
ZIP: 22040-0747
                                                          ADDRESSEE: BIRCH, STREET: PO BOX 747
CITY: FALLS CHURCH
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STREET: 1880 Centur
CITY: Los Angeles
STATE: California
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5886152
                                                                               E: BIRCH, STEWART, KOLASCH AND BIRCH PO BOX 747
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1880 Century Park East - Suite 500
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75.2%;
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Pred. No. 7.7e-43;
9; Mismatches 14;
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-57
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US-09-025-769B-57
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Best Local Similarity 76.9%;
Matches 100; Conservative
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Patent No. 63000
                                                                                                                                                                                                                                                                                                               TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: JEM PC compatible
COMPUTER: JEM PC compatible
COMPUTER: JEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
APPLICATION DATA;
APPLICATION UMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
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APPLICANT: 1
APPLICANT: 1
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STREET: New York
CITY: New York
TTATE: New York
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APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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121 GQGTMVTVSS 130
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                                             AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                             OVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEMMGGIIPIFGTANY 60
                                                                                                                OVQLVOSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY 60
                            AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARWGGDGFY-----
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                                                                                                                                                                                                                                                                                                                                                                        (212)596-9090
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Ilag, Vic
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                                                                                                                                                                 Score 512; DB 4; Le
Pred. No. 1.1e-45;
"" smatches 11;
                                                                                                                                                                                                      Length 120;
                                                                                                                                                                   Indels 10;
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RESULT 4
US-08-488-197-12
; Sequence 12, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:
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; MOLECULE TYPE: protein
US-09-025-769B-21
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US-09-025-769B-21
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Best Local Similarity
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILLING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Moroney, Šimon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373.
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APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 119 amino acids
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111 GQGTLVTVSS 120
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ilarity 76.2%;
Conservative
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Liming
v, Simon
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Pred. No. 4.4e-44;
B; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 119;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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416.677 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-025-769B-27

US-09-025-769B-21

US-08-428-197-12

PCT-US93-10555-12

US-08-983-607-50

US-08-983-10555-13

US-08-652-816A-8

US-08-652-816A-9

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US-08-652-816A-9

US-08-652-816A-9

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US-08-525-816A-9

US-08-525-539A-77

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              Sequence 57,
Sequence 21,
Sequence 12,
Sequence 12,
Sequence 13,
Sequence 13,
Sequence 13,
Sequence 13,
Sequence 13,
Sequence 14,
Sequence 2,
Sequence 4,
Sequence 4,
Sequence 45,
Sequence 5,
Sequence 5,
Sequence 10,
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Sequence 53,
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           35, Appl
57, Appl
21, Appl
12, Appl
12, Appl
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                                               CIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-EB-1998
PRIOR APPLICATION UNBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-09-025-769B-35
Query Match 74.4%;
Best Local Similarity 76.9%;
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1251 Avenue of the Americas CITY: New York
STATE: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPITED
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APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462.5
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US-08-714-017-53
US-08-657-680-53
US-08-652-16A-7
US-09-199-149-3
US-09-355-925-8
US-09-355-925-8
US-09-355-925-8
US-08-579-378A-12
US-08-579-378A-12
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US-08-579-378A-12
US-08-653-1612-12
US-08-653-1642-19
US-08-653-024-18
US-08-603-024-18
        9;
Score 512; DB 4; Length 120; Pred. No. 1.1e-45; 9; Mismatches 11; Indels
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Sequence 53, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 22, Appli
Sequence 8, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 19, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 12, Appli
Sequence 13, Appli
Sequence 63, Appli
10;
Gaps
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Result

Database

Minimum DB Maximum DB

Sequence:

on:

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Sequence 1866, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
ITITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
FILE REFERENCE: PF553
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
FRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,379
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR FILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIAL DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQ ID NO 1866
; LENGTH: 254
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-880-748-1866
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                                                                                                                                                                                   US-10-269-805-35
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                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 35
LENGTH: 125
                                                                                        Matches
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                                                                                                                                     Query Match
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Best Local (
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TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                   Local Similarity 78.5 tos 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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Similarity 71.4%; Pred. No. 5.1e-39;
00; Conservative 10; Mismatches 8; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAREQGYDILTGYYPEGGWF----- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQ-----NGGWYEGPLL 110
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                                                                       73.8%; Score 507.5; DB 15; Length 125; 78.5%; Pred. No. 2.7e-39; Live 9; Mismatches 14; Indels 5;
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                                                                    Gaps
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Search completed: December 30, 2003, 11:45:22 Job time : 28.8798 secs
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US-10-269-805-9
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SEQ ID NO 9
LENGTH: 121
TYPE: PRT
                                                                                                                                                                                                                                                               Query Match 73.6%; Score 506.5; DB 15; Length 121; Best Local Similarity 78.5%; Pred. No. 3.2e-39; Matches 102; Conservative 6; Mismatches 13; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT APPLICATION UNDBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
                                                                      112 GOGTMVTVSS 121
                                                                                                   121 GOGTMVTVSS 130
                                                                                                                               61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAA-----FSPFTE--TDAFDIW
                                                                                                                                               61 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
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FITTLE OF INVENTION: CHARGE TILE REFERENCE: PRESS
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/27,379
PRIOR APPLICATION NUMBER: 60/27,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1509
LENGTH: 253
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1509
                                                                                                                                                                                            US-10-047-542-47
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Best Local Similarity 76.9
Matches 100; Conservative
                                                                                                                            Sequence 47, Application US/10047542 Publication No. US20020168367A1 GENERAL INFORMATION:
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Best Local
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APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOPF, KEITH L.
TITLE OP INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OP INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
CURRENT APPLICATION NUMBER: US/10/047,542
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Local Similarity 72.1%;
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-DPWGKGTMVTVSS 128
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLy.
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILLING DATE: 2000-06-15
PRIOR FILLING DATE: 2000-06-15
PRIOR FILLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILLING DATE: 2001-03-16
PRIOR FILLING DATE: 2001-03-16
PRIOR FILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
NUMBER OF SEQ ID NOS: 3239
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US-09-880-748-1880
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SEQ ID NO 1880
LENGTH: 253
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Publication No. US20
GENERAL INFORMATION:
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SEQ ID NO 47
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PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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TYPE: PRT
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ORGANISM: Homo sapiens
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Local Similarity 74.6%; Pred. No. 4.6e-39;
mes 100; Conservative 11; Mismatches 12; Indels 11;
114
                                          117 LDIWGQGTMVTVSS 130
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                                                                                                                                                                          AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAKTGILGPYSSGWY-----PNSD 133
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FDIWGRGTMVTVSS 127
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                                             ; ORGANISM: Homo sapiens US-10-269-805-25
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2000-10-17
PRIOR PRIOR DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
                                                                                                                             APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR PRILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/102 Publication No. US20030124129A1 GENERAL INFORMATION:
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LENGTH: 244
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
Query Match
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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                                                                                         LENGTH: 124
TYPE: PRT
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Local Similarity 76.9%;
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74.6%;
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Pred. No. 1.2e-39;
Score 513;
DB 15;
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Length 124;
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-10-125-687-1
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TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
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Publication No. US20020142255A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             Sequence 1, Application US/10125687 Publication No. US20030054407A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 74.4%;
Best Local Similarity 76.9%;
Matches 100; Conservative
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                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                 Human consensus antibody heavy chain variable region
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Pred. No. 9.8e-40;
9; Mismatches 11
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9; Mismatches 12;
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TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT APPLICATION NUMBER: US 09/989,901
PRIOR APPLICATION NUMBER: US 09/989,901
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 118
TYPE: PRT
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US-10-300-675-6
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Best Local S
Matches 99
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Watkins, Jeffry D.

TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 09/989,901
PRIOR FILING DATE: 2001-11-19
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Publication No. US20030198638A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                     LENGTH: 118
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   109
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                              GOGTMYTYSS 130
                                                         AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREDSSGWYH-----
                                                                         AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                                                       QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWNGGIIPIFGTANY 60
GQGTLVTVSS 118
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                                                                                                                                                                                                   Conservative
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76.2%;
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                                                                                                                                                                                           Score 517; DB 12;
Pred. No. 3.3e-40;
9; Mismatches 10;
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Pred. No. 1.2e-40;
B; Mismatches 10;
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                                                                                                                                                                                                                            Length 118;
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, Sequence 12, Application US/10300675
, Publication No. US20030198638A1
, GENERAL INFORMATION:
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US-10-300-675-10
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SOPTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                         Matches
                                                                                                                                                                          Query Match
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Best Local Similarity 76.2%;
Matches 99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 09/989,901
PRIOR FILING DATE: 2001-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
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ITILE OF INVENTION: Tumor Specific Monoclonal Antibodies

FILE REFERENCE: P-IX 5519

CURRENT APPLICATION NUMBER: US/10/300,675

CURRENT FILING DATE: 2002-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 09/989,901
PRIOR FILING DATE: 2001-11-19
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                                                                                                                                                                                                                                                     FEATURE:
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                         Local
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                                                                                                                                                         Similarity
AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                            QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEMMGGIIPIFGSTKY 60
                                                      QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
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                                                                                                                                     Conservative
                                                                                                                                                   75.0%;
76.2%;
                                                                                                                               Score 516; DB 12;
Pred. No. 4.1e-40;
8; Mismatches 11
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Pred. No. 4.1e-40;
8; Mismatches 11;
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Sequence 2, Appli
Sequence 1733, Ap
Sequence 1734, Ap
Sequence 1718, Ap
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Sequence 1873, Ap
Sequence 1737, Ap
Sequence 1737, Ap
Sequence 1741, Ap
Sequence 1741, Ap
Sequence 1746, Ap
Sequence 1727, Ap
Sequence 1727, Ap
Sequence 1728, Ap
Sequence 1728, Ap
Sequence 1728, Ap
Sequence 1736, Ap
Sequence 1748, Ap
Sequence 171, Ap
Sequence 171, Ap
Sequence 171, Ap
Sequence 173, Appli
Sequence 1813, Ap
Sequence 1813, Ap
Sequence 17, Appl
Sequence 37, Appl
Sequence 17, Appl

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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688
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Copyright (c) 1993 - 2003 Compugen Ltd.
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          BB
     US-10-269-805-19
US-10-300-675-14
US-10-300-675-6
US-10-300-675-10
US-10-300-675-12
US-09-880-748-1881
US-10-269-805-25
US-10-025-687-1
US-09-880-748-1509
US-10-047-542-47
US-09-880-748-1880
US-09-880-748-1880
US-09-880-748-1866
US-10-269-805-35
US-10-269-805-9
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Sequence 19, Appl Sequence 6, Appli Sequence 6, Appli Sequence 10, Appli Sequence 112, Appli Sequence 1881, Appli Sequence 1891, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1509, Appli Sequence 1880, Appli Sequence 1860, Appli Sequence 9, Appli
                                                                                                                                                                                           Description
                                                                                                                                                                                                                   RESULT 1

US-10-269-805-19

Sequence 19, Application US/10269805

Publication No. US20030124129A1

GENERAL INFORMATION:

APPLICANT: OLINER, JONATHAN D.

TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BIN

FILE REFERENCE: A-722

CURRENT APPLICATION NUMBER: US/10/269,805

CURRENT APPLICATION NUMBER: US 60/328,604

PRIOR APPLICATION NUMBER: US 60/328,604

PRIOR FILING DATE: 2001-10-11

NUMBER OF SEQ ID NOS: 76

SOFTMARE: Patentin version 3.1

SEQ ID NO 19

LENGTH: 121

TYPE: PAT

ORGANISM: Homo sapiens

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sest Local Similarity 78.5%;
Matches 102; Conservation
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                                                                                     AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQQQGWYEGPLLEPRPDALDIW 120
                                                                                                                      GOGTMVTVSS
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Pred. No. 7e-41;
9; Mismatches 10; Indels 9;
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BINDING AGENTS

Result No.

1143 1133 1143 1143

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Gaps

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                                                                                                                                                                                                                                              Query Match 73.0
Best Local Similarity 75.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 2470-2471; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-114799/15
113 DYWGOGTLVTVSS 125
                                 118 DIWGQGTMVTVSS 130
                                                                     61 AQXFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARMEYDILTGYYGG-----YF 112
                                                                                           61 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONG---GWYEGPLLEPRPDAL 117
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                                                                                                                                                     QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY 60
                                                                                                                                                                                                                                                                                                                                         248 AA;
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Search completed: December 30, 2003, 10:54:29 Job time: 41.903 Becs

cancer

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RESULT 14
ABR01518
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Best Local S
Matches 100
                                           New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a in which TIMP-1 is elevated, e.g. liver fibrosis, benign pros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; Cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer; lupus nephrotease; lupus lupu
                                    hypertrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to human anti-epidermal growth factor receptor single-chain antibodies (anti-EGFR-scFvs) isolated from a human IgM phage display library using EGFR as antigen. Two isolates with different amino acid sequences were identified. The anti-EGFR-scFvs are useful for treating cancer, and for the diagnostic location and assessment of tumour growth, where the anti-EGFR-scFv is radiolabelled. The present sequence represents human anti-EGFR single-chain antibody isolated from clone pSEX81-63.
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                                                                                                                                                                                                                      Pan C,
                                                                                                                                                                                                                                                                    (FARB )
(MORP-)
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                               or lung cancer
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Pred. No. 2.2e-40;
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Claim

20; Page 158-159;

228pp;

English

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RESULT 15
ABP45722
ID ABP457
XX ABP457
XX 19-AUI
DE Human
XX Humou
KW Immun
KW System
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                                                                                                                                                               16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240B1EP.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                    (HUMA-)
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                                                                                                                                                                                                                                                                                                                                          15-JUN-2001; 2001WO-US19110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                              HUMAN GENOME SCI II
CAMBRIDGE ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VWGOGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; Protein; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IWGQGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARWSDQSYHYYWHPY------PD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCAR--QQNGGWYEGDLLEPRDDALD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
                           Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                           SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.0%;
                           Choi GH,
                                                                                                            INC
                                                                                 TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 502.5; 1
Pred. No. 2.6e
10; Mismatches
                     Vaughan
                     H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .6e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                     Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                     ū
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TIMP-1)
ty of
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RESULT 12
AAB36083
ID AAB36
XX AAB36
XX 16-FE
XX 16-FE
XX Human
XX CTN-C
XX CTN-C
XX HOMO
XX H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid complements of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the cinvention. The antibodies can be used in the treatment of obesity and complements. The antibodies can be used to deliver drugs or components of the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to delipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a complement mediated lysis. The antibodies may be labeled with a complement mediated lysis. The antibodies may be labeled with a complement of dagnosis in human subjects e.g. to determine the cells of determine the presence or level of adipocytes e.g. to determine the complement of adipocytes antigen on the surface of an adipocyte to detect or complement of the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies complement of adiposite can also be produced e.g. intra-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 日
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sim
Matches 101;
                                                                                                                                                                                                                                                                                                     Human; antibody cTN-C.
   20-APR-1999;
                                                           19-APR-2000;
                                                                                                                      26-OCT-2000
                                                                                                                                                                              WO200063699-A1
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         Recombinant human antibody scrv TN11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36083 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CAMB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 DIWGQGTMVTVSS 130
||||:||:||:||
113 DIWGRGTLVTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Page 127; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPD---AL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVQLVQSGAEVXXPGSSVXVSCKASGGTFSSYAISWVRQAPGQGLEMMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREAS-----LNLWPDPTWAF 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                           2000WO-EP03550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Main SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.
99IT-FI00094
                                                                                                                                                                                                                                                                                                                                 scFv; TN11; Tenascin-C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.3%;
75.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          members of antibody molecules which bind in the treatment of obesity and obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 504.5; DB 2
Pred. No. 8.4e-41;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                 TN-C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                              domain C-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT 13
AAU97198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope recognised by TN11 is located inside domain C of TN-C. TN11 is therefore only capable of recognising TN-C isoforms containing domain C (TN-C). TN11 is useful for detecting the presence of TN-C isoforms in vitro or in vivo for diagnosing pathologies expressing the cTN-C isoforms of TN-C. It is useful for the preparation of formulations for the treatment of human neoplasias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ligands used for diagnosis and treatment of human neoplasias, capable of identifying the tenascin-C isoform containing domatenascin-C -
                                  WPI; 2002-463261/49
                                                                                                                                                                                                                     anti-EGFR-scFv;
                                                                                                                                                                                                                                 Human; anti-epidermal growth
                                                                                                                                                                                                                                                       Human anti-EGFR single-chain antibody isolated from clone
                                                                                                                                                                                                                                                                               27-AUG-2002
                                                                                                                                                                                                                                                                                                                          AAU97198 standard; protein; 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                           12-OCT-2001; 2001WO-US31857
                                                                                                                                                                        WO200230984-A1
                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                      AAU97198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 5-6; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                               (UABR-) UAB
                                                                                                     13-OCT-2000; 2000US-240353P
                                                                                                                                                   18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PHIL-) PHILOGEN SRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-687225/67.
DB; AAC67868.
                                                                                                                                                                                                                                                                                                                                                                                     114
                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                        ξĐ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGABAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                     GRGTMVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                          GOGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGG1IPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSRRITIFGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 AA;
                                                        Curiel DT,
                                                                               RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                     IgM; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.3%;
76.9%;
                                                       Bonner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                   factor receptor single-chain antibody;
tumour growth; clone pSEX81-63; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 504.5;
Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                           $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8e-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sias, are
domain C
                                                                                                                                                                                                                                                        pSEX81-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        얁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
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Novel human anti-epidermal growth factor receptor single-chain antibody useful for diagnostic location and assessment of tumour growth, and in

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RESULT 10
ABP45855
ID ABP45
XX ABP45
XX ABP45
XX IP-AU
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240B16P.
16-MAR-2001; 2001US-276246P.
21-MAR-2001; 2001US-277379P.
                                                                                                                                                                                                                                                                                                                                                          BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antitheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                              15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic, immunosuppressive, immunostrimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in abiological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and immunodeficiency (e.g. common variable immunodeficiency (evil) and the antibodies and fragments of the antibodies described in the method of the invention.
                                                                                                                                                                                                            10-JAN-2002
                                                                                                                                                                                                                                                                       WO200202641-A1
                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human BLyS binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP45855 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP45855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 2645-2646; 3148pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQN----GGWYEGPLLEPRPDA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDIWGRGTMVTVSS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARESHYDILTGYYSNP-----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLQQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQCLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCFV SEQ ID 1866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 508.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibodies that immunospecifically bind polypeptides. BLyS is a member of the uper family and induces B cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel antibodies that immunospecifically bind to CB Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNF) super family and induces B cell CC proliferation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC antirheumatic and antiAlDS activity and can be used in vaccines to cinhibit the expression and activity of BLyS. The antibodies bind to BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be and activity such as cancer, immune, and autoimmune disorders and CC and activity such as cancer, immune, and autoimmune disorders and CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and cquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the antibodies and fragments of the antibodies described in the method
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Best Local (
                         11-OCT-2000; 2000WO-GB03900
                                                                                       WO200127279-A1
                                                                                                                     Homo sapiens.
                                                                                                                                             Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                         Anti-adipocyte monoclonal antibody heavy chain, FAT 41
                                                                                                                                                                                                                            29-AUG-2001
                                                                                                                                                                                                                                                                                    AAU02555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention.
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                                                                                                                                                                                                                                                                                  standard; Protein; 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQ------NGGWYEGPLL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                     EPRPDALDIWGOGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 AA;
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 508; DB
Pred. No. 8.5e
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides, useful for immune disorders -
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity. The human antibody is useful for decreasing an MMP-inhibiting activity of a TIMP-1. It is especially useful for ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The antibody is also useful for detecting a TIMP-1 in a test preparation, or in diagnosing a disorder in which a TIMP-1 level is elevated. The sequences shown in ABR01502-ABR01545 represent the heavy chain regions of a human anti-TIMP-1 antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                        16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                               Claim 1; Page 2203-2204; 3148pp; English
                                                                                       Antibodies against B Lymphocyte Stimulating polypothe diagnosis and treatment of cancers and immune
                                                                                                                                                                                    WPI; 2002-114799/15
                                                                                                                                                                                                                                               Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human BLyS binding scFv SEQ ID 1509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-AUG-2002
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                                                                                                                                                                                                                                                                                                          (CAMB-)
                                                                                                                                                                                                                                                                                                                                      (HUMA-)
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                                                                                                                                                                                                                                                                                                    HUMAN GENOME SCI INC
CAMBRIDGE ANTIBODY TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQGTLVTVSS 116
                                                                                                                                                                                                                                         Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 AA;
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                                                                                                                                                                                                                                         Choi GH,
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Pred. No. 3e-41;
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                                                                                          polypeptides, useful for
immune disorders -
                                                                                                                                                                                                                                            Hilbert
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RESULT 9
ABP45869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                16-JUN-2000; 2000US-212210P: 17-OCT-2000; 2000US-240816P: 16-MAR-2001; 2001US-276248P: 21-MAR-2001; 2001US-277379P: 25-MAY-2001; 2001US-293499P
                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human BLyS binding scFv SEQ ID 1880.
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                                                                                          (HUMA-) HUMAN GENOME SCI INC
(CAMB-) CAMBRIDGE ANTIBODY T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                Barash SC,
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                                Choi GH,
                                                                                                TECHNOLOGY.
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                                Vaughan T,
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RESULT 6
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Best Local Similarity
Matches 100; Conserv
                       The invention relates to a novel method for the construction of a library of recombinant antibodies. The novel method comprises clustering variable regions of a collection of antibodies having known 3D structures into at different antibody sequences but with substantially identical main chain conformations. The method is useful for constructing a library of artificial antibodies in silico which provides a structurally diverse and yet functionally more relevant source of antibody candidates which can including small molecules, and biomacromolecules such as proteins, a peptides and nucleic acids. The libraries constructed are useful as a proteins of a constructed are useful as a constructed are 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Constructing a library of recombinant antibodies useful as source antibody candidates for screening antigens comprises clustering variable regions of antibodies having known 3-dimensional structurinto structural ensembles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 13B; 119pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library; recombinant antibody; clustering variable region; in silico; immunogenecity; antibody therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABJ18718
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Pred. No. 1.5e-41;
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ul as a a antibodies
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The invention relates to a novel purified preparation of a human antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1) and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and a variable light chain (VLC)DR3 region. An antibody preparation of the invention has hepatotropic, cytostatic, nephrotropic and cardiant

(TIMP-1)

Claim 20; Page 173; 228pp; English.

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RESULT 7
ABROL538
ID ABROL538
ID ABROL538
ID ABRO
XX ABRO
XX ABRO
XX ABRO
XX ABRO
XX ABRO
XX Humw
XW mat
XW mat
XW alc
XW lup
XX Idi
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Best Local S
Matches 100
                                                                                                                                                                                                       New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a in which TIMP-1 is elevated, e.g. liver fibrosis, benign proshypertrophy or lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer; lupus nephritis; glomerulosclerotic renal disease; lung cancer;
                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FARB )
(MORP-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human anti-TIMP-1 antibody heavy chain #36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-2003
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DB; ABZ74809.
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No. 1.5e-41;
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Claim 1; Page 2646-2647; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have CC cytostatic. immunosuppressive, immunostimulant, immunomodulatory, compared to and antiALDS activity and can be used in vaccines to CC antirheumatic and antiALDS activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression CC and activity such as cancer, immune, and autoimmune disorders and CC immunodeficiency (e.g. common variable immunodeficiency (CUTD) and cc acquired immunodeficiency (e.g. common variable immunodeficiency (c.g. acquired immunodeficiency (PLYD) and cc acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent CC of the invention.

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RESULT 4
AAW27550
ID AAW2
XX AAW2
AC AAW2
AC AAW2
AC AAW2
AC Huma
XX Huma
XX Homc
XX H
                 Preparation of human derived antibody gene library - using synthetic consensus sequences, and signal consensus antibody gene as universal framework for highly diverse antibody libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
heavy c
                                                                                                                                                                                                                                                                                                                              Ge L,
                                                                                                                                                                                                                                                                                                                                                                                      (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
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                                                                                                                                                                                                                                            1997-179277/16.
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                                                                                                                                                                                                                                                                                                                     Ilag V,
                                                                                                                                                                                                     AAT87948.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-EP03647
                                                                                                                                                                                                                                                                                                                 Knappik A,
                                                                                                                                                                                                                                                                                                             Moroney S,
                                                                                                                                                                                                                                                                                                        Pack P,
                                                                                                                                                                                                                                                                                                    Plueckthun A;
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RESULT 5
ABJ18672
ID ABJ1
XX A
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Best Local S
Matches 100
The invention relates to a novel method for the construction of a library of recombinant antibodies. The novel method comprises clustering variable regions of a collection of antibodies having known 3D structures into at least two families of structural ensembles, each comprising at least two conformations. The method is useful for constructing a library of artificial antibodies in silico which provides a structurally diverse and yet functionally more relevant source of antibody candidates which can including small molecules, and biomacromolecules such as proteins, peptides and nucleic acids. The libraries constructed are useful as a source of antibody candidates for further screening for novel antibodies
                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 98-99; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Constructing a library of recombinant antibodies useful as source of antibody candidates for screening antigens comprises clustering variable regions of antibodies having known 3-dimensional structures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-093043/08
                                                                                                                                                                                                                                                                                                                                                                                                                                   into structural ensembles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Luo P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-APR-2001; 2001US-284407P.
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Pred. No. 1.
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Similarity

74.8%; 76.9%;

Score 514.5; Pred. No. 1.9 Mismatches

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The present sequence is the heavy chain variable region of a human tumour-specific monoclonal antibody. Neoplastic cells selectively antigens which are not present on normal cells. Thus monoclonal antibodies can be produced that are specifically directed against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; LH13 monoclonal antibody; hybridoma; tumour-specific; cancer; cytostatic; cytotoxic; heavy chain variable region.
                                                                                                                                              Claim
                                                                                                                                                                                                  determining region
                                                                                                                                                                                                                         New tumor-specific human and diagnosis of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                  Watkins JD,
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DB; AAA48411.
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                                                                                                                                           10; Page 82-83; 84pp; English
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Pred. No. 2.2e-58;
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17-OCT-2000; 2000US-240B16P
16-MAR-2001; 2001US-27624BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficie systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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                                                                                                              WPI; 2002-114799/15
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CAMBRIDGE ANTIBODY TE
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2001US-276248P.
2001US-277379P.
2001US-293499P.
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Pred. No. 5e-42;
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Antibodies aga

against

: B Lymphocyte treatment of c

cancers

Stimulating polypeptides, useful for cancers and immune disorders -

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Copyright (c) 1993 - 2003 Compugen Ltd
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ABJ18718
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Human BLyS binding
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Human anti-TIMP-1
Human BLyS binding
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APKIL DINGING SCFV Human BLyS binding Human BLyS binding	anti-		Human anti-TIMP- Human leukocyte	2 3	scFv 1b4 antibody Human leukocyte a	n BLy	anti	-		ВЬУЅ	Human BLyS binding	anti	u	nce c	Human BLyS binding			BLyS	BLyS	anti-	(T)	Recombinant human	adipoc	Human BLyS binding

RESULT 1 AAY50948 Human; heavy chain; antibody; factor VIII; hemostatic; hemophilia A; VH gene. AAY50948 standard; Protein; 130 08-MAY-1998; 07-MAY-1999; Homo sapiens Human anti-factor VIII antibody VH clone EL-14 encoded protein. 23-MAR-2000 (first entry) AAY50948; 18-NOV-1999. WO9958680-A2 (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING 98EP-0201543. 99WO-NL00285 ₹

New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -

WPI; 2000-053102/04.

Voorberg JJ, Van Den Brink EN,

Turenhout EAM

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RESULT 14

Q924Q1

ID Q924Q

AC Q924Q

DT 01-DE

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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

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SEQUENCE 142 AA; 15622 MW;
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"Direct Estimation of Relative Affinity by Flow Cytometry Reveals

"finity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl) Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB069913; BAB63929.1; -.
                                                                                                                                         O95978;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
VH1 protein precursor (Fragment).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TISSUE=Peripheral blood;
Jox A., Zander T., Kuepp
                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                              095978
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                             NCBI_TaxID=9606;
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Kueppers R.,
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   Kornacker
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Best Local Similarity
Matches 81; Conserva
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InterPro; IPRO03006; Ig_MC.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                Bohlen H., Diehl V., Wolf J.;

"Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a patient with mixed cellularity Hodgkin's disease is associated w somatic mutations within the untranslated regions of rearranged class switch recombinated Ig genes.";

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ005570; CAA06599.1; -.

HSSB; P01772; ZFB4.

HSSB; P01772; ZFB4.
                                                                                                                                                                                                                                                                                        Signal.
SIGNAL
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                                                                         LDIWGQGTMVTVSS 130
                                                                                                                        AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGW----YEGPLLEPRPDA 116
                                                                                                       AEKFOGRLTMTRNTSTTTVYMELSRLRFEDTAVYFCGR--GGRWRSGNYNGH-----
                                                                                                                                                                                                                                                       1 21 POTENTIAL.
157 157
157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                           55.6%; Score 382.5; DB 60.4%; Pred. No. 5e-32; tive 10; Mismatches
              2003,
              11:01:02
                                                                                                                                                                                                                                     DB 4;
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RESULT 12

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CS Mus m

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                                        Q9Z1C4 PRELIMINARY; PRT; 118 AA.

Q9Z1C4;
Q9Z1C4;
Q9Z1C4;
Q9Z1C4;
Q9Z1C4;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-MAY-1999 (TrEMBLrel. 23, Last annotation update)
Anti-porcine VCAM mAb 3F4 heavy chain variable region
B Anti-porcine VCAM mAb 3F4 heavy chain variable region
S Mus musculus (Mouse).

E Lekaryota; Metazoa; Chordata; Craniata; Vertebrata;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Best Local 9
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 SEQUENCE FROM N.A. STRAIN=Balb/c;
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Q9GYZ2;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Song X.T., Feng Z.Q., Guan X.H.,
Yamplification, cloning and sequence analysis of the heavy chain
variable region gene of monoclonal anti-idiotypic antibody NP30 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Fragment).
Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; D
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG_LIKE;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schistosoma japonicum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF282622; AAG01452.1; -.
HSSP; P01772; 2FB4.
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                                                                                                                                                                                                                                                                                                     AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                                                                                                                                                                                                                                                                            QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
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119 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13567 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                    57.0%; Score 392.5; DB 5; Length 119; 60.8%; Pred. No. 3.2e-33; tive 14; Mismatches 26; Indels 11
                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BA893873FD5FA6AB CRC64;
                                                                                         tation update)
variable region
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Best Local S
Matches 77
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC013490, AAH13490.1; -.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003056; Ig_v.
R Ffam; PF00047; ig; 4.
R Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
R PROSITE; PS05093; IG_LIKE; 4.
R PROSITE; PS05093; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
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Best Local :
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
NOW TEP
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.1 kDa protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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01-DEC-2001
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NON_TER
SEQUENCE
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"Humanized porcine VCAM-specific monoclonal antibodies was IgG2/G4 constant regions block human leukocyte binding the endothelial cells.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U78801; AAD00293.1; -.
HSSP; P01810; ZFBJ.
HSSP; P01810; ZFBJ.
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                                                                                           l Similarity
77; Conserva
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75; Conserv
                                                   QVQLVQSGAEAKKPGSSVKVSCKASGDTENSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                      QVQLLQSGPELVKPGASVKISCKASGYTFTSYYIHWVKQRPGQGLVWIGWIYPGDGNTKY
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118 AA; 13036 MW;
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57.7%;
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                                                                                     Score 388.5; DB 11;
Pred. No. 4.8e-32;
7; Mismatches 23;
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Pred. No. 3
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AC Q9
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A Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
A Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
A Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
Kawakami B., Nagai K., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
REMBL; AKO58027; BAB71633.1; -.
InterPro; IPR003106; Ig-1ike.
InterPro; IPR003106; Ig-1ike.
InterPro; IPR003006; Ig-V.
R InterPro; IPR003596; Ig-V.
R InterPro; IPR003596; Ig-V.
R PROSITE; PS00490; IG-MHC; 1.
R PROSITE; PS00490; IG-MHC; 1.
R PROSITE; PS00290; IG-MHC; 1.
R PROSITE; PS00290; IG-MHC; 1.
R SEQUENCE 496 AA; 53532 MW; C72EE1E247C86FED CRC64;
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Best Local S
Matches 83
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
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Hypothetical protein.
Homo sapiens (Human)
Eukaryota, Metazoa; Chordata,
Mammalia; Eutheria; Primates;
                                                                                                      Q9BRV0;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                                                                                                                         LDIWGQGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQKFQGRVIMTADGSTSTAYMELNSLRSEDTAIYYCAR----QQNGGWYEGPLLEPRPDA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVHLVQSGAELKMPGSSVKVSCKASANMFRSYAFTWVRQAPGQGLQMMGGIIPNFGAPNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQNFQDRVTISADDSTTTVYMELTSLTFEDTAFYYCGRGLTYYGSGSYY---
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                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.4%;
61.9%;
                                                                                                                                                                                                                                                                                                                                                     143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 409; DB 4; 2003-
Pred. No. 3.6e-34;
Pred. No. 3.6e-36; Indels 14;
                                                                                                         Last sequence update)
                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 496
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RESULT 10
Q8VCX7
ID Q8VCX
AC Q8VCY
AC Q8VCY
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DT 01-M
IGH
OS Mus
OC Euk
OC Man
OX NCI
RN [1]
RN [2]
RN [3]
RP SE
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RA SI
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Best Local S
Matches 81
                                                           Query Match
Best Local :
                                                 Matches
                                                                                              InterPro; IPR007010; Ig-like.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 5.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50835; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67855 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 500 AA; 54154 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005951; AAH05951.1; -.
HSSP; P01799; IMCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                              Q8VCX7
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Cro
01-MAR-2002 (TrEMBLrel. 20, Lan
01-MAR-2003 (TrEMBLrel. 23, Lan
01-MAR-2003 (TrEMBLrel. 23, Lan
Hypothetical 67.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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[1]
                                                                                                                                                                                                           EMBL; BC018315; AAH18315.1; MGD; MGI:96448; Igh-6.
                                                                                                                                                                                                                                    Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                           TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   GH-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 -- YMDVWGKGTTVTVSS
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                      1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
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                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDALDIWGQGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQ-----QNGGWYEGPLLEPR
AKKFQGRVTLTTDTSTSTVYMELRSLRSDDTAVYYCARRYCSYSSCONDYYYY---
                                                                                            protein.
613 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.2%;
ilarity 59.1%;
Conservative 1
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                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54154 MW;
                                                                                                  67855 MW;
                                                            57.7%;
59.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147
                                               Score 397; DB
Pred. No. 8.5e
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 407; DB 4
Pred. No. 6e-34;
7; Mismatches
                                                                                                                                                                                                                                                                                                              Sciurognathi;
                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OA9BF43F2A3CC6D9 CRC64;
                                                                                                  41A9384DD4C22862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             613
                                                  DB 11;
3.5e-33;
hes 22;
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                                                   Indels
                                                                            613;
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                                                   Gaps
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RESULT QO COSO OCCUPANT OCCUPA
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Best Local
                                                                                                                                                                                                                                                                                                Q9Y298
Q9Y298;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; iravo-
Pfam; PP00047; ig; 1.
SMART; SM00406; iGv; 1.
SMOSITE; PS50835; iG_LIKE; 1.
PROSITE; PS50835; iG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative matrix cell adhesion molecule-3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q96QS0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Homo sapiens putative microfibrillar protein with Ig-like mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3)."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY039025; AAK82649.1; -.
SEQUENCE FROM N.A.
MEDLINE=98322155; PubMed=9657749;
Jacquemin M.G., Vander Elst L.P.L
                                                                                           Homo gapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                 IGG VH.
                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQ------QNGGWYEGPLLE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                  InterPro; IPR003006; Ig_MHC.
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119 AA;
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150 AA;
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[1]
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ224083; CAA11829.1; -. HSSP; P01772; 2FB4.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Myosin-reactive immunoglobulin heavy chain variab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mechanism and kinetics of factor VIII inactivation: study with an IgG4 monclonal antibody derived from a hemophilia A patient with
                                                                                                                                                                                                                                                                                                                                  "Myosin-reactive autoantibodies in rheumatic carditis
                                                                                                                                                                                                                                                            AF035020; AAD56256.1; -. P01810; 2FBJ.
                                                                                                                                                                                                                                                                                               Immunol. Immunopathol. 87:184-192(1998)
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Primates;
                                                                                                     13205 MW; 13E64F5345F4A16E CRC64;
                                 12;
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                             Score 420.5; DB 4;
Pred. No. 3.9e-36;
2; Mismatches 21;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                            Q9UL92
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HSSP; P01810; 2FBJ
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Mammalia; Eutheria; Primates;
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                                                                                                    (Fragment)
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125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESULT 4
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Best Local S
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Matches 89
                                                                                                                                           Pfam; PF00047; ig; 5. SMARR; SM0406; IGV; 1. SMARR; SM0406; IGV; 1. PROSITE; PS00041; HTH ARAC_FAMILY_1; 1. PROSITE; PS50835; IG_LIKE; 5. PROSITE; PS00290; IG_MHC; 3. Hypothetical protein.
SEQUENCE 614 AA; 67921 MW; 55EF536F
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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NON_TER
SEQUENCE
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O96GA6; PRELIMINARY;
O1-DEC-2001 (TrEMBLrel. 19,
O1-DEC-2001 (TrEMBLrel. 19,
O1-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (UTL-2001) to the EMBL/GenBank/DDBJ
EMBL; BC00985; AAH09851.1; -
InterPro; IPR000005; HTHAraC.
InterPro; IPR003110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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MEDLINE=982771139; PubMed=9614934;
Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pı
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF035022; AAI
HSSP; P01772; 2FB4
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EMBL; AF035022; AAD56258.1; -.
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    QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
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124 AA;
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Primates;
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Last sequence update)

Last annotation updat
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                                               Score 438.5; DB
Pred. No. 4e-37;
8; Mismatches
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Q9ul92 homo sapien
Q96ga6 homo sapien
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Q90ul94 homo sapien
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Q9z1c4 mus musculu
Q91vt1 mus musculu
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•	52.5			•	•	•	52.9	•	53.0	53.1	53.4	53.6	53.7	53.8	53.8	•	53.9	53.9	54.0	54.2	54.5	٠	•	•	•	•	55.3	
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RESULT 1
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Best Local Similarity
Matches 92; Conserv
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; AF035025; AAD56261.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fragment)
5 VQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKYAQKF 64
                                                                                                                                                                                                                                                                116
116 AA;
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                              116
12605 MW; C8F9131DE13EA898 CRC64;
                                                                                                                                               67.2%;
72.4%;
                                                                                                                8;
                                                                                                             Score 462; DB 4; Length 116;
Pred. No. 1.8e-40;
B; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116
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                                                                                                                Indels 12;
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HV48
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                    Matches
P03980;

P03980;

23-OCT-1986 (Rel. 02, Created)

23-OCT-1986 (Rel. 02, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

15 heavy chain V region TEPC 1017 precursor.

Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1; swarr; SM00406; IGv; 1. PROSITE; PS50835; IG I.T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibodies: somatic m
Cell 24:625-637(1981)
                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00539; AAA38172.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                   HV48_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A02038; G2MS43.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bothwell A.L.M., Paskind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NPB ANTIBODIES).

SWISS-PROT entry is copyright. It is produced through a collaboration and the EMBL outsteen the Swiss Institute of Bioinformatics and the EMBL outsteen the Swiss Institute. There are no restrictions in
                                                                                                                                                                                 128
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                                                                                                                                                                                                                                  80
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                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                     70;
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                           GOGTMVTVSS 130
                                                                                                                                                                                                                               NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARYRLGRYF--
                                                                                                                                                                                                                                                                                                       QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50835; IG LIKE;
                                                                                                                                                                                GQGTTLTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                   20
50
55
69
69
118
113
123
141
137 AA;
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                         49
54
68
85
117
122
137
                                                                                                                                                                                                                                                                                                                                                                                    15200 MW;
                                                                                                                                                                                                                                                                                                                                              51.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۲.
                                                                                                                                                                                                                                                                                                                                 19; Mismatches
                                                                                                                                                                                                                                                                                                                                              Score 354; DB 1;
Pred. No. 1.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG HEAVY CHAIN V REGION S43.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
D SEGMENT.
                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                    ADD5881BF44B8EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            2 SEGMENT.
SIMILARITY.
                                                                                                                   138 AA
                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                       Length 137;
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Best Local
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DOMAIN
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DOMAIN
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SEQUENCE FROM N.A.
MEDLINE=84248078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J
                                                                                                                                                                                                                                                                                                                                                          "Illegitimate recombination generates a class switch delta in an IgD-secreting plasmacytoma."; Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                  PIR; A02033; HVMST7.
                                                                                                                                                       SEQUENCE
                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                            InterPro; IPR007110;
InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                           HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                         Tucker P.W.;
                                                                                                                                                                                                                                                                       mmunoglobulin V region;
 129
                  121
                                      80
                                                        61
                                                                           20
                                                                                             Н
                                                                                                                69;
                                                                                                                          Similarity
                                                AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
GOGTLVTFSA 138
                   GQGTMVTVSS 130
                                     NEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCAR--SDGYY----
                                                                                            QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                           QVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRPGQGLEWIGEINPNDGRSNY
                                                                                                                                                                                                                                                                                  PS50835;
                                                                                                                                                       138 AA;
                                                                                                                Conservative
                                                                                                                                                                                   21
50
55
69
86
118
128
                                                                                                                                                                                                                                                                                Gv; 1.
IG_LIKE;
                                                                                                                                                                         138
49
54
68
85
117
127
138
115
                                                                                                                                                                                                                                                                                                           Ig-like.
Ig_MHC.
Ig_v.
                                                                                                                                                       15576
                                                                                                                        50.1%;
                                                                                                                                                                                                                                                                       Signal.
                                                                                                                                                       ¥.
                                                                                                                21;
                                                                                                                        Score 344.5;
Pred. No. 1.
                                                                                                                                                                                                              IG HEAVY CHAIN V REGION TEPC 1017.
FRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEMORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                         FRAMEWORK-4.
BY SIMILARITY
                                                                                                                                                                                            FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3
                                                                                                                                                       748157E4C6907B8E CRC64;
                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 J.E., Blattner F.R., Mushinski
                                                                                                                No. 1.6e-28;
smatches 29;
                                                                                                                                   DB 1;
                                                                                                                 Indels
                                                                                                                                  Length 138;
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                                                                                                                11;
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                                                                                                                                                                                                                                                                                                                                                                                                  J.F.,
                                       DWEVYW
                                                                                                                Gaps
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Search completed: December 30, 2003, 10:55:49 Job time : 7.96994 secs

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Interpro,
Interpro,
Interpro,
Interpro,
Interpro,
Interpro,
Interpro,
Interpro,
IpR0035v,
Pfam; PF00047; ig; 1.

« SMART; SM00406; IGv; 1.

» RPOSITE; PS50835; IG LIKE; 1.

KW Immunglobulin V region.
FT DOMAIN
PT DOMAIN
PT DOMAIN
PT DOMAIN
106
120
120
120
121
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                                                                                         RESULT 12
HV50_MOUSE
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                                               Query Match
Best Local S
Matches 71
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Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPRO07110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
DOMAIN
NON TER 114 114
NON TER 114 114
                                                                                                                                                                                                                                                                                                                                                                                                           HV50_MOUSE
P06329;
                                                                                                                                                                                       HSSP, P01810; 2FBJ.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                    lymphocytes is encode
EMBO J. 3:517-523(19)
PIR; A02037; MHMS15.
                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
19 heavy chain V region AC38 15.3.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                    Dildrop R.,
"A V region
                                                                                                                                                                                                                                                                                          MEDLINE=84182519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Cont.
PIR; A02022; G1MSAA.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                          \vdash
                                             Similarity 71; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    =84182519; PubMed=6201362;
R., Bovens J., Siekevitz M.,
gion determinant (idiotope) e
ytes is encoded by a large se
3:517-523(1984).
QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQKFQGRVTITADESTNTAYMELSSLRSEDTAVYFCAVRVISRYFDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AOKFOGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQGTLV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOGTMV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.3%; milarity 58.7%; Conservative 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114
114 AA;
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114
12555 MW; 99DD8F0B6A69F4BE
                                                     52.0%;
54.2%;
                                            18;
                                      Score 358; DB
Pred. No. 5.7e-
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 360; DB
Pred. No. 3.4e
17; Mismatches
                                                                                                          A G C
                                                                                                         V SEGMENT.
D SEGMENT.
F SEGMENT.
SY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG-LIKE
                                                                                   914453F426F09834 CRC64;
                                                                                                                                                                                                                                                    M., Beyreuther K., Rajewsky K.;
) expressed at high frequency in B
set of antibody structural genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                    120 AA
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                                  DB 1;
5.7e-30;
30;
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3.4e-30;
23;
                                                              Length 120;
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                                           Indels
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; Murinae; Mus
                                         12;
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                                         Gaps
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RESULT 14
HV11_MOUSI
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Best Local S
Matches 71
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                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.

SMART; SM00406; IG; 1.

PROSITE; PS50835; IG LIKE; 1

Immunoglobulin V region.

DOMAIN

1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-84182519; PubMed=6201362;
Dildrop R., Bovens J., Siekevitz M.,
"A V region determinant (idiotope) e:
lymphocytes is encoded by a large sei
EMBO J. 3:517-523(1984).
PIR; A02040; MIMS38.
HSSP; P01789; 1MCP.
InterPro; IPR007010; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003096; Ig-MHC.
InterPro; IPR003596; Ig-V.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Havy chain V region S43 precursor.
Bukaryota; Metazoa; Chordata; Craniata; Vertel
Mammalia; Eutheria; Rodentia; Sciurognathi; Me
                                                                                  HV11 MOUSE
P01755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (Rel. 06,
01-JAN-1988 (Rel. 06,
15-JUL-1999 (Rel. 38,
1g heavy chain V regi
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                       DOMAIN
DISULFID
NON_TER
SEQUENCE
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P06330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                      109
                                                                                                                                                                           121
                                                                                                                                                                                                  61
                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                            AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW
                                                                                                                                                     GTGTTVTVSS
                                                                                                                                                                           GOGTMVTVSS 130
                                                                                                                                                                                                                                          EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMMWVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                       QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFFISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                 NOKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCAR---GYGY--
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ilarity 54.6%;
Conservative 1
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in V region AC38 205.12.
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                                                                                             STANDARD;
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                        Score 354; DB 1; 1
Pred. No. 1.4e-29;
7; Mismatches 30;
Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                      94F7BEE4C762A018 CRC64;
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expressed at high frequency in B
ext of antibody structural genes.";
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                                                                                                                                                                                                                                                                                                             Length 118;
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Best Local :
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DOWAIN 1 98
DOWAIN 99 107
DOWAIN 108 125
DISULFID 22 96
NON_TER 125 125
                                                                                                                                                                                                                                                                                                                                        HV07 MOUSE STANDARD,
P01751; P01752;
P01751; P01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                      Ig heavy chain V regi
Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Amino acid sequence of the variable region of heavy chain immunoglobulin (Mot) having unusual papain cleavage sites." Mol. Immunol. 23:169-174(1986).
PIR, A02025; HVHUMO.
HSSP; P01777. http://doi.org/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.0001/10.00
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NON TER
SEQUENCE
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
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                                                                                                                         "Heavy chain variable region contribution antibodies: somatic mutation evident in a
                                                                                                                                                                                        MEDLINE=81234548; PubMed=6788376; Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                      STRAIN=C57BL/6;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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Mammalia; Eutheria; Primates;
    Thie
                                                                                                                                                                      Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86203277; PubMed=3084950;
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GO:0005576; C:extracellular; NAS.
GO:000352; F:antigen binding activ
GO:0006955; P:immune response; NAS.
                                                           1 24:625-637(1981).
MISCELLANEOUS: THE B1-8 MU CHAIN
MAKING ANTIBODIES TO THE HAPTEN
SWISS-PROT entry is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115
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                                          ANTIBODIES)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLVQSGAEVKKPGSSARLSCKVSGDDFNTYDIHWVRQAPGRGLEWMAVVHPSDDRTTY
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Rodentia;
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copyright.
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Pred. No. 2.6e
12; Mismatches
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                                                                                                                                                                                          Reth
                                                                                                                                                                                                                                                                                                                      Craniata; Veri
Sciurognathi;
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F4C4285D6DF0C8EA CRC64;
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  Ιt
                                                              N MRNA WAS CLONED FROM A HYBRIDOMA (4-HYDROXY-3-NITROPHENYL) ACETYL
                                                                                                                                                                                     Imanishi-Kari T.,
  18
                                                                                                                                                                                                                                                                                                                      Vertebrata;
thi; Muridae;
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produced
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through
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, Murinae; Mus.
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                                                                                                                                                                                        Rajewsky K.,
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collaboration
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RESULT 11
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Best Local
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P01741;
21-JUL-1986
21-JUL-1986
15-SEP-2003
                              STRAIN=A/J;

MEDLINE=79195438; PubMed=109536;

Capra J.D., Nisonoff A.;

Capra J.D., Nisonoff A.;

"Structural studies on induced antibodies with defined i specificities. VII. The complete amino acid sequence of chain variable region of anti-p-azophenylarsenate antibo mice bearing a cross-reactive idiotype.";

J. Immunol. 123:279-284(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
CHAIN
DOMAIN
DOMAIN
                                                                                                                                                         Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region (Anti-arsonate anti
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                          SEQUENCE
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SMART; SM00406; IGv;
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                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal;
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PDB; 1A6W; 15-JUL-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110;
InterPro; IPR003006;
InterPro; IPR003596;
MISCELLANEOUS: ANTIBODY THE IGG1 SUBCLASS. THERE REGION SEQUENCE.
                                                                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                            GOGTTLTVSS
                                                                                                                                                                                                                                                                                                                                   GOGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                         NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYD---
                                                                                                                                                                                                                                                                                                                                                                              AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                                                                                                                                                                                                                                                                                                                                    QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
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139
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                                                                                                                                                                                                                                                    STANDARD;
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54
68
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117
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                                                                                                                                                           Chordata;
Rodentia;
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Ig_MHC.
Ig_v.
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             THERE
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                       ISOLATED
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Pred. No. 3.3e
17; Mismatches
             WAS
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D SEGMENT
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                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG HEAVY
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           ö
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           HETEROGENEITY 1
                                                                                                                                                                                                                                                    114
                                                                                                                                                                                            update)
e antibody).
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           IN THE HEAVY CHAIN
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of the heavy
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Best Local :
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Matches
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                                                                                                                                                                                                                                                                                                          MEDLINE=80078170; PubMed=6765983;
Schilling J. Clevinger B., Davie J.M., Hood L.;
"Amino acid sequence of homogeneous antibodies to dextran rearrangements in heavy chain V-region gene segments.";
Nature 283:35-40(1980).

-i- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS BIND DEXYRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS,
WHICH OCCUR IN THE D AND J SEGMENTS.

-i- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
-i- SIMILDARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                             DOMAIN
DISULFID
                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region J558.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                       PIR; A26242; MHMSJ5.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                              HSSP; P01789; 1MCP
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                                                                                                                                        Similarity
                                                     AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                           GOGTMVTVSS
                                      NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
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117
117 AA;
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ilarity 55.4%;
Conservative 10
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                 130
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Pred. No. 5.9e
18; Mismatches
                                                                                                                          Score 366.5; DB 1
Pred. No. 7.4e-31;
8; Mismatches 27
                                                                                                                                                                                         IG-LIKE.
BY SIMILARITY.
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RESULT 9
HV1F HUMAN STANDARD; PRT; 125 AA
ID HV1F HUMAN STANDARD; PRT; 125 AA
AC P06326;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V-I region Mot.
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Best Local S
Matches 74
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NON TER
SEQUENCE
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P01746;
P01746;
P01746;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
11-SEP-2003 (Rel. 42, Last annotation update)
11-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region 93G7 precursor.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J00493; AAA38128.1; -. PIR; A94264; HVMSG7. HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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Science 216:309-311(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Somatic mutation in genes for the variable immunoglobulin heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sims J., Rabbitts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=82152818;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                                                                                                             AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQ-NGGWYEGPLLEPRPDALDI 119
                                                                                                                                                                                  WGQGTMVTVSS
                                                                                                                                                                                                             NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYYGGSYD----
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T.H., Estess P.,
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                                                                                                                                                                                                                                                                                                                              Score 363.5; DB 1;
Pred. No. 1.9e-30;
8; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                          IG HEAVY CHAIN V REGION IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                            25A4CBBE31DASCE8 CRC64;
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RESULT
HV03_M
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Matches 74
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequ
15-SEP-2003 (Rel. 42, Last anno
15 heavy chain V region 36-65.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
NCBI TaxID=10090;
                                       Siekevitz M., Gefter M.L.,
Marshak-Rothstein A.;
                                                                          SEQUENCE FROM N.A.
MEDLINE=83131846; PubMed=6186498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
DOMAIN
NON TER
                                                                                                                                                                                                                                                                                                                                                                             MOUSE
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE
Immunoglobulin V region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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GO; GO
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MEDIJNE=88296408; PubMed=2841108;
Matsuda F. Lee K.H., Nakai S., Sato
Ohno H., Fukuhara S., Honjo T.;
Dispersed localization of D segments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X07448; -; NOT_ANNOTATED_CDS.
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heavy-chain locus
                     genetic
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74; Conserv
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117
117 AA;
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A.;
s of antibody production: the
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117
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LIKE; 1.
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75.5%;
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                                                     Brodeur P.,
                                                                                                                                                                                                                                                        sequence up
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Pred. No. 3e-32;
6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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         dominant
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   DISULFID CARBOHYD NON_TER
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Theavy chain V region MOPC 104E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete amino acid sequence of a m heavy chain constant region domains. Biochemistry 21:5415-5424(1982).
-i- MISCELLANEOUS: THE SEQUENCE OF T PROTEIN HAS ALSO BEEN DETERMINED
                                                                                                     Immunoglobulin
DOMAIN
                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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HV12
                                                                                                                                                                   PROSITE;
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
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HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN HAS ALSO BEEN DETERMINED.
-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
-!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE MEDLINE-83075344; PubMed-6816276; Kehry M.R., Fuhrman J.S., Schilling J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Mus musculus (Mouse)
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1023-1032(1982)
-!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL
DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE
CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED
SEGMENT, JH2.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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-!- SIMILARITY: COT
HSSP; P01789; 1MCP.
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                             ; Glycoprotein.
IG-LIKE.
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N-LINKED (GLCN)
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V-I region HG3 precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=83144028; PubMed=6298778;
Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HV1B
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003956; Ig_v.
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:. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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5; Mismatches 12;
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HUMAN HV1G HUMAN P23083; 01-NOV-1991 01-NOV-1991 15-SEP-2003

STANDARD;

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(Rel. 20, Created)
(Rel. 20, Last sequence update)
(Rel. 42, Last annotation updat

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RESULT 4
HV1G HUMF
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AC P23G
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Matches 79
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0003823; F:immune response; NAS.
InterPro; IPR0077110; Ig-like.
InterPro; IPR007016; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; ig: 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V regin; Signal; Pyrrolidone carboxylic acid.
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21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V-I region ND precursor (Fragmu Homo sapiens (Human)
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MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
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tive 14; Mismatches 33
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IH -> HI (IN REF. 2).
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KKPGS	61.1 67.4 ative	IGv; 1. ; IG_LIKE region; 112 112 96 117 A; 12472	tiger	J.M.; G.M.; Gure of bond -3196 THE SI HAS J	4024; PubMed=5489 A., Rutishauser Edelman G.M.; t structure of a e of heavy-chain 9:3161-3170(1970	l, Creat. 1, Last 2, Last region E Chordat. Primate	DARD;	1119 1122 1122 1124 1114 1120 1126 1117 1117 1117
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QQNGGWYEGPLLEPRPDALD

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RESULT 7
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ID Q9F0M3
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O1-MAR-2001 (TrEMBLrel. 16, Created)

O1-MAR-2001 (TrEMBLrel. 21, Last sequence

O1-MAR-2003 (TrEMBLrel. 23, Last annotat)

D-alanine:D-alanine ligase.

Enterooccus faecium (Streptococcus faeci

Bacteria; Firmicutes; Lactobacillales; En

NCBI_TaxID=1352;
   STRAIN=A902;
Gold H.S., Eliopoulos G.M., M.
"D-alanine:D-alanine ligase o.
Submitted (DEC-1999) to the El
EMBL; AF515736; AAG49141.1;
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InterPro; IPR005905; Dala Dala.
Pfam; PF01820; Dala Dala la 1.
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PROSITE; PS00843; DALA DALA LIGASE 1;
PROSITE; PS00844; DALA DALA LIGASE 2;
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Tulkens P.M., Courvalin P.,
"Sequencing of the ddl gene
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U39790; AAB17902.2; HSSP; P07862; 110V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alanine ligase in glycopeptide-dependent faecium.";
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SEQUENCE FROM
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
D-alanine:D-alanine ligase
Enterococcus faecium (Streptococcus faecium).
Bacteria: Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
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Q1-MAR-2001 (TrEMBLrel. 16, Created)

Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)

Q1-CCT-2002 (TrEMBLrel. 22, Last annotation update)

Hypothetical protein FLJ22501.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., K. Hosoyama A., Fukui S., Nagai Y., Nishijina K., Nakazawa H., Takamiya M., Maguda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Kubota K., "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Ki."; DNA Res. 6:83-101(1999).

EMBL; Aepo00061; BAA8534.1; -...
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PROSITE; PS00334; MYB 2; 1.
Lyase; Pyruvate; Complete proteome.
SEQUENCE 403 AA; 47103 MW; 6B6852
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01-NOV-1999 (TrEMBLrel.
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403AA long hypothetical
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Desulfurococcaceae; Aeropyrum.
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01-NOV-1999
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InterPro; IPR005905; Dala Dala.
Pfam; PF01820; Dala Dala ligas; 1.
TIGRFAM6; TIGR01205; Dala DalaTIGR; 1.
PROSITE; PS00843; DALA DALA LIGASE 1; 1.
PROSITE; PS00844; DALA DALA LIGASE 2; 1.
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New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies .	WPI; 2000-053102/04.	Voorberg JJ, Van Den Brink EN, Turenhout EAM;	(SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.	08-MAY-1998; 98EP-0201543.	07-MAY-1999; 99WO-NL00285.	18-NOV-1999.	WO9958680-A2.	Homo sapiens.	hemophilia A; VH protein.	Human; heavy chain; antibody; factor VIII; hemostatic.	Human anti-factor VIII antibody VH protein VH EL-14 CDR3 fragment.	23-MAR-2000 (first entry)			AAY50956 standard; Protein: 21 AA	0956

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Best Local
                             hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human antibody value of the invention and the antibodies in the method of the invention
                                                                                                                                                                                        Example 4; Fig 4A; 6lpp; English.
                                                                                                                                                                                                              New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                 This invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY50948;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention
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                                                                                                                                                      describes a novel polynucleotide (I) (and complements and
                                                                                                                                                                                                                                                                                                                                                                              98EP-0201543.
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Pred. No. 1.1e-11;
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                                                                                                                                                                                                                                                                                                               Turenhout EAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
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the invention.

Query Match Best Local

Similarity

43.3**%**; 69.2**%**;

Pred. No. 7.2

22;

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CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC ond gene mapping, and in recombinant production of (II). The
CC and gene mapping, and in recombinant production of (II). The
CC polynuclectides are also used in disgnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC disorders involving aberrant protein expression or biological activity.
CC disorders involving aberrant protein expression or biological activity.
CC disorders involving aberrant protein expression or biological activity.
CC disorders for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC camino acid sequences. ABG00010-ABG30377 represent novel human
CC specification, but was obtained in electronic format directly from WIPO
CX at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
ABG00057
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Sequence
                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation
                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 30416; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73.
N-PSDB; AAS64244.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
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Pred. No. 8.4e-11;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                          ion of mutations and to assess
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                                                                                                                                                  pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

C P. acnes is also involved in infections of bone, joints and the central concerved system, however it is particularly involved in the inflammatory clesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a condition of the binds of the invention conditions and determining the amount of bound protein in the sample. The conditions may be used as antigens in the production of antibodies convergulate expression and activity of P. acnes proteins can be used to convergulate expression and activity of P. acnes protein and activity of P. acnes proteins. The antibodies may also be used as converging the acnes infections. The antibodies may also be used as convergence treat P. acnes infections. The antibodies may also be used as convergence inked immunosorbent assay (ELISA).

C enzyme linked immunosorbent assay (ELISA).

C Note: The sequence data for this patent did not form part of the printed convergence convergence data for this patent did not format directly from WIPO
      Query Match
Best Local Similarity
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                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID No 4390; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating acne vulgaris
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatological; osteopathic; neuroprotectant
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e J, Zhang
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Score
Pred.
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51.5;
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                     Length 118,
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                                                                          cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; noctropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune modulation; haematopoiesis regulation; tissue growth; angiogenasis; activin; inhibin; chemotactic; chemokinetic; http://doi.org/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ORF;
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sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  open reading frame; ORFX; drug screening; diagnosis;
itoring; cytokine; cell proliferation; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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29-NOV-2001 WO200190366-A2

24-MAY-2000; 2000US-206690P 24-MAY-2001; 2001WO-US17076. (CURA-) CURAGEN CORP

Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperprollferative disorders and disorders related to organ transplantation

N-PSDB; ABN77579. WPI; 2002-106200/14 Leach MD,

Shimkets RA

Claim 10; Page 1516; 2508pp; English

Sequences ABB31028-ABB35561 represent 4534 novel human proteins CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-CC ABN75897 represent cDNAs encoding them. The invention also encompasses CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively CC referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORF1-ORF4534 (collectively CC RFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and cctivity, and methods of screening for modulators of ORFX persession or CC polypeptides, methods of screening individuals for a predisposition to an CC crange of biological activities, such as Cytokine, cell proliferation, timmune modulation, hamatopoiesis regulation, tissue growth, angiogenesis, activin or inhibin activity, chemotactic/ cc receptor/ligand, antiinflammatory activity, thmombolytic activity, and may also be involved in the determination of boddily characteristics, fertility and behaviour. ORFX proteins,

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Best Local :
              The invention rel
prokaryotic cellu
genes, their use
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23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                          N-PSDB;
                                                                                                                               antibiotics,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU35179 standard; Protein;
                                                                                                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM INC.
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invention relates to antisense inhibitors of genes essential karyotic cellular proliferation, their use in identifying the lear, their use in the discovery of novel antibiotics, the esse
                                                                                                                     polynucleotides for the identification and development biotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                           2001-611495/70
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9; Conserv
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2000US-206848P.

2000US-207727P.

2000US-242578P.

2000US-253625P.

2000US-257931P.

2000US-2569308P.
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Xu HH;
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                                                                                   511pp; English
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design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC genes themselves and the encoded proteins. The prokaryotes used are CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense mucleic acid sequence is also useful to screen CC awide variety of organisms. The present sequence represents an CC awide variety of organisms. The present sequence represents an CC essential prokaryotic cellular proliferation protein. CC Note: The sequence data for this patent did not form part CC format directly from WIDO at
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Best Local
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The present invention describes a method (MI) of evaluating the potential of a chemical entity (CE) to associate with a molecule or molecular complex comprising a binding pocket (BP) defined by specific structural coordinates (SC) of D-Ala-D-Ala ligase (I) E coli amino acids Lys144, Glu180, Lys181, Leu183, Glu187, Asp257 and Glu270, by employing a computational unit to perform a fitting operation between CE and BP defined by SC and analysing the results of the fitting operation to
                                                                                                                                                                                   Evaluating association binding pocket defined computational unit for
                                                                                                                                                                                                                                                                                   Navia MA,
Magee AS,
                                                                                                                                      Example 8; Fig 10; 115pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecalis D-Ala-D-Ala ligase enzyme SEQ ID
                                                                                                                                                                                                                                                                                                                                 (ESSE-) ESSENTIAL THERAPEUTICS (PLIV) PLIVA DD ZAGREB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
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Connelly PR,
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                                                                                                                                                                                                                                                                                               Griffith JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.7%;
                                                                                                                                                                             potential of chemical entity to complex having by structural coordinates, by employing entity-pocket fitting operation and analyzing
                                                                                                                                                                                                                                                                                  Perola E;
                                                                                                                                      English.
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Pred. No. 20;
5; Mismatches
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RESULT 8
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Best Local S
Matches 8
                      The present invention describes a method (M1) of evaluating the potential of a chemical entity (CE) to associate with a molecule or molecular complex comprising a binding pocket (BP) defined by specific structural coordinates (SC) of D-Ala-D-Ala ligase (I) E. coli amino acids Lys144, Glu180, Lys181, Leu183, Glu187, Asp257 and Glu270, by employing a computational unit to perform a fitting operation between CE and BP defined by SC and analysing the results of the fitting operation to quantify the association between CE and BP. Also described is a method (M2) for identifying a potential inhibitor of (I). M1 is useful for evaluating the potential of a chemical entity to associate with a constitution of the potential of a chemical entity to associate with a constitution of the potential of a chemical entity to associate with a constitution of the constitution
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                                                                                                                                                                                                                                                                                                                                                                                                                                Example 8; Fig 10; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evaluating association binding pocket defined computational unit for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Navia MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ESSE-)
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   molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            faecium D-Ala-D-Ala ligase enzyme SEQ ID NO:30
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PR, Perola I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme; bacterial; structure-based data; D-Ala-D-Ala ligase inhibitor;
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complex
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comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ali JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         operation
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pocket.
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   is useful
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Best Local
                         biodiversity and producing many other types of data and products dependent on DNA and amino acid sequences. They are also useful for preventing, treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell disorders, osteoporosis, osteoarthritis, bone
                                                                                                                                                                                                                                                                                                                                                             neurodegenerative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; genetic disorder; gene mapping; medical imaging; cancer; neurodegenerative disorder; lymphoid cell disorder; osteoporosis; Parkinson's disease; Alzheimer's disease; bone degenerative disorder; osteoarthritis; periodontal disease; liver fibrosis; viral infection; fungal infection; bacterial infection; autoimmune disease; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                   The invention relates to human polynucleotides and the polypeptides they encode. The polynucleotides and polypeptides are useful in diagnostics,
                                                                                                                                                                                                                                                                                                     Claim 9;
                                                                                                                                                                                                                                                                                                                                                          disorders, and
                                                                                                                                                             encode. The polynucleotides and polypeptides are useful in diagnostic forensics, gene mapping, medical imaging, identification of mutations responsible for genetic disorders or other traits, assessing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polypeptides and polynucleotides, useful for preventing, treating or ameliorating medical conditions, such as cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xue AJ,
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T, Wang J,
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                                                                                                                                                                                                                                                                                                  SEQ ID NO 609; 235pp; English.
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R, Wang Z,
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                                                                                                                                                                                                                                                                                                                                                                                   bone
                                                                                                                                                                                                                                                                                                                                                                                   degenerative
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The present sequence represents rat TAO2 protein kinase, which is capable of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related polypeptides, are used to screen for modulators of stress-responsive mitogen activated protein (MAP) kinase pathways. These modulators are cc potentially useful for treating or preventing: (1) inflammation, c protein (Map) kinase pathways. These modulators are cc autoimmune disease, cancer and degeneration (inhibitors of phosphorylation); or (2) insulin-resistant diabetes, metabolic disorders can neurodegeneration (enhancers of phosphorylation). TAO kinases are modulators and as immunoassay reagents for detecting TAO kinases.

CC modulators and as immunoassay reagents for detecting TAO kinases, and (b) in the form of fragments, for detecting TAO kinase polynucleotides can be used: (a) for recombinant expression cc fao kinase polynucleotides in standard hybridisation and amplification cc tests. TAO kinases are highly specific for MEK3.
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Best Local
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                                                                                                                                                                                                                                             Claim 7; Page 84-87; 95pp; English
                                                                                                                                                                                                                                                                                  modulators
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation; p38; protein kinase; cancer; inflammation; autoimmune disease; degeneration; insulin-resistant diabetes; metabolic disorder; neurodegeneration; MAP kinase; MAP/ERK kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (e.g. viral, fungal or bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis). Sequences ABG99888-ABG99989 and ABU00010-ABU00433 represent human polypeptides of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY49897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
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 993
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Pred. No. 48;
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11-JUL-2000; 2000US-0217496

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26-JUL-2000; 2000US-022963

14-AUG-2000; 2000US-022951

14-AUG-2000; 2000US-022521

14-AUG-2000; 2000US-022521

14-AUG-2000; 2000US-022526

14-AUG-2000; 2000US-022526

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14-AUG-2000; 2000US-022526

14-AUG-2000; 2000US-022527

14-AUG-2000; 2000US-022527

14-AUG-2000; 2000US-022527

14-AUG-2000; 2000US-022575

16-AUG-2000; 2000US-022579

22-AUG-2000; 2000US-0225868

22-AUG-2000; 2000US-02258924

01-SEP-2000; 2000US-0229343

01-SEP-2000; 2000US-0229344

01-SEP-2000; 2000US-0229344
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Matches 7; Conserv
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28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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17-MAR-2000;
18-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
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2000US-0216647.
2000US-0216880.
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2000US-0190076.
2000US-0198123.
2000US-0205515.
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3; Mismatches 3;
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2000US-0229509. 2000US-0229513. 2000US-0230437. 2000US-0230438.

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RESULT 12
ABG24835
ID ABG24
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        ABG24835 standard; Protein; 564
                                                                                                                                                                                                                                                specification, at ftp.winc '-
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Note: The sequence data for this patent did not specification, but was obtained in electronic fo at ftp.wipo.int/pub/published_pct_sequences.
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06-DEC-2000;
08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11;
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N-PSDB; AAS41213.
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9; Conservative
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2000US-0249297
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2000US-0250160
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2000US-0251988
2000US-0251988
2000US-0251479
2000US-0251866
2000US-0251868
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20-OCT-2000
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; 2000US-0237037 ; 2000US-0237038 ; 2000US-0237039 ; 2000US-0237040 ; 2000US-0239935 ; 2000US-0239937

2000US-0236370. 2000US-0236802.

3-0236367. 3-0236368. 3-0236369.

2000US-0232399 2000US-0232401 2000US-0233063 2000US-0233063 2000US-0233063 2000US-0233063 2000US-0234274 2000US-0234274 2000US-0234997 2000US-0234998 2000US-0234998 2000US-0235834 2000US-0235834 2000US-0235834 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836

2000US-0231968. 2000US-0232397. 2000US-0232398.

2000US-0231414. 2000US-0232080. 2000US-0232081.

2000US-0231413

2000US-024617 2000US-024186 2000US-024186 2000US-024186 2000US-024180 2000US-0244617 2000US-0244617 2000US-024647 2000US-024647 2000US-024647 2000US-024647 2000US-024647 2000US-024647 2000US-024647 2000US-024647 2000US-024652 2000US-024652

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RESULT 13
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                                                        ABG24833 standard; Protein; 816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisati
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23-AUG-2000; 2000US-0649167.
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Pred. No. 1e+02;
4; Mismatches
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CC Note: The sequence data for this patent did not appear in the printed consection in but was obtained in electronic format directly from WIPO CC at figure and polymblished_pct_sequences.
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                                                   ABG04046;
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23-AUG-2000;
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                                                                                                                                                                                                                                          Similarity
                                                                                                                                                          WYEAVVLAPOPETLPL 112
                                                                                                                                                                                         WYEGPLLEPRPDALDI 21
                                                                                                                                                                                                                                                                                          918
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2000US-0649167.
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Pred. No. 1.5e+02;
4; Mismatches 5
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13-FEB-2002

(first entry)

Novel

human diagnostic protein #4037

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RESULT 15
ABG25828
ID ABG25
XX
AC ABG25
XX
DT 18-FF
XX
DE Novel
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CC Note: The sequence data for this patent did not appear in the printed CC at ftp.wino.int/mnh/mhishad not sequences.
                                                                                                                                                                                                                                                                  Matches
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Best Local 9
          Novel human diagnostic protein #25819
                                              18-FEB-2002 (first entry)
                                                                                 ABG25828
                                                                                                            ABG25828 standard; Protein; 897
                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 34405; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
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23-AUG-2000; 2000US-0649167
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39 WYEAVVLAPQPETLPL 154
                                                                                                                                                                                                                                                                  Similarity 7; Conserv
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                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                             39.2%;
43.8%;
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Pred. No. 1.6e+02;
4; Mismatches 5
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II) and for chromosome CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC imaging of sites expressing (II). (I) and (II) are useful in medical CC disorders involving aberrant protein expression or biological activity. CC disponsible for genetic disorders are useful in medical CC disorders involving aberrant protein expression or biological activity. CC disponsible for genetic disorders sor other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed construction, but was obtained in electronic format directly from WIPO can first the printed construction.
                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 56187; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS90015
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23-AUG-2000; 2000US-0649167.
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Matches
                          Query Match
Best Local
                                                  Sequence
  6
                  Similarity 7; Conserv
WYEGPLLEPRPDALDI
                                                  897
                Conservative
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                       39.2%;
 21
              Score 47; DB 22;
Pred. No. 1.7e+02;
4; Mismatches 5
                              Length 897
              0
              Gaps
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91

WYEAVVLAPOPETLPL

106

Search completed: December 30, 2003, 10:54:32 Job time : 7.83882 Becs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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pea
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1: /cgn2=6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2-6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*

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length: 2000000000
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Match Length DB
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120
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    341.7
39.23
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37.53
36.77
36.77
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                                                                                    362
4150
355
163
76
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358
451
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12
11
15
9
5 US-10-186-886-31

5 US-10-186-886-30

US-10-156-761-8003

2 US-10-369-493-20793

2 US-10-369-493-748

1 US-09-808-880-2

2 US-10-156-761-11806

US-09-815-242-11403

US-10-186-886-29

3 US-10-186-886-29

3 US-10-186-886-2963

5 US-10-156-761-12356

2 US-10-369-493-16825
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US-09-815-242-10772
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Sequence 3841, Ap
Sequence 10772, A
Sequence 31, Appl
Sequence 30, Appl
Sequence 20793, Ap
Sequence 20793, Ap
Sequence 2, Appli
Sequence 4, Appl
Sequence 11806, A
Sequence 11806, A
Sequence 2963, A
Sequence 2963, A
Sequence 22963, A
Sequence 12356, A
Sequence 12356, A
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ALIGNMENTS

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
FILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE OF INVENTION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
INUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3841
LENGTH: 1427
TYPE: PRT
TYPE: PRT
                 US-09-815-242-10772
; Sequence 10772, Application US/09815242
; Patent No. US20020061569A1
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GENERAL INFORMATION:
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Best Local Similarity
Matches 10; Conserv
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QQQGGWHTKP-LPPTPD 1114
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58.8%;
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Pred. No. 1.2e+02;
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; TYPE: PRT ; ORGANISM: Enterococcus faecalis US-10-186-886-31
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FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-2
PRIOR PRICING DATE: 2000-12-2
PRIOR PRICING DATE: 2001-12-2
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31, Application US/10186886 Publication No. US20030119061A1
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10772
LENGTH: 341
                                                                                                                                                                                                          APPLICANT: Magée, Andréw S.
APPLICANT: Connelly, Patrick R.
APPLICANT: Connelly, Patrick R.
APPLICANT: Perola, Emanuele
TITLE OF INVENTION: STRUCTURE-BASED DRUG DESIGN METHODS FOR
TITLE OF INVENTION: IDENTIFYING D-ALA-D-ALA LIGASE INHIBITORS AS ANTIBACTERIAL
TITLE OF INVENTION: DRUGS
FILE REFERENCE: 10283-014001
CURRENT APPLICATION NUMBER: US/10/186,886
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION TUMBER: US/10/186,886
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                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/301,676
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Navia, Manuel A.
APPLICANT: Ala, Paul J.
APPLICANT: Griffith, James P.
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                                                                            ENGTH:
                                                                            348
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8; Conserv
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Xu, H. Howard
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Pred. No. 35;
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Sequence 8003, Application US/10156761
Publication No. US20030119018A1
GENERAL IMFORMATION:
APPLICANT: OMUTA, SATOSHI
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHTA
TITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 10283-014001
CURRENT APPLICATION NUMBER: US/10/186,886
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 60/301,676
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 52
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 358
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APPLICANT: Navia, Manuel A.

APPLICANT: Ala, Paul J.

APPLICANT: Griffith, James P.

APPLICANT: Ali, Janid A.

APPLICANT: Faerman, Carlos H.
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Best Local Similarity 40.0%;
Matches 8; Conservative
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Best Local Similarity 40.0
Matches 8; Conservative
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TITLE OF INVENTION: STRUCTURE-BASED DRUG DESIGN METHODS FOR
TITLE OF INVENTION: IDENTIFYING D-ALA-D-ALA LIGASE INHIBITORS AS ANTIBACTERIAL
TITLE OF INVENTION: DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 KEGOWVKGPLLTEKPASKDV 61
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Connelly, Patrick R.
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No. US20030119061A1
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; Pred. No. 35;
5; Mismatches
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US50/0/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 748
LENGTH: 362
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Query Match
Best Local Similarity
Thehes 7; Conserva
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Best Local Similarity
""" Conserv
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20793
LENGTH: 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
FILE REFERENCE: 38-10 (52052) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28
                                                                                                                 ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434 QERGGWHRGPVL 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 GGWYEG-----PLLEPRPDALDI 21
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                  Conservative
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                                  39.2%;
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 Mismatches

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Pred. No. 56;
3; Mismatches
                  4; Mismatches
                                  Score 47; DB 12;
Pred. No. 98;
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Pred. No. 1e+02;
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                                                       Length 362;
                  Indels
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APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.1.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GPS0013
CURRENT APPLICATION NUMBER: US/10/203,708
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 44
LENGTH: 355
TYPE: DET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence; FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Recombinant; OTHER INFORMATION: Oleandolide PKS
US-09-808-880-2
                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-203-708-44
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US-09-808-880-2
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Best Local Similarity 45.0%; Matches 9; Conservation
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Publication No. US20030149238A1
GENERAL INFORMATION:
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SEQ ID NO 2
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Best Local :
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APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US/09/428,517
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/120,254
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/106,100
PRIOR FILING DATE: 1998-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE FILE REFERENCE: 30062-20029:00 CURRENT APPLICATION NUMBER: US/09/808,880 CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 39.2%; Score 47; DB 11; Length 4150;
Local Similarity 56.2%; Pred. No. 1.1e+03;
nes 9; Conservative 1; Mismatches 6; Indels
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                                    Score 46; DB 12;
Pred. No. 1.3e+02;
                                                              Length 355;
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Gaps

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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length: 2000000000
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Match Length
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416.677 Million cell updates/sec
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    Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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 US-08-454-196-8
US-08-454-196-17
US-09-064-033-8
US-09-064-033-17
US-09-064-033-17
US-09-291-046-18
US-09-291-046-18
US-09-291-046-18
US-09-291-046-17
US-09-107-532A-5920
US-09-252-991A-3135-17-2
US-09-252-991A-3135-18
US-09-252-991A-20263
US-09-252-991A-20263
US-09-252-991A-202518
US-08-556-422A-2
US-09-252-991A-23201
US-08-138-641-2
US-09-252-991A-330-3
US-08-138-641-2
US-08-138-641-2
US-08-138-133-2
US-08-138-133-2
US-08-471-058-16
US-08-690-095-3
US-08-690-095-3
US-08-471-058-16
US-08-471-058-16
US-08-471-058-16
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Sequence 17, Appli
Sequence 8, Appli
Sequence 17, Appli
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Sequence 17, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 31355, A
Sequence 1438, Ap
Sequence 1438, Ap
Sequence 43, Appl
Sequence 23201, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 30437, A
Sequence 16, Appli
Sequence 16, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 16, Appli
Sequence 16, Appli
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7, Appli
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US-08-454-196-8
                 STRANDEDNESS:
TOPOLOGY: lir
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ZIP: 22202
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42 35.0 433 1 US-07-661-610C-2 42 35.0 519 3 US-09-172-841-55 42 35.0 519 4 US-08-951-621-55 42 35.0 888 2 US-08-951-621-56 42 35.0 888 2 US-08-396-001-6 42 35.0 888 3 US-08-396-001-6 42 35.0 2710 2 US-08-568-459A-12 42 35.0 2710 2 US-08-568-459A-12 42 35.0 2710 2 US-08-487-8268-12 42 35.0 2710 2 US-08-487-8268-12 42 35.0 2710 2 US-08-487-8268-12 42 35.0 3060 2 US-08-487-8268-14 41 34.2 16 1 US-08-248-819A-50 41 34.2 16 2 US-08-37-5646A-68 41 34.2 16 2 US-08-978-523-42 41 34.2 16 3 US-08-978-523-42 41 34.2 16 3 US-08-978-523-42 41 34.2 17 1 US-08-337-565-68 41 34.2 17 2 US-08-661-479-14	45	44	3	42	41	40	39	38	37	36	ü	4	33	32	31	30	29	
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	14, App]	14, Appl	68, App	42, App.	68, App	•	50, Appl	14, App	-	•	12, Appl	6, Appl:	6, Appl:	6, Appl	55, Appl	55, App	2, Appl	111111

ALIGNMENTS

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Sequence 8, Application US/08454196
Patent No. 5770361
                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/454,196
FILING DATE: 07-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/15671
FILING DATE: 18-DEC-1992
PRIOR APPLICATION NUMBER: FR 93/08356
FILING DATE: 07-JUL-1993
ATTORNEY/ACENT INFORMATION:
NAME: OBLON, NORMAN F:
REFERENCE/DOCKET NUMBER: 660-101-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: EVERS, STEFF
APPLICANT: COURVALIN, IE
TITLE OF INVENTION: PRC
TITLE OF INVENTION: REC
TITLE OF INVENTION: BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CTTY: ARLINGTON
                                         LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DUTKA-MALEN,
EVERS, STEFAN
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linear
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                   not relevant
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-454-196-17
RESULT 3
US-09-064-033-8
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                                                                                                                                                                                                                                                                                                     TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FR 9:
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F
REGISTRATION NUMBER: 24,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: COURVALIN, PATKICE
TITLE OF INVENTION: PROTEIN COMPERRING AN INDUCIBLE
TITLE OF INVENTION: RESISTANCE TO GLYCOPEPTIDES, PARTICULARLY IN GRAM-POSITIVE
TITLE OF INVENTION: BACTERIA
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FR 9:
FILING DATE: 18-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ARTHUR, MICHEL APPLICANT: DUTKA-MALEN, SYLVIE APPLICANT: EVERS, STEFAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 STATE: VA
                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/OFFILING DATE: 07-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
                                                        42 KDGQWVKGPLLSERPQNKEV 61
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                                                                                                                      Similarity 40.0%; Pred. No. 9
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ilarity 40.0%;
Conservative
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                                                                                                                   5; Mismatches
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US-09-064-033-17; Sequence 17, A
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Best Local Similarity
Warches 8; Conserva
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; MOLECULE TYPE:
US-09-064-033-8
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Patent No. 606, 110
Patent No. 606, 110
PATENT INFORMATION:
                                                                                                                     GENERAL INFORM
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09064033 Patent No. 6087106
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
              APPLICANT: DUTKA-MALEN, SYLVIE
APPLICANT: EVERS, STEFAN
APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE
TITLE OF INVENTION: RESISTANCE TO GLYCOPEPTIDES, PARTICULARLY IN GRAM-POSITIVE
TITLE OF INVENTION: BACTERIA
TITLE OF INVENTION: BACTERIA
TUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PROTEIN OF TITLE OF INVENTION: BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ARTHUR, MICHEL APPLICANT: DUTKA-MALEN, SYAPPLICANT: EVERS, STEFAN APPLICANT: COURVALIN, PATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ARLINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
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                                                                                                                                                                                      Application US/09064033
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1755 S.
                                                                                                                                     ARTHUR, MICHEL
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ilarity 40.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FR 93/08356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             660-101-0 PCT
                                                                                                                                                                                                                                                                                                                                                                            Length 348
                                                                                                                                                                                                                                                                                                                                          Indels
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; MOLECULE TYPE: protein US-09-064-033-17
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Patent No. 6569622
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/064,033
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FR 93/083
FILING DATE: 07-JUL-1993
ATTORNEY AGENT INFORMATION:
NAME: OBLOW, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acid
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                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PATRICE
COURVALIN, PATRICE
TO GLYCOPEPTIDES, PARTICULARLY IN GRAM-POSITIVE
RESISTANCE TO GLYCOPEPTIDES, PARTICULARLY IN GRAM-POSITIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1755 S. CITY: ARLINGTON
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                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ARTHUR, MICHEL
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8; Conserv
                                                                                                                                                                       CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 348 amino acida
amino acid
                     APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                 DUTKA-MALEN, SYLVIE
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40.0%;
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                                 Version #1.30
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i Sequence 17, Applicatic
patent No. 6569622
GENERAL INFORMATION:
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Best Local Similarity 40.0
Matches 8; Conservative
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                                                 APPLICATION NUMBER: US/09/291,046
FILING DATE: 14-Apr-1999
CLASSIFICATION: <URNOwn>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,196
FILING DATE: <UNKnown>
APPLICATION NUMBER: FR 93/08356
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                     ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:
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FILING DATE: 14-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/454,196
FILING DATE: <Unknown>
APPLICATION NUMBER: FR 93/08356
FILING DATE: 07-UUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE
RESISTANCE TO GLYCOPEPTIDES, PARTICULARLY IN GRAM-POSITIVE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-101-0 PCT
TELECOMMUNICATION INFORMATION:
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                   NAME: OBLON, NORMAN F. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                 STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1755 S.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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EVERS, STEFAN
COURVALIN, PAT
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40.0%; Pred. No. 9.
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                     24,618
660-101-0 PCT
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Query Match Best Local (Matches

TOPOLOGY:

FILING DATE:

US-09-291-046-8 RESULT 5

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                                      US-09-107-532A-5920
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Patent No. 6589275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
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Query Match
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                             NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE,DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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                                                     NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...370
SEQUENCE DESCRIPTION: SEQ ID NO: 5920:
                                                                                                             FEATURE:
                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: YES
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TYPE: amino acid
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STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02354
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                                                                                                                                                                                                  LENGTH: 370 amino acids
TYPE: amino acid
TOPOLOGY: linear
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ilarity 40.0%;
Conservative
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41.7%; Score 50;
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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 DB 4;
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Length 370;
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US-09-060-410-4
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FILING DATE: 14-APR-10^
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Matches 8; Conserv
                                                                                                               Sequence 4, Application Patent No. 6586242
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-60
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: SEED and BERRY LLP
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TITLE OF INVENTION: TAO PROT
TITLE OF INVENTION: THEREFOR
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APPLICANT: Hutchinson, Michele
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 86
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 993 amino acids
NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                          TITLE OF INVENTION:
                                                                                                  APPLICANT: Cobb, Melanie
                                                                                                                                                                                                                   888 GWVQGPVLTPVPE 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5<u>4</u>
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                                                                                                                                                                                                                                              5 GWYEGPLLEPRPD 17
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                                                                                                                                                                                                                                                                       40.0%;
Similarity 53.8%;
7; Conservation
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                                                                                                                                           Application US/09723458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (206) 622-4900
                                                                    Hutchinson, Michele
Chen, Zhu
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                                                         Kevin
                            THEREFOR
                                          TAO PROTEIN KINASES AND METHODS OF USE
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APPLICANT: Selach, Mary C.

APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Tang, Li

APPLICANT: Tang, Li

TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20029.00

CURRENT APPLICATION NUMBER: US/09/428,517

CURRENT FILING DATE: 1999-10-28
EARLIER FILING DATE: 1999-02-16
EARLIER APPLICATION NUMBER: 60/120,254
EARLIER APPLICATION NUMBER: 60/106,100
EARLIER APPLICATION NUMBER: 60/106,100
EARLIER APPLICATION NUMBER: 050/106,100
EARLIER APPLICATION NUMBER: 050/106,100
EARLIER FILING DATE: 1998-10-29

SOFTMARE: Patentin Ver. 2.1
                                                                    US-09-428-517-2
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-723-458-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-428-517-2
                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 4150
        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09428517 Patent No. 6251636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                  OTHER INFORMATION:
                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (206) 622-49
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.421
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/060,410
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       888 GWVQGPVLTPVPE 900
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7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/723,458
FILING DATE: 27-No. 6586242-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 993 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
                                                                            Description of Artificial Sequence: Recombinant Oleandolide PKS
        39.2%;
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53.8%;
    Score 47;
Pred. No.
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Pred. No. 57;
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DB 3; Length 4150; 3.9e+02;
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PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 1438
LENGTH: 76
TYPE: PRT
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US-09-252-991A-31355
                                                                         Query Match 37.1%;
Best Local Similarity 36.0%;
Matches 9; Conservative
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APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION UMMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
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Best Local Similarity
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SEQ ID NO 31355
LENGTH: 605
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Mittanck, Cindy A.
APPLICANT: Mittanck, Cindy M.
APPLICANT: Mittanck, Cindy M.
                                                                                                                                                    ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US OF PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
27 RRDGGWIESIGYYNPLSEPKDIKID 51
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5. 6573361
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                              1 QQNGGW-----YEGPLLEPRPDALD 20
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                                                                     Conservative
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IBER: US 60/074,788
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                                                                   <u>ن</u>
                                                                                  Score 44.5;
Pred. No. 1
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Pred. No. 66;
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                                                                   Mismatches
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                                                                                                DB 4;
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                                                                                                Length 76;
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CURRENT FILLE REFERENCE: 107196.136
CURRENT FILLING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILLING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20263
ENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,925
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US-09-227-357-409
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20263, Application US/09252991A Patent No. 6551795
                                       EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 60/051, 929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052, 803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052, 732
EARLIER FILING DATE: 1997-07-08
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TITLE OF INVENTION: 123 Human Secreted Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 396
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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tent No. 634258
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ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,932
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,916
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,930
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,918
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ER APPLICATION NUMBER: 60/051,920
APPLICATION NUMBER: 60/051,919 FILING DATE: 1997-07-08
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8; Conserva
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Pred. No. 82;
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; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 425

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-556-422A-7
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US-09-227-357-409
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            sequence 7, Application US/08556422A Patent No. 6576754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 409
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                    APPLICANT: SCHULTZE, Joachim L.
APPLICANT: BOUSSIOTIS, Vassiliki
APPLICANT: NADLER, Lee
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
FILE REFERENCE: DFN-005CPA2
CURRENT APPLICATION NUMBER: US/08/556,422A
CURRENT FILLING DATE: 1995-11-09
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                APPLICANT: HALL, APPLICANT: FREE
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NUMBER OF SEQ ID NOS: 672
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APPLICATION NUMBER: 60/058,664
FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/058,660
FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/055,964
FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/056,360
FILING DATE: 1997-08-18
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APPLICATION NUMBER: 60/055,950
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APPLICATION NUMBER: 60/055,948
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APPLICATION NUMBER: 60/
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SCHULTZE, Joachim L.
BOUSSIOTIS, Vassiliki
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53.3%;
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Query Match

35.8%;

Score 43;

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Matches 9; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

Cy 1 QONGGW--YEGFLIESEPDN 18

Db 180 GSTRWHTRYNGHVERFOR 193

Search completed: December 30, 2003, 11:05:33

Job time: 3 21575 secs
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Post-processing:
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Perfect score:
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Match
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1: pir1:*
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Gapop 10.0 , Gapext 0.5
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Listing first 45
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134
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Copyright (c) 1993 - 2003 Compugen Ltd.
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T28621
S26646
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A473651
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9

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	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	34.3	34.3	34.3
į	528	463	459	457	456	456	456	453	449	319	276	276	172	894	826	741
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1.1771	P71011	S29170	AH0349	897828	H85894	C91050	NCEC7	F71673	AF0820	S54100	JC4161	G83304	HIZVWM	C86756	T02753	I48694
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ALIGNMENTS

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Ig heavy chain V region - human
C;Species; Home sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: 826792
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7, A;Reference number: $26786; MUID:92111632; PMID:1730251
A;Accession: $26792
A;Status: preliminary
A;Rolecule type: mRNA
A;Residues: 1-131 <MOR>
A;Cross-references: EMBL:X61012; NID:g32804; PIDN:CAA43346.1; PID:g1335131
C;Keywords: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C/Superfamily: immunoglobulin V region; immunoglobulin homology (Keywords: heterotetramer; immunoglobulin F;1-30/Region; framework 1 region; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>F;15-98/Domain: immunoglobulin homology <IMM>F;31-35/Region: complementarity-determining 1 F;36-50/Region: framework 2 region: framework 2 region: framework 3 region: complementarity-determining 3 F;68-98/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-132 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0954
A;Sterior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
(;Species: Homo sapiens (man)
(;Date: 17-Apr-1934 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
(;Accession: PH0954
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for sommatic selection of natural autoantibodies.
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Pred. No. 0.58;
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D15R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Bate: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
C;Accession: B72175
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim vA;Reference number: A72150
A;Accession: B72175
A;Accession: B72175
                                                                                                                                            A; Notatus, r.-..
A; Molecule type: DNA
A; Residues: 1-1896 <SHC>
A; Cross-references: GB: Y16780; NID: g5830555; PIDN: CAB54796.1; PID: e1542752;
A; Cross-references: Strain Garcia-1986
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A; Residues: 1-1264 <BLI>
A; Residues: 1-1264 <BLI>
A; Residues: GB: X69198
A; Experimental source: strain India-1967, ssp. major, isolate Ind3
R; Experimental source: v.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.;
Submitted to the EMBL Data Library, April 1992
A; Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O
A; Reference number: S46868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A36859
A;Accession: A36858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G2R protein - variola virus (strain India-1967)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to GenBank, November 1992
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                                                                                             Query Match
Best Local
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;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
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Best Local Similarity
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                                                                                           Local
1559 SYEDIWKSDWPDY 1571
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                                     AYEDVWSGEYPEY 18
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ilarity 56.5%;
Conservative
                                                                                       39.6%;
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                                                                                                                                                                                                                                                                                                  the complete coding sequence of DNA of alastrim variola minor
                                                                  Score 53; DB
Pred. No. 58;
5; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 1264; 37;
                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                      V.V.; Safronov, P.F.; Massung, R.F.; Lopa:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                     Length 1896;
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                                                                  Indels
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A;Map position: 4
A;Introns: 228/2; 261/3
C;Superfamily: Caenorhal
                                                                                                                                                                                                                                      submitted to the EMBL Data
A;Reference number: Z20285
A;Accession: T26908
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T26908
                                                                                                                                                                                                                                                                                                                                  hypothetical protein Y45F10A.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex
                                                                                                   A; Gene: CESP:Y45F10A.1
                                                                                                                          C; Genetics:
                                                                                                                                                  A;Cross-references: EMBL:AL021488; PIDN:CAA16365.1; GSPDB:GN00022; CESP:Y45F10A.1
                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-292 <WIL>
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R;McMurray, A.
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R;Ohkuma, Y; Hashimoto, S.; Roeder, R.G.; Horikoshi, M.

Nucleic Acids Res. 20, 5838, 1992

A;Title: Identification of two large subdomains in TFIIE-alpha on A;Reference number: $26646; MUID:93087200; PMID:1454543

A;Accession: $26646
                                                                                                                                         A; Experimental source: clone Y45F10A
                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-433 <OHK>
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C;Species: Kenopus laevis (African clawed frog)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
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S26646
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A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60931.1; PID:g439100
A;Experimental source: strain Bangladesh 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aub. Mature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox viru A;Reference number: Z20488; MUID:94088747; PMID:8264798
A;Accession: T28621
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 GASGTQKEVWSSKGPSYEDLYTQDV
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                               Caenorhabditis elegans hypothetical protein Y45F10A.1
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    37.3%;
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    Score 50;

 Mismatches

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Pred. No. 2
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Pred. No.
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DB 2;
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Length 292;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR PELICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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SOFTWARE: FastSEQ for Windows Version SEQ ID NO 325
LENGTH: 127
Type: """
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. SEQ ID NO 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Best Local Similarity 78.9%;
                                                                                                                                                                                                                                                                                         Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/041,860 CURRENT FILING DATE: 2002-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 252
TYPE: PRT
                                                                                                                                                                                                                                                                                                       Match 73.7%;
Local Similarity 78.0%;
                                                        115
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                                                                                            121 VWGQGTTVTVSS 132
                                                                                                                                    61
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                                                                                                                                                      AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                                                                                                                                                                               QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEY-PEYYAM 119
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                                                        VWGQGTLVTVSS 126
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                                                                                                                                    AQKLQGRVTLTTDTSTSTAYMELRSLRSDDTAVYYCAR---
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                                                                                                                                                                                                                                                                                     Score 524; DB 11;
Pred. No. 3.2e-42;
7; Mismatches 16;
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Pred. No. 1.4e-42;
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FILE REFERENCE: PESSA

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/273,499

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTMARE: PACENTIN Ver. 2.0

SEQ ID NO 1921

LENGTH: 251
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                                                          US-09-880-748-973
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                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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                                                                                                                                                                    SEQ ID NO 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 973, A Publication No.
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     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ruben et al. TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                              SOFTWARE: PatentIn
                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                ENGTH: 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 EYYAMDVWGQGTTVTVSS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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5. US20030059937A1
     73.3%;
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Pred. No. 4e-42;
5; Mismatches 14; Indels 1
     Score 521
     DB
Length
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113

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APPLICATION NUMBER: 00/270, 379
PRIOR APPLICATION NUMBER: 60/212, 210
PRIOR APPLICATION NUMBER: 60/212, 210
PRIOR APPLICATION NUMBER: 60/212, 210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/212, 210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/270, 316
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276, 248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277, 379
PRIOR APPLICATION NUMBER: 60/277, 379
PRIOR APPLICATION NUMBER: 60/279, 399
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/293, 499
PRIOR APPLICATION NUMBER: 60/293, 499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
SEQ ID NOS: 3239
SOPTWARE: Patentin Ver. 2.0
SOPTWARE: Patentin Ver. 2.0
                                                                                                                          RESULT 10
US-09-880-748-1778
Sequence 1778, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
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US-09-880-748-1777
i Sequence 1777, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
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US-09-880-748-1777
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Best Local S
Matches 100
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity Matches 102; Conser
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                                                                                                                                                                                                                                                                                                            121 VWGQGTTVTVSS 132
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100; Conservative
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                                                                                                                                                                                                                                                                        VWGQGTMVTVSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.1%; Score 520; DB 11; 75.8%; Pred. No. 7.8e-42; ative 12; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.5%; Pred. No. 5.8e-42; ative 8; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 253;
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                                                                                                                                                                                                                                          ; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo s
US-09-880-748-1610
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US-09-880-748-1610
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; ORGANISM: Homo sapiens
US-09-880-748-1778
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1610
LENGTH: 257
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
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Best Local
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
VATABERS OF SECTION NOTES: 2001-05-25
                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Antibodies that Immunospecifically Bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ruben et al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 248
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                                                                                                    1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEMMGWISIYSGNTDY
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                                                                                                                                                              h 72.4%;
Similarity 77.0%;
04; Conservative
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    AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGBYPE---YY 117
                                                                              QVQLQQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                6; Mismatches
                                                                                                                                                                            Score 514.5; DB 1
Pred. No. 2.7e-41;
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Pred. No. 2.6
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                                                                                                                                                                                                DB 11;
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                                                                                                                                                          18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                              Length 257;
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TITLE OF INCURTION, Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
FRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,349
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEG ID NOS: 3239
SOFTWARE: DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-05-12
PRIOR PELLING DATE: 2000-06-15
PRIOR PELLING DATE: 2000-06-15
PRIOR PELLING DATE: 2000-06-15
PRIOR PELLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-27,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PALENTIN Ver. 2.0
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US-09-880-748-1576
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US-09-880-748-1425
                                                                                                                                                                                                                                                                                                                                                                     Sequence 1576, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-880-748-1425
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SOFTWARE:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLySFILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ruben et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 FDIWGQGTLVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 MDVWGQGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYY--A 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR---GGNY-DILTG----YYIGA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OVOLLOSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
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76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 513; DB 11; Length 249; Pred. No. 3.6e-41;
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RESULT 15
US-09-880-748-1452
US-09-880-748-1452; Sequence 1452, Application US/09880748; Publication No. US20030059937A1; GENERAL INFORMATION:
APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLy:
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR PPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-16
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION SUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1576
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SEQ ID NO 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 101; Conservative
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Publication No. US20
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                          121 VWGQGTTVTVSS 132
                                                                                                                                                                                                                                                               114 YWGQGTTVTVSS 125
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                                                                                                                                                                                                                                                                                                                                                                     AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR-----MEYDILTGYYGGYF--D
                                                                                                                                                                                                                                                                                                                                                                                                             AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLVQSGAEVKKÞGÁSVKVSCKÁSGYTFTSYGISMVRQAÞGQGLEMMGWÍSAYNGNTNY
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
CURRENT PILIK PRES23
CURRENT APPLICATION WIMBER: 05/09/880,748
PRIOR APPLICATION WIMBER: 60/212,210
PRIOR APPLICATION WIMBER: 60/212,210
PRIOR APPLICATION WIMBER: 60/276,248
PRIOR APPLICATION WIMBER: 60/276,248
PRIOR APPLICATION WIMBER: 60/277,379
PRIOR APPLICATION WIMBER: 60/273,499
PRIOR APPLICATION WIMBER: 60/27
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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452.5
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Gapop 10.0 , Gapext 0.5
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711
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1 (cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2 (cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3 (cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4 (cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5 (cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6 (cgn2_6/ptodata/1/iaa/backfiles1.pep:*
       QVQLLQSATEVKKPGASMKV.....YPEYYAMDVWGQGTTVTVSS 132
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Copyright (c) 1993 - 2003 Compugen Ltd
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                                               US-09-025-769B-36
US-09-025-769B-59
US-09-025-769B-22
US-08-264-093-3
US-08-561-521-45
US-08-561-521-45
US-08-561-521-45
US-08-562-690-22
US-08-964-690-22
US-08-964-690-22
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US-08-652-8164A-19
US-08-652-8164A-19
US-08-652-769B-57
US-08-652-769B-57
US-08-651-521-10
US-09-025-769B-57
US-08-899-575-155
US-08-899-575-155
US-08-899-575-155
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US-08-899-575-155
US-08-899-575-155
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Sequence 36, Appl
Sequence 22, Appl
Sequence 27, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 19, Appl
Sequence 115, Appl
Sequence 115, Appl
Sequence 114, Appl
Sequence 118, Appl
Sequence 118, Appl
Sequence 118, Appl
Sequence 119, Appl
Sequence 110, Appl
Sequence 115, Appl
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US-09-025-769B-36
       Matches
                                 Query Match
       Local Similarity
les 96; Conserv
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45	44	43	42	41	40	39	38	37	36	35	<u>ب</u>	U U	32	31	30	29	28
432	432	433	433	433.5	433.5	434.5	434.5	434.5	435.5	435.5	436.5	436.5	436.5	438	438	438	438
60.8	60.8	60.9	60.9	61.0	61.0	61.1	61.1	61.1	61.3	61.3	61.4	61.4	61.4	61.6	61.6	61.6	61.6
135	135	135	135	140	140	123	123	123	119	119	119	119	119	135	135	116	116
N	μ	N		4	w	N	N	-	v	N	v	w	۲	N	_	ຫ	N
US-08-436-717-112	US-08-137-117D-112	US-08-436-717-100	US-08-137-117D-100	US-09-434-122-63	US-08-836-561-63	US-08-477-989B-94	US-08-472-281A-94	US-08-477-877B-94	PCT-US95-01219-12	US-08-561-521-12	PCT-US95-11235-65	US-08-931-645-65	US-08-300-386A-65	US-08-436-717-102	US-08-137-117D-102	PCT-US95-01219-41	US-08-561-521-41
Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence
112	112	100	100	63,	63,	94,	94,	94,	12,	12,	65,	65,	65,	102	102	41,	41,
•	•	•	•	Appl					App	App	App	App	App	, Apı	, Api	App	App

ALIGNMENTS

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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-09-025-769B-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6300064
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
                                                                                                                                                                                                             TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                APPLICATION NUMBER: EP 95 11 3021.0 FILLING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 18-FEB-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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STREET: 1251 Avei
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                              LENGTH: 120 amino TYPE: amino acid
                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                 120 amino acids
                                                                                  protein
  68.2%;
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Score 485; DB 4;
Pred. No. 5.3e-39;
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                     DB 4; Length 120;
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Conservative

Mismatches

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US-09-025-769B-59
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Matches
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                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                             TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: EP 95
FILING DATE: 18-AUG-1007
ATTORNEY
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. 1
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APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Procein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                NAME: James F. Haley, Jr., REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
FILING DATE: 18-FEB
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121 VWGQGTTVTVSS 132
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                                                        AOKFOGRVIMITDISRRIAYMELRSLRSDDIAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                     QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTNY
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Ge, Liming
Geney, Simon
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Ilag, Vic
                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                             59:
                                                                                                                                               7; Mismatches
                                                                                                                                            Score 485; DB 4; Length 120; Pred. No. 5.3e-39; 7; Mismatches 17; Indel8
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US-09-025-769B-22
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
FRIGTH: 117 amino acids
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                                                                                                                                                                                               Matches
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FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esg.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                          Query Match
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APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
US/09/025,769B
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                             TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
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 106
                       121 VWGQGTTVTVSS 132
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                                                             AQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCARDGDGG
                                                                                        AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                                                              QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGNTNY
                                                                                                                                                    QVQLLQSATEVKKPGASMKVSCMASGYPPTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
YWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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Ilag, Vic
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                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                              68.1%;
72.7%;
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                                                                                                                                                                                             Score 484.5; DB 4
Pred. No. 5.7e-39;
5; Mismatches 16
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                                                                                                                                                                                                                             DB 4;
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                                                                                                                                                                                                                             Length 117;
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RESULT 4 US-08-264-093-3

Sequence 3, Application US/08264093 Patent No. 5639863 GENERAL INFORMATION:

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US-08-561-521-45
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                                                                                     GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: H
TITLE OF INVENTION: OF INVENTION: A
NUMBER OF SEQUENCES.
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NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
ADDRESSEE: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS: not
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                                                                                                                                                                                                                                                                                                                                                    110
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                   San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                  VWGQGTTVTVSS 132
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California
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HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
CELL CYCLE-INDEPENDENT GLIOMA SURPACE
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72.0%; Pred. No. 2.2e-38;
tive 11; Mismatches 15
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US-08-525-539A-77
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SEQUENCE CHARACTERISTICS:
LENGTH: 129 amin
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                           APPLICANT: DO COUTO, FE.
APPLICANT: CERIANI, ROB
APPLICANT: ETERSON, JE.
TITLE OF INVENTION: REC
TITLE OF INVENTION: MC3
TITLE OF INVENTION: MC3
TITLE OF INVENTION: MET
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
                                                            ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/525,539A FILING DATE: 14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 415-543-9600
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                 STATE:
                                                                                                                                                                             STREET: 755 Pag
CITY: Palo Alto
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                COUNTRY:
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                                                                                                                                                                                              755 Page Mill Road
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                                                                                                                                                                                                                                              METHODS OF HUMANIZING ANTIBODY PEPTIDES 81
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                                                                                                                                                                                                                                                                                                                                                FERNANDO J.R.
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PCT-US95-01219-45
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
"ENGTH: 129 amino acids
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NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 2763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
               TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
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APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
SEQUENCE CHARACTERISTICS:
                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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STRANDEDNESS: sir
                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 25-JAN CLASSIFICATION:
                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
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linear
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                                                                                                                                                                                                                                        UMBER: PCT/US95/01219
25-JAN-1995
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                 45:
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                                                                                                                      TELEFAX: 415-320 IN TELEFAX: 415-320 IN NO: 22: INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: FUNCTH: 128 amino acids
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Best Local Similarity
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APPLICANT:
                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Rcl-ease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
CLASSIFICATION: 424
CLASSIFICATION: 424
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BENDIG, Mary M.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                          TELEPHONE: 415-326-2400
                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                        FEATURE:
                                                                                             TENGTH: 128 amino
TYPE: amino acid
STRANDEDNESS: sinc
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 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                     LOCATION:
                                  NAME/KEY: Protein
                                                                                     TOPOLOGY:
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One Market Plaza, Steuart Tower, Suite 2000
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SALDANHA, Jose W.
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                                                                                       linear
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                                                                       protein
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                                                                                                      single
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/label= HUMAN_I
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US-08-964-690-22
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         Best Local Similarity Matches 95; Conserv
                                           Query Match
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                                                                                                                                                                                                                  TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local S
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                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 25-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CHESNUT, Robert W. APPLICANT: POLLEY, Margaret J. APPLICANT: PAULSON, James C. APPLICANT: JONES, S. Tarran APPLICANT: SALDANHA, JOSE W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                NAME/KEY: Protein LOCATION: 1.128 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF
                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 22, APP-
NO. 6033667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVENTION: Antibodies to P-Selectin and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCARAPGYGSGGGCYRGDY-----F 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OVOLVOSGAEVKKÉGASVKVSCKÁSGYTETSYAISWVRÓAPGÓGLEWMGWINPYGNGDTN 60
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                                                                                                                                                                                                     128 amino acids
         Conservative
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                                                                                                                                              protein
                                                                                                                                                                      single
66.9%; Score 476; DB 3; Length 128; 71.4%; Pred. No. 4.1e-38; cive 11; Mismatches 21; Indels
                                                                             /label= HUMAN_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.9%; Score 476; DB 1; 71.4%; Pred. No. 4.1e-38; tive 11; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                         US/08/202,047
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 Gaps
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2;
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APPLICANT: Jonak, Zdenka L.

APPLICANT: Taylor, Alexander H.

APPLICANT: Trulli Jr., Stephen H.

APPLICANT: Trulli Jr., Stephen H.

APPLICANT: Johanson, Kyung O.

ITILE OF INVENTION: Humanized Monoclonal Antibodies

FILE REFERENCE: 950860

CURRENT APPLICATION NUMBER: US/09/199,149

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-08-652-816A-19
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US-09-199-149-3
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                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: OBbourn, JK

APPLICANT: Allen, DJ

APPLICANT: McCafferty, JG

TITLE OF INVENTION: Specific binding members, materials and

TITLE OF INVENTION: methods.

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESS:
                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/08652816A Patent No. 5872215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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COUNTRY: United States of America
COMPUTER READABLE FORM;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 125
TYPE: PRT
                                                                                                    STREET: 6300 Sea
CITY: Chicago
STATE: Illinois
COUNTRY: United:
                                                                                                                                                                        ADDRESSES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YAQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCARAPGYGSGGGCYRGDY-----F 115
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                                                                                                                                                   6300 Sears Tower,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ÓVQLVQSGABVKKÞGASVKVSCKASGYTFTSYA I SWVRQAÞGQGLEWNGW I NÞYGNGDTN
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                                                                                                                                                   Marshall, O'Toole,
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71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Pred. No. 1.1e-37;
8; Mismatches 18;
                                                                                                                                            Gerstein, Murray &
South Wacker Drive
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RESULT 12
US-08-933-983-21
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US-08-652-816A-19
                                                                                                                                                                                                     Sequence 21
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATE: 01-JUN-13.

ATTORNEY/AGENT INFORMATION:

NAME: David W. Clough

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 28111

TELECOMMUNICATION INFORMATION:

TRI.EPHONE: 312-474-6300

TRI.EPHONE: 312-474-6300

TRI.EPHONE: 312-474-6300
                                                                                                                                                                                        GENERAL
                                        APPLICANT: REED, GUY L
APPLICANT: HARRIS, LINDA
APPLICANT: HARRIS, LINDA
APPLICANT: BAJORATH, JURGEN
APPLICANT: MATSUEDA, GARY
APPLICANT: HSU, MEI-YIN
APPLICANT: NOVOTRY, JIRI
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING
TITLE OF INVENTION: FIBRINOLYSIS
                     CORRESPONDENCE
                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
FILING DATE: 02-DEC-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 23-MAY-
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APPLICATION NUMBER:
FILING DATE: 07-DEC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
FILING DATE: 23-MAY-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/244,597 FILING DATE: 01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 02-DE
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    Application US/08933983
    6114506

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                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
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                                                                                                                                                                                                                                                                                                      VWGQGTMVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                    AQKFQGRVTMTTDTSTSTAYMELRSLRSEDTAVYYCAGRRGGFRFR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 amino acids
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STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                   ADDRESS
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02-DEC-1992
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23-MAY-1996
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07-DEC-1995
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23-SEP-1992
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Pred. No. 5.2e-37;
5; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28111/33308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 120;
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RESULT 13
US-08-545-809A-105
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                                                                                                                                                                                                                                                                                                                        Sequence 105, Application US/08545809A Patent No. 6096878
                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTINUES OF SEQUENCES: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 20-SEICLASSIFICATION: 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: GOLDSTEIN, JORGE A
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 19-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1100 NEW CITY: WASHINGTON
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65.2%; Pred. No. 7.5e
ative 14; Mismatches
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Best Local Similarity
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                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,877C
FILING DATE: 03-JUN-1994
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tent No. 577300;
                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
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                                                                                                                                                                                                                                                                               STATE: New Jersey COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                  CITY: Wayne
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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TOPOLOGY: lino-
LECTION
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REGISTRATION NUMBER:
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REFERENCE/DOCKET NUMBER: 06501/004001
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Weiss, Martin J.
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Hallett, William
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27-MAR-1996
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der, Irwin
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                                      32,368
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RESULT 15
US-08-452-164A-19
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          Query Match
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                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE PC-DOS/MS-DOS SOFTWARE: PATENTIAL RELEASE #1.0, VE CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/452,164A FILING DATE: 26-MAY-1995 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: BETINATION NUMBER: 31,088 PERFENTATION NUMBER: 31,088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5877296
GENERAL INFORMATION:
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Best Local Similarity 65.2
Marches 86; Conservative
                                                                                                                                                        TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO:
                                                        TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: American |
STREET: One Campus D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Conjugates of Methyltrithic Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
                                                                     STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Parsippany
STATE: New Jersey
COUNTRY: U.S.A.
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amino acid
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Weiss, Martin J.
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Hollander, Irwin
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Hallett, William
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63.0%; Score 448;
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                                                                                                                                                                                                                                                                                                                    US/08/452,164A
                                                                                                                                                                                                                        32,368-04
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Title:
Perfect score:
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Maximum
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     Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being possessions.
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     derived by analysis
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.
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Maximum Match 100%
Listing first 45 summaries
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A;Cross-references: EMBL:Z12316; NID:g32855; PIDN:CAA78186.1; PID:g32856 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>

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Query Match Local

Similarity

87.5%; 87.8%;

Length 98;

30	382	73.3	118	N	PH1666	Ιg	heavy	chain	
31	381	73.1	142	N	A32483		heavy	chain	V r
32	380	72.9	171	N	S23623		heavy	chain	< r
33	379	72.7	98	N	PH0871		heavy		۷ r
34	378	72.6	119	N	JN0295	Ig	heavy		V-D
35	377	72.4	116	N	S31667		heavy	chain	۷ r
36	377	72.4	117	-	HVHU35		heavy	chain	pre
37	377	72.4	120	N	S31999		heavy		V'r
38	377	72.4	135	N	B32274		heavy		pre
39	376	72.2	126	N	I44151		heavy	chain	< r
40	372	71.4	98	N	S24680		heavy	chain	٧1
41	370	71.0	98	Ν	S26921		heavy	chain	V r
42	369	70.8	104	N	PH1665	Ιg	heavy	chain	< r
43	369	70.8	109	Ν	PH1668		heavy	chain	V r
44	367	70.4	98	N	\$26915		heavy	chain	V r
45	367	70.4	116	N	S31698		heavy	chain	pre
					ALIGNMENTS				
RESULT 1 S26919									
Ig heavy chain V region	hain V		(DP-14)		 human (fragment) 				
C;Date: 22-Nov-1993 #se	-Nov-1		nence.	re	#sequence_revision 10-Nov-1995 #tex	#text_change	e 23-	23-Jul-1999	99
R; Tomlinson, I.M.;	n, I.M.;	i; Walter,		3	G.; Marks, J.D.; Llewelyn, M	M.B.; Winter.		<u>ဂ</u>	
J. Mol. Biol. 227, 776-798, 1992	01. 22	7, 776-7	98, 1	992					
A, Title: T	he rep	റ	of hu	nan	oire of human germline V(H) sequences	s reveals	le about		fifty groups
A; Reference number:	e numb		85; M	gib	:93021117; PMID:1404388				
A:Status: preliminary	prelim	inary							
A; Molecule type:	type:	DNA							
A;Residues: 1-98 <t< td=""><td>: 1-98</td><td>Ŕ</td><td>. 9133</td><td>5</td><td>M></td><td></td><td>313.233056</td><td>2</td><td></td></t<>	: 1-98	Ŕ	. 9133	5	M>		313.233056	2	

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C; Keywords: .....
F; 15-98/Domain:
                                                      A;Residues: 1-129 <GRI>
A;Cross-references: EMBL:Z18851; NID:g33124; PIDN:CAA79303.1; PID:g939903
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                             C;Accession: S36260
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, CEMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; EMID:7679990
A;Accession: S36260
                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                              RESULT
S36260
                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA
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                                        immunoglobulin homology <IMM>
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    Score 453;
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Pred. No. 1.7e-39;
4; Mismatches B
    BB
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Length 129;
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A;Molecule type: mRNA
A;Residues: 1-40, 'GLSGWDGSALTMVTQSILDK',61-118,'T',120-124 <JON>
A;Residues: 1-40, 'GLSGWDGSALTMVTQSILDK',61-118,'T',120-124 <JON>
A;Residues: The difference for residues 41-60 results from misplacement of 10 |
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotettamer; immunoglobulin
F;15-98/Dcmain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                           submitted to the EMBL Data Library, A:Reference number: $24442 A;Accession: $24442
                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-124 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                      A;Title: By-passing immunization. Human antibodies from V-gene A;Reference number: S19663; MUID:92085276; PMID:1748994 A;Accession: S19665...
                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Marks, J.D.; Hoogenboom, H.R.; Bonnert, J. Mol. Biol. 222, 581-597, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region (alpha-phOx15) - human (fragment)
C:Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C:Accession: S19665; S24442
                                                                                                                                                                                                                                                                                                                    R;Jones,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36271
A;Status: preliminary; nucleic acid sequence not shown
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             Query Match
Best Local S
Matches 85
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    Score 450; DB 2;
Pred. No. 9.1e-39;
3; Mismatches 10
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Pred. No. 7.1e-39;
4; Mismatches 8;
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                                                                                                                                                                                                                                                                                    October 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T.P.; McCafferty, J.; Griffiths, A.D.; Winter
    10;
                                           Length 124
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R/Silberstein, L.E.; Litwin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1989

A;Title: Relationship of variable region genes expressed by a human B cell lymph, Reference number: PL0106; MUID:89235583; PMID:2541221

A;Reference number: B10105

A;Rolecule type: mRNA

A;Residues: 1-160 <SIL>
A;Note: the authors translated the codon GAC for residues 108 and 109 as Glu C;Comment: The antibody is one of the cold agglutinins that preferentially bind C;Keywords: autoantibody; hemagglutinin

C;Keywords: autoantibody; hemagglutinin

C;Keywords: autoantibody; hemagglutinin

C;Keywords: autoantibody; hemagglutinin

C;Keywords: immunoglobulin V region; immunoglobulin homology

F;J4-117/Domain: signal sequence #status predicted <SIG>
F;J4-117/Domain: immunoglobulin homology 
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                                                                                                                                 F;118-131/Domain: D region cDRG>
F;132-144/Domain: J4 segment <JS
F;145-160/Domain: C region <CRG>
                                                                                                                                                                                              F;49-54/Region: complementarity-determining F;69-84/Region: complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-PR2 erythrocyte autoantibody heavy chain precursor - human (fragment)
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-131 <FRI>
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Best Local (
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Similarity 82.7%;
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                                                      Conservative
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                                                                        82.1%;
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                                                    6,
                                                                   Score 428; DB 2;
Pred. No. 2.1e-36;
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Pred. No. 6.5e-37;
                                               Mismatches
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                                                                                      Length 160
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                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region (DP-15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26918
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26918
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-111 <FRI>
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A; Accession: S21925
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                                                               AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR
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78.6%;
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                                                                                                                                                                                                             Score 407; DB 2; Length 98; Pred. No. 1.7e-34;
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Pred. No. 9.1e-36;
4; Mismatches 8; Indels
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A; Residues: 20-117 < TOM>
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A; Residues: 1-117 <SHI>
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AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR 117
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A;Molecule type: mRNA
A;Residues: 1-136 <CUI>
A;Residues: 1-136 <CUI>
A;Crose'references: BMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, submitted to the EMBL Data Library, June 1992 A;Description: Mechanisms that generate human immunoglobulin diversit. A;Reference number: S31585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin hom C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin P;i-19/Domain: signal sequence #status predicted <SIG>F;20-117/Product: Ig heavy chain V region (VI-3b) #status F;34-117/Domain: immunoglobulin homology <IMM>
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Ig heavy chain V region precursor (VI-3b) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18553; 826916
C;Accession: Maranda. F.: Naqaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A/Cross-references: EMBL:X62109

R/TOMINSON, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Blol. 227, 776-798, 1992

A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups

A;Reference number: S26885; MUID:93021117; PMID:1404388

A;Accession: S26916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Pukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E., EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: A;Reference number: $18551; MUID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: translation not shown
61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                             61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAR
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78.6%;
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78.6%;
                                                                                                                                                                         9;
                                                                                                                                                                    Score 407; DB 2;
Pred. No. 2.4e-34;
9; Mismatches 12
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Pred. No. 2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                 Length 136;
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Ig heavy chain V region - human (fragment)
N;Alternate names: anti-cytomegalovirus glycoprotein B antibody
C;Species: Homo sapiens (man)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C;Accession: S68170
R;Boeldicke, T; Hasse, B. Boecher, M.; Lindenmaier, W.
A;Title: Human monoclonal antibodies to cytomegalovirus. Characterization and r.
A;Reference number: S68170; MUID:96128166; PMID:8536681
A;Accession: S68170
A;Status: preliminary
A;Kolecule type: mRNA
A;Ressidues: 1-125 <BOE>
A;Cross-references: GB:S80750; NID:g1246061; PIDN:AAB35861.1; PID:g1246062
C;Superfamily: immunoglobulin
C;Keywords: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                         RESULT
S31680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region (DP-75) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-193 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: $26938
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups
A;Reference number: $26885; MUID:93021117; PMID:1404388
A;Accession: $26938
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A;Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, iC;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Best Local S
Matches 75
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Best Local
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Pred. No. 3.5e-34;
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A;Title: Physical map of the 3' region of the human immunoglobulin A;Reference number: S18551; MUID:92037524; PMID:1935893
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S18551
                                                                                                                                                                                                                                                                C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG>F;20-117/Product: Ig heavy chain V region (VI-2) #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832 R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, J. Exp. Med. 175, 831-842, 1992 A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors A;Reference number: S23623; MUID:92156804; PMID:1740665
                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
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A; Residues: 1-117 < OLE>
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A; Residues: 1-117 <SHI>
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1955 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18551; S23625
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-117 <CUI>
A;Cross-references: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796
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A;Description: Mechanisms that generate human immunoglobulin diversity operate from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
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A; Accession: S31680
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                                                                                                                                                                                        Similarity
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                               AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                      QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                           QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY
AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAR 117
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Pred. No. 8.2e-34;
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Title:
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Sequence:
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Maximum Match 100%
Listing first 45 summaries
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                Score
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1 QVQLLQSATEVKKP
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HV1B HUMAN

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AC P01743;

DT 21-JUL-1986

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DT 15-CSE-2026
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ALIGNMENTS

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Searched:

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NCBI_TaxID=9606;	2
C Mammalia; Eutherja: Primaros. Catarrhin: Vertebrata; Euteleostomi;	88
Fukarvota: Metazon Charles	2 6
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Pfam; PF00047; ig; 1,
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SMOSITE; PS50835; IG LIKE;
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HV1C_HUMAN
P01744;
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16-OCT-2001
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01-NOV-1991 (Rel. 20
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Id heavy chain V-I I
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GO; GO
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MEDLINE=88296408; PubMed=2841108;
Matsuda F., Lee K.H., Nakai S., S
Ohno H., Fukuhara S., Honjo T.;
"Dispersed localization of D segn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30; GO:00055/6; C:extracellular; NAS.
30; GO:0003823; F:antigen binding activity; NAS.
GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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EMBO J. 7:1047-1051
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Homo sapiens (Human)
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Pred. No. 5.1e-37;
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                                               01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat.
Ig heavy chain V region VH558 Al/A4 precurs
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Rodentia; Sciurognathi;
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SEQUENCE FROM N.A.
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
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GO; GO:0003823; F:antigen binding activity; NAS
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007711); Ig-like
InterPro; IPR003006; Ig_MHC.
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(In) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.:
Marcel Dekker, New York (1978).
-i- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110;
InterPro; IPR003006;
InterPro; IPR003596;
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HSSP; P01789; IMCP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and sequence determination of the gene for immunoglobulin epsilon chain expressed in a myeloma Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                    APRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAK 117
                         AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
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Pred. No. 8.3e-35;
3; Mismatches 19
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IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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|l line.";
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                                                                                                                                             Gaps
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Murinae; Mus

precursor

update)

PRT;

117

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RESULT 5
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Best Local
      MEDLINE=71064027;
Gall W.E., Edelman
"The covalent stru
                                                                                                                                                                                     HVIA HUMAN STANDARD;
P01742;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
                                                       "The covalent structure of a human gamma acid sequence of heavy-chain cyanogen brobiochemistry 9:3161-3170(1970).
                                                                       "The
acid
                                                                                       Cunningham B.A., Rutish Waxdal M.J., Edelman G.
                                     DISULFIDE BOND
                                                                                              MEDLINE=71064024; PubMed=5489771; Cunningham B.A., Rutishauser U.,
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                           HUMAN
                                                                                                                           SEQUENCE.
                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                   Ig heavy chain V-I region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003906; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unrearranged VH gene segments."; Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=85099340; PubMed=2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unrearranged VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mmunoglobulin
     l W.E., Ede
e covalent
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                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                    QVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPGQGLEWIGWIYPGDGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50835; IG LIC.
                Edelman
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X
                       PubMed=4923144;
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68
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 human gamma
                                                                                                                                                                                                                                                                                                                                                                                           Score 340; DB 1
Pred. No. 1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY-DETERMINING-2 FRAMEWORK-3.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION VH558 A1/A4.

FRAMEWORK-1.

COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                            8B0BC138856DFC9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                              Gall W.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY
                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                          117
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                                                             nma G-immunoglobulin. VII. Amino
bromide fragments H1-H4.";
                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
G-immunoglobulin.
                                                                                                                                                                                                                                         ₿
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                                                                                               Gottlieb
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 117
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Best Local S
Matches 66
                                                                                                                                                                                               PIR; A02022; GIMSAA.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                  Capra J.D., Nisonoff A.;
"Structural studies on induced antibodies with defined idiotypic specificities. VII. The complete amino acid sequence of the heavy chain variable region of anti-p-azophenylarsenate antibodies from mice bearing a cross-reactive idiotype.";

J. Immunol. 123:279-284(1979).

-I-MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVED THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CH.
                           DOMAIN
NON_TER
                                                                                                                                        Pfam; PF00047; ig; 1
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region (Anti-arsonate antibody).
Mus musculus (Mouse)
                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
STRAIN=A/J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=79195438; PubMed=109536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                         mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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DISULFID
NON TER
SEQUENCE
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SMART; SM00406; IGv; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Pyrrolidone carboxylic acid.

DOMAIN

1 112

IG-LIKE.

PYRROLITHONE CARBOXYLIC P
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A90563; G1HUEU.
HSSP; P01772; 2FB4.
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.PR0035.
.PR0035.
.047; ig; 1.
.M00406; iGV; 1.
.PS50835; IG LIKE; 1
.PS50835; IG LIKE; 1
.PST0835; IG LIKE; 1
.PS
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56; Conservative
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117
117 AA;
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                                               IG-LIKE.
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Pred. No. 1
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RESULT 7
HV14 M
HV045
ID HV045
ID HV14 M
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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MGD; MGI:96486; Igh-VJ558.
InterPro; IPR003006; Ig_MIC.
InterPro; IPR003006; Ig_MIC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PRO0047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J00488; AAA38519.1; -. PIR; A02041; HVMS8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=81245215; PubMed=6789211;
Givol D., Zakut R., Effron K., Rechavi G., Ram D., Coh
"Diversity of germ-line immunoglobulin VH genes.";
Nature 292:426-430(1981).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region 108A precursor.
IGH-VJ558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P01758;
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                                                                               AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                    NOKEKSKATLTVDNSSSTAYMELSSLTSEDSAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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117
117
                                                                                                                                                                                                                                                                                  62.6%; Score 326; DB 1;
larity 60.2%; Pred. No. 4.5e-31;
Conservative 16; Mismatches 22
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                                                                                                                                                                                                                                                                                                                                                                                                             12972 MW; 428CB44DF25D1BC2 CRC64;
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Rodentia;
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Pred. No. 4.4e-31;
.7; Mismatches 18
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                 Length 117
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RESULT 9
HV04 MOUSE
TO HV04 MOUSE
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HV03 MOUSE
ID HV03 MOUSE
AC P01747;
DT 21-JUL-1986 0
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Best Local
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Interpro; IPROUSSE.
Pfam; PPO0047; 1g; 1.
SMART; SM00406; IGv; 1.
SMART; SS0835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
Tmmunoglobulin V region; Hybrid
                                                                                                                                                                        P01748;
P01748;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
~~ heavy chain V region 23 precursor.
                Baltimore D.;
"Heavy chain variable region
antibodies: somatic mutation
Cell 24:625-637(1981).
                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6;
STRAIN=C57BL/6;
MCDLINE=81234548; PubMed=6788376;
Mothwell A.L.M., Paskind M., Reth M.,
                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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NON TER
SEQUENCE
                                                                                                                                        NCBI_TaxID=10090;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1023-1032(1982).
-I- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME (TRANSPORTED TO THE SAME).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=83131846; PubMed=6186498;
Siekevitz M., Gefter M.L., Brodeur P.,
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-!- SIMILARITY: COL
HSSP; P01789; 1MCP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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21-JUL-1986 (Rel. 01, Last seq
15-SEP-2003 (Rel. 42, Last ann
19 heavy chain V region 36-65.
    MISCELLANEOUS:
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120 AA;
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13307 MW; FF04E4A167B654AF CRC64;
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  GERMLINE
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annotation update)
                       contribution to the NPb evident in a gamma 2a va
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Pred. No. 4.6e-31;
B; Mismatches 20
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                 PRT;
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 GENE BELONGS
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                                                                 Imanishi-Kari T.,
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 SET OF CLOSELY
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                        variable region.";
                                                                                                                                                                 Euteleostomi;
                                       family of
                                                                                                                                                 Murinae; Mus
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                                                                 Rajewsky
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Best Local S
Matches 61
                                                                                              EMBL; J00493; AAA38128.1;
PIR; A94264; HVMSG7.
HSSP; P01810; 2FBJ.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03096; Ig_MHC.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; ig; 1.
3MART; SMON400
                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                             use by non-profit institutions as modified and this statement is not reentities requires a license agreement
                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                 "Somatic mutation in genes for the variable portion immunoglobulin heavy chain."; Science 216:309-311(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=82152818;
Sims J., Rabbitts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capra J.D.;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region 93G7 precursor.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RELATED GENES T
PIR; A02030; HVMS23
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROSITE; PS50835; IG LIKE; 1.
mmunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AQKFQGRVIMITDISRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEKFKSKVTLTVDKSSSTAYTQLSSLTSEDSAVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OVOLOOPGTELVKPGASVKLSCKASGYTETSYWMHWVKORPGOGLEWIGNINPGNGGTNY 79
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,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=6801765;
T.H., Estess P.,
                                                                                                                                                                                             institutions as long as its content is in no way atement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THAT COULD ENCODE V REGIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 325;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V REGION 23.

FRAMEWORK-1.

COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Slaughter C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325; DB 1;
No. 5.9e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPB ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                          of.
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                                                                Query Match
Best Local S
Matches 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPREER
                                                                                                                                                                                                                                                                                                                                                                                                                                HV09 MOUSE
P01753; P11271;
1 21-JUL-1986 (Rel. 01, Created)
T 01-JUL-1989 (Rel. 11, Last sequence update)
T 15-JUL-1999 (Rel. 38, Last annotation update)
T 15-JUL-1999 (Rel. 38, Last annotation update)
T 15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                       NON TER
                                                                                                                DOMAIN
DISULFID
NON_TER
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Immunoglobulin V region; Hybrid
SIGNAL 1 19
CHAIN 20 140
DOMAIN 20 139 IO
NON TER 140 NA; 15514 MW;
                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                     SIGNAL
                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                            PIR; D90809; HVMS61.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                    antibodies: somatic n
Cell 24:625-637(1981)
                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                      ROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                        Heavy chain variable region contribution to the NPb family antibodies: somatic mutation evident in a gamma 2a variable
                                                                                                                                                                                                                                                                                                                                                          WEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                 Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                            MISCELLANEOUS: THIS GERMLINE GENE BELONGS RELATED GENES THAT COULD ENCODE V REGIONS
                         20
                                                                                                                                                                                                                           PF00047; ig; 1; SM00406; IGv;
                                                                59;
                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
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AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                   QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEMVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
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69
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41
                                                               Conservative
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54
68
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117
115
                                                                                                  12890 MW; 16191A088CB17F5A CRC64;
                                                                       61.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15514 MW;
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59.2%;
                                                              15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                     Score 319;
Pred. No. 2.
                                                                                                                                 COMPLEMENTARITY-DETERMINING-2 FRAMEWORK-3.
                                                                                                                                                    IG HEAVY CHAIN V REGION 186-1.

FRAMEWORK-1.

COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                         Reth M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 324;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG HEAVY CHAIN V REGION 93G7 IG-LIKE.
                                                          Mismatches
                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25A4CBBE31DA5CE8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                       Imanishi-Kari T.,
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                                                          DB 1; I
2.9e-30;
les 24;
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.5e-31;
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                                                                          Length 117;
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                                                         Indels
                                                                                                                                                                                                                                                                                                      SET OF CLOSELY
                                                                                                                                                                                                                                                                                                                       variable
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                                                                                                                                                                                                                                                                                                                                                      Rajewsky
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                                                                                                                                                                                                                                                                                                                        region.";
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Best Local S
Matches 58
                                                                                                                                                                             HV06 MOUSE STANDARD; PRT; 117
P01750; P01750; Pr17-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence updat
15-UUL-1999 (Rel. 38, Last annotation updat
15-UUL-1999 (Rel. 38, Last annotation updat
15 Heavy chain V region 102 precursor.
Mus musculus (Mouse).
Ekkaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Rodentia; Sciurognat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dildrop R., Bovens J., Siek
"A V region determinant (id
lymphocytes is encoded by a
EMBO J. 3:517-523 (1984).
PIR; A02040; MHMS38.
HSSP; P01789; IMCP.
                                                         STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M.,
"Heavy chain variable antibodies: somatic mu Cell 24:625-637(1981).
                                                       Baltimore D.;
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
DISULFID
NON_TER
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                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1988 (Rel. 06, Created 01-JAN-1988 (Rel. 06, Last se 15-JUL-1999 (Rel. 38, Last an Ig heavy chain V region AC38 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=84182519; PubMed=6201362; Dildrop R., Bovens J., Siekevitz M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                             NOKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVŐLQÓSGPÉLVKPGÁSVKISCKÁSGYTFTDYYMNWVKOSHGKSLEWIGDINPNNGGTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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99
105
22
118
118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      835; IG_LIKE;
n V region.
1 98
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                   mutation
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118
96
118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12934 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 315; DB
Pred. No. 8.7e.
16; Mismatches
             contribution to the evident in a gamma 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               large set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY CO
                                                                                                                                                                                 Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94F7BEE4C762A018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ., Beyreuther K., Rajewsky K.;
expressed at high frequency in B
set of antibody structural genes.";
                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                   Imanishi-Kari T.,
                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118
                                                                                                                                                                               Vertebrata; E
thi; Muridae;
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Dildrop R., Bovens J., Siekevitz M., B.
"A V region determinant (idiotope) exp:
lymphocytes is encoded by a large set of EMBO J. 3:517-523(1984).
PIR; A02037; MHMS15.
HSSP, P01810; 2FBJ.
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InterPro; IPR003006; Ig MHC.
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Pfam; PF00047; ig; 1
SMART; SM00406; IGv; 1.
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01-JAN-1988 (Rel. 06, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig heavy chain v region AC38 15.3.
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Mammalia; Eutheria; Rodentia;
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HSSP; P01810; 2FBJ.
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              l Similarity
57; Conserv
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Score 314; DB 1;
Pred. No. 1.2e-29;
6; Mismatches 25
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BY SIMILARITY.
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                                                                                                         914453F426F09834 CRC64;
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HV05_MOUSE
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InterPro; IPR007710; Ig-like.
InterPro; IPR003706; Ig-MHC.
InterPro; IPR003596; Ig_V.
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                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                            EMBL; J00536; AAA38605.1; -. PIR; A02031; HVMS3. HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV05-MOUSE STANDARD; PRT; 117 AA. P01749; 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
19 heavy chain v region 3 precursor.
IGH-VJ558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
        20
                                                             58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
                                                                        Similarity
              QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
OVQLQQPGAELVRPGSSVKLSCKASGYTFTSYWMDWVKQRPGQGLEWIGNIYPSDSETHY
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117 AA;
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ilarity 59.2%;
Conservative 1:
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86
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68
85
117
117
                                                                                                             13016 MW;
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                                                          15;
                                                    Score 313; DB 1; Length 117;
Pred. No. 1.5e-29;
5; Mismatches 25; Indels
                                                                                                                                                    IG HEAVY CHAIN V REGION 3.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                       BY SIMILARITY.
                                                                                                            427C861C53975EDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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                                                   Gaps
 79
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61 AQKFQGRV[MTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
|||:::|:|| ||||:||||:||||||||
80 NQKFKDKA[LTVDKSSSTAYMQLSSLTSEDSAVYYCAR 117
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Search completed: December 30, 2003, 10:55:49 Job time : 5.25426 secs

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Result
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Maximum DB
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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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73.7
73.7
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69.7
68.7
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64.3
63.3
63.3
63.3
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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521
1 QVQLLQSATEVKKPGASMKV......AYMELRSLRSDDTAVYYCAR 98
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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sp_organelle:*
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sp_mammal:*
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Q925S3
Q91WT1
Q9Y298
Q9Y298
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Q9GYZ2
Q8WY24
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Q9UL94
Q9BRV0
Q9UL92
Q9GA6
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Q9u192 homo g
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Best Local S
Matches 72
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HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=98277139; PubMed=9614934;

Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

Young D.C.;

"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035019; AAD56255.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                            72;
Similarity
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125 AA; 13516 MW;
                                                                                                                                                                                73.9%; Score 385; DB 4; Length 125; ilarity 73.5%; Pred. No. 7.3e-35; Conservative 10; Mismatches 16; Indels
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79 60

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Query Match
Best Local S
Matches 72
                           SEQUENCE FROM N.A.

TISSUE=Prostate;

Strausberg R.;

Submitted (APR-2001) to the E
EMBL; BC005951; AAH05951.1; -
HSSP; P01789; IMCP.
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Q9UL94;
Q9UL94;
Q9UL94;
Q9UL94;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 23, Last sequence update)
Q1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                            Q9BRVO; PRELIMINARY;
Q9BRVO;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                         Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia, Eutheria; Primates;
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SEQUENCE
                                                                                                                                                       NCBI_TaxID=9606;
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MEDLINE=98277139; PubMed=9614934;
Wan der Merwe P.L.,
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HSSP; P01810; 2FBJ
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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[1]
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AF035020; AAD56256.1; -.
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         IPR007110;
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119 AA;
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         Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.7%; Score 384; DE 73.5%; Préd. No. 8.96 tive 10; Mismatches
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Last sequence update)
Last annotation update)
                                                               EMBL/GenBank/DDBJ
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Q9UL92
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Best Local S
Matches 72
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
NON TEP
Q96GA6;
Q96GA6;
01-DEC-2001
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50290; IG_MfC; 1.
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Q9UL92;
01-MAY-2000
01-MAY-2000
01-MAR-2003
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NON_TER
SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE=98277119; PubMed=9614934;
Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol.
EMBL; AF035022; AAD56258.1; -
HSSP; P01772; 2FB4.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                  72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                            Similarity 73.5
72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71;
                                                                                                                                                                                               Similarity
                                                                                                                            AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
                                                                                                                                                   AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKKFOGRVTLTTDTSTSTVYMELRSLRSDDTAVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                       124 AA;
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 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                          124
                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3MBLrel. 13, Last sequence update)
BMBLrel. 23, Last annotation update)
immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                       13580 MW;
                                                                                                                                                                                                                                                                                               72.6%;
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19,
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                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                        Score 378; DB 4;
Pred. No. 4.3e-34;
10; Mismatches 16
 Created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 382; DB 4;
Pred. No. 8.2e-34;
9; Mismatches 18
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; 
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                     1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rheumatic
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                                   614
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                                                                                                                                                                                                                                                                            16;
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Best Local S
Matches 69
                                             Query Match
Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2001) to the EMB EMBL; BC009851; AAH09851.1; ... InterPro; IPR000005; HTHATAC. InterPro; IPR007110; Ig-like. InterPro; IPR003106; Ig_MHC. InterPro; IPR003596; Ig_WHC. InterPro; IPR003596; Ig_V. pfam; PF00047; 19; 5. SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Hypothetical protein.
                                                                                                                                   "Homo sapiens putative microfibrillar protein with Ig-like mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3)."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AY039025; AAK82649.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003066; Ig_MHC. InterPro; IPR003596; Ig_V. Pfam; PF00047; ig: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                Q96QS0 PRELIMINARY; PRT; 159 AA.

Q96QSO;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative matrix cell adhesion molecule-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00041; HTH ARAC_FAMILY_1; PROSITE; PS50835; IG_LIKE; 5. PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LI
                                                                                                                                                                                                                                                                              Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein
                                                                                                                                                                                                                                Tilson M.D.;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                               SEQUENCE
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                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLLQSATEVKKPGASMKVSCWASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                         AQKFQDRVTITRDRSMNTAYMELSSLRSEDTAMYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QMQLVQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMGWITPFNGNTNY
               QVQLLQSATEVKXPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
OVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY
                                                                                               159
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                                                Conservative
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                                                                                             ; IG LIKE;
A; 17497 M
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                                                                                                                                                                                                                                                                                Primates;
                                                                                                                                                                                                                                                                                         Chordata;
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                                                          69.7%;
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23,
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Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 371; DB 4;
Pred. No. 1.7e-32;
                                              Score 363; DB 4;
Pred. No. 2.6e-32;
3; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                               Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                               5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
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RESULT
Q9GYZ2
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RESULT QRWY24
ID WY24
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AC Q8
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE;
NON_TER 1 1 119
NON_TER 119 119
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HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Song X.T., Feng Z.Q., Guan X.H.;

"Amplification, cloning and sequence analysis of the heavy variable region gene of monoclonal anti-idiotypic antibody variable region gene of monoclonal anti-idiotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schistosoma japonicum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCB1
                        Zheng S., Shao X., Cao J., Geng L., Pang Y., D
"Identification and characterization of SNC66,
down-regulated in colorectal cancer.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
EMBL, AF283666; AAL36897.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8WY24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8WY24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNC66 protein.
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Zheng S., Shao X.,
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _TaxID=6182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 AA;
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13567 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.7%; Score 358; DB 5; 68.4%; Pred. No. 6.7e-32; tive 14; Mismatches 17
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annotation update)
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6, a 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                       g Q.;
Ig-like
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Best Local S
Matches 67
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Best Local S
Matches 65
                                                                                                                                                                                                               Q925S3;
Q925S3;
Q1-DEC-2001
01-DEC-2001
01-MAR-2003
          MRP3
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Y'' H. Van der Merwe P.L.,
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01-MAY-2000
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                  "Myosin-reactive autoantibodies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 497 AA; 53665 MW;
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musculus
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                                                                                                                                                                           . Similarity 67; Conserv
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                                                                                                             QGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCA
                                                                                                                                  VOSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANYAQKF
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                                                                                                 QGRVTITADKSTSTAYMELSSLRSEDTAVYYCA
                                                                                                                                                  LOSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHYAQKF
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              (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
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(TrEMBLrel.)
(TrEMBLrel.)
                                                     PRELIMINARY;
                                                                                                                                                                          Conservative
(Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                               12605 MW;
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72.0%;
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               19,
19,
23,
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              Created)
Last seq
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                                                                                                                                                                       Score 340; DB 4; Le
Pred. No. 6.3e-30;
8; Mismatches 18;
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 357;
Pred. No. 4
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Catarrhini; Hominidae; Homo
                                                                                                                                                                                                             C8F9131DE13EA898 CRC64;
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             sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                  rheumatic
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                                                     147
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4.7e-31;
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                                                                                                                                                                                                                                                                                                                                   carditis
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                                                                                                                                                                                          Length 116;
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Best Local S
Matches 62
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Best Local S
Matches 63
                                                                                      Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ day
EMBL; BC013490; AAH13490.1; -
InterPro; IPR0077110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003566; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS0035; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the same strain.";

Int. J. Radiat. Biol. Relat. Stutement. AP240166; AAK3731.1; -.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGy 1.

PROSITE; PS50835; IG_LIKE; 1.

SEQUENCE 147 AA; 16274 MW; 8
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                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.1 kDa protein.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q91WT1
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE=Colon;
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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"Mechanism of exogenous nucleic acids and
the repair of intestinal epithelium after
World J. Gastroenterol. 6:709-717(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BALB/c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cui D., Zeng G., 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
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         62; Conserv
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         Conservative
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64.3%;
64.3%; Score 335; DB 11;
63.3%; Pred. No. 1.2e-28;
cive 13; Mismatches 23
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Pred. No. 1
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Sciurognathi; Muridae;
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repairing
it with the
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                                        DB 11;
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.8e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Murinae;
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A of mice o
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RESULT
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Best Local S
Matches 65
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SEQUENCE FROM N.A.
TISSUE=Breast tumor;
Strausberg R.;
                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                       Similar to expressed sequence Mus musculus (Mouse).
                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                          Q8K0Z4
                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
SIGNAL
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ224083; CAA11829.1; -. HSSP; P01772; 2FB4.
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MEDLINE=99322155; PubMed=9657749;

Jacquemin M.G., Vander Elet L.P.L.;

Jacquemin and kinetics of factor VIII inactivation: study with an ING4 monclonal antibody derived from a hemophilia A patient with inhibitor.";
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
IgG VH protein precursor (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blood 92:496-506(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                AREFOGSVIMTADISTDIAYMELSSLRSDDTAVYYCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAPGKGLEWVGSFDPESGESIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS50835; IG_LIKE;
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Last sequence update)
Last annotation updat
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Pred. No. 4e-2
8; Mismatches
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Murinae; Mus
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Best Local :
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003596; Ig-w.
InterPro; IPR003596; Ig-w.
Pfam; PP000407; Ig; 4.
SMART; SM00409; IG; 3.
SMART; SM004007; IGc1; 3.
SMART; SM00406; IGcv; 1.
PROSITE; PS50035; IG LIKE: 4.
PROSITE; PS00290; IG-MHC; 2.
SEQUENCE 480 AA; 51645 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkes "Differences in V kappa gene utilization and VH CDR3 sequence anti-DNA from C3H-lpr mice and lupus mice with nephritis."; EMBL; U59154; AAB02916.1; -... InterPro; IPR007110; Ig-like. InterPro; IPR003106; Ig MIC. InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C3H/HeJ-lpr/lpr;
MEDLINE=96409289; PubMed=8814271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Anti-DNA heavy chain (Fragment).
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01-MAR-2002
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BC029188; AAH29188.1; -.
                                                                                                                                                                                                                Similarity
                                                                                                            1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                            AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
SOKFKDKATLTVDKSSRTAYMQLNSLTSEDSAVYYCAR
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                                                                                                                                                                                 63.3%;
milarity 60.2%;
Conservative 19
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                                                                                                                                                                                                                                                                            13806 MW;
                                                                                    /KPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWVGDINPYYGGTRY
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                                                                                                                                                                            Score 330; DB 11;
Pred. No. 8.6e-29;
9; Mismatches 20
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Sciurognathi; Muridae; Murinae; Mus
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RESULT 15
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Search completed: Job time : 23.883
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peeole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peeole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Hyons P., Rang B., Ringwald M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.,
Functional annotation of a full-length mouse cDNA collection.";
RI Nature 409:685-690(2001).
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Best Local S
Matches 60
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EMBL; AK007918; BAB25349.1; -.
HSSP; P01842; 7FAB.
MGD; MGI:96443; Igh-1.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00356; Ig_v.
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Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUR-2003 (TrEMBLrel. 23, Last annotation update)
1810060009Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00229; IG_MHC; 1.

SEQUENCE 473 AA; 51699 MW;
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                                                                                                                                                                                               61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                                                                                                                                                                                                                                                                                                                                                        1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ch 63.3%; Score 330; DB 11; Length 473; Similarity 61.2%; Pred. No. 4.3e-28; 60; Conservative 17; Mismatches 21; Indels
                                                                                                                                        PRELIMINARY;
                                   December 30, 2003, 11:01:02
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RESULT 15
ABP45461
ID ABP45
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DT 19-AU
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BLy8;
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                                                                                                                                                                                                                                              BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Honjo
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  15-JUN-2001; 2001WO-US19110.
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                                                                                                             WO200202641-A1
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                                                        10-JAN-2002
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)B; AAQ78956.
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                                                                                                                                                                                                                       erythematosus; rheumatoid arthritis; CVID; AIDS; immunodeficiency; acquired immunodeficiency syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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Pred. No. 2.5e-39;
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bulin in mammalian
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Search completed: December 30, Job time: 32.6089 secs

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                                                                                                                                                                                                                                                     This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the thumour necrosis factor (TNF) super family and induces B cell thumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated with aberrant expression of BLyS. They may also be immunostrated to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (eyg. common variable immunodeficiency (CVD) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                     Query Match
Best Local
                                                                                                                                         Matches
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 2159-2160; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibodies against B Lymphocyte Stimulating the diagnosis and treatment of cancers and i
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                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                            invention.
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                                                                                                                                                       Similarity
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                                                                                                 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEWVGWISAYNGNTHY
                   AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                  QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
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                                                                                                                                                                                                          248
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; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
                                                                                                                                         Conservative
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                                                                                                                                                       87.5%;
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                                                                                                                                     Score 456; DB 23;
Pred. No. 5.6e-39;
4; Mismatches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides, useful immune disorders -
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   98
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                               measuring human game expression in a sample derived from human adult cliver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high cliver (1) may be used for predicting, measuring and displaying gene cexpression in samples derived from human adult liver. The genes clientified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which clients associated with coronary heart disease. A89/3748-A855930 represent cliver the sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly crom wipo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                            Query Match
Best Local
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-068408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
Peptide #8044 encoded by human foetal liver single exon probe
                                     04-FEB-2002
                                                                   ABB40538
                                                                                          ABB40538 standard;
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nuclectide sequences given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analysing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488898/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human liver peptide, SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG,
                                                                                                                                                                 64
                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome-derived single exon nucleic acid probes useful sing gene expression in human adult liver -
                                                                                                                                                                                                                        4.
                                                                                                                                                                                                                                                                               86;
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                           AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                               QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                         AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 101
                                                                                                                                                                                                             QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID No 34543; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                      104
                                                                                                                                                                                                                                                                          Conservative
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                          Peptide;
                                                                                                                                                                                                                                                                                        87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                          104
                                                                                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                                                      Score 456; DB 22;
Pred. No. 2.2e-39;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR;
                                                                                         ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34543.
                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                  Length 104;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                      0,:
                                                                                                                                                                                                                                                                    Gaps
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RESULT 14
AAR66311
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                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 86
                                                      Primer; cosmid;
          WO9426895-A1
                                                                                 Human immunoglobulin variable heavy chain #17.
                               Homo sapiens
                                                                                                                25-MAR-2003
03-AUG-1995
                                                                                                                                                  AAR66311;
                                                                                                                                                                     AAR66311 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 33173; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; foetal liver; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157277-A2
                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG,
                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                               66;
                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                         p=4
                                              PCR; amplify; human; immunoglobulin; variable; heavy chain; placenta; vector; pUB81; E.coli; mammalian.
                                                                                                                                                                                                                             AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 101
                                                                                                                                                                                                                                                                                          QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
                                                                                                                                                                                                                                               AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                        QVQĹVQSGAEVKKPĠASVKVŠČKASGYTFTSYGTŠWVRQAPGQĞLEWMĞWISAYNĞNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel
                                                                                                                                                                                                                                                                                                                                                                               104 AA;
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                             (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2000US-0180312.
2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000US-0226359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DK,
                                                                                                                                                                                                                                                                                                                                       87.5%;
87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank
                                                                                                                                                                                                                                                                                                                              4.
                                                                                                                                                                                                                                                                                                                          Score 456; DB 22;
Pred. No. 2.2e-39;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                            8;
                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                 Length 104;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English
                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                            63
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                                                                                                                                                                                                                                                                      The invention relates to an isolated epitope present on cancer cells and comportant in physiological phenomena such as cell rolling, metastasis and important in physiological phenomena such as cell rolling, metastasis and confident in the pitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one captions are useful for inhibiting cell rolling, inflammation, autoimmune continuous or leukaemia cells, increase in number of tumour or leukaemia cells in a patient, cell-matrix, platelet-matrix, for platelet-platelet and/or cell-platelet adhesion or aggregation, for concreasing mortality of tumour or leukaemia cells, for increasing the concreasing mortality of diseased cells to damage by anti-disease, anti-cancer concreasing cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diseases concretaing diseases such as cancer, leukaemia, autoimmune diseases, cardiovascular diseases such as myocardial confiarction, retinopathic diseases and other diseases mediated by abnormal concretain interactions of the concretain a human antibody.
                                                                                                                                                Query Match
Best Local S
Matches 86
                                                                                                                                                                                                                                                       fragment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 246-247; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases, and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lazarovits J, Hagai Y, Szanthon E, Richter T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-2000; 2000US-258948P.
29-DEC-2000; 2000US-0751181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-DEC-2001; 2001WO-US49442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200253700-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOT-) BIO-TECHNOLOGY GEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human antibody fragment #46
     61
                                      61
                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody;
                                                                                     QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                   AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                        87.5%;
milarity 87.8%;
Conservative
                                                                                                                                                                                                                     86
                                                                                                                                                                                                                                                   tein interactions. This sequence represents a human
                                                                                                                                                                                                                     $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plaksin D, Vogel T, Amit B, Kooperman L,
                                                                                                                                     Score 456; DB 23
Pred. No. 2e-39;
4; Mismatches
                                                                                                                                                                       DB 23;
                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nimrod A,
Peretz T,
98
                                                                                                                                                                       Length
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mar-Haim
Levanon
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                                                                                                                                     Gaps
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RESULT 11 ABG78171

> RESULT 12 ABG55895

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ABG55895

standard; Peptide;

104

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                                                                                                                                                                                                            The invention relates to a peptide or polypeptide comprising an FV CC molecule, a construct of fragment with schools and a construct of a fragment with CC enhanced binding characteristics which selectively and/or specifically CC binds to a target cell in favour of other cells, where binding is a single CC primarily determined by a first hypervariable region and FV is a single CC chain FV (scFV) or a disulfide FV (dsFV). The peptide, optionally in CC association with or attached, coupled, combined, linked or fused to a CC pharmaceutical agent, is useful in the manufacture of a medicament, where CC the medicament has activity against a diseased cell, preferably a cancer CC cell (selected from carcinoma, sarcoma, leukaemia, leukaemia, lymphoma, CC myloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a CC composition for use in inhibiting the growth of a diseased or cancer CC cell. This sequence represents a human FV molecule hypervariable region CC related peptide of the invention.
                                                                                                                             Matches
                                                                                                                                                            Query Match
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel peptide/polypeptide for cancer therapy has Fv molecule, or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favoucells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-619166/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plaksin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hagai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-DEC-2000; 2000US-0751181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-DEC-2001; 2001WO-US49440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Fv molecule hypervariable region related peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BIOT-) BIO-TECHNOLOGY GEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200259264-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG78171 standard; Protein; 98 AA
                                                                                                                                               rocal
      61
                               19
                                                                                               ш
                                                                                                                               86;
                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ō
                   AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                        QVQLVQSGAEVKXPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                           OVOLLOSATEVKKPGASMKVSCMASGYPFTSYDISWVROAPGOGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lazarovits J,
, Peretz T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 169; 232pp; English
                                                                                                                                                                                          98
                                                                                                                           Conservative
                                                                                                                                                                                          ¥,
                                                                                                                                        87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guy R,
                                                                                                                           4.
                                                                                                                     Score 456; DB 2:
Pred. No. 2e-39;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipschitz O,
                                                                                                                                                  23:
                                                                                                                      8
                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Szanton
98
                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell in favour of other
                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levanon A;
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                                                                                                                                                                                                                                                          reparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            construct
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                                                                                                                                        Query Match
Best Local S
Matches 87
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ABP45584
                                                                                                                                                                                                                                This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) Super family and induces B cell proliferation and differentiation. The antibodies of the invention have entirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases. An averant blys expression of BLyS.
                                                                                                                                                                       diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-114799/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUN-2000; 2000US-212210P.
17-CCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomoulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune discorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CAMB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200202641-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP45584 standard; Protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human BLyS binding scFv SEQ ID 1595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP45584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MS
                                                                       87;
                                                                                                                                                                    invention.
                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN GENOME SCI INC
CAMBRIDGE ANTIBODY TI
                 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
OVQLVQSAAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                     250 AA;
                                                                    88.3%;
ilarity 88.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2306-2307; 3148pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi GH,
                                                               Score 460; DB
Pred. No. 2.2e-
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaughan T,
                                                               DB 23;
2.2e-39;
1es 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hilbert
                                                                                              Length
                                                               Indels
                                                                                              250;
                                                             0;
                                                           Gaps
60
                             60
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DXXXX DXXX DXXX

04-DEC-2002 ABG91862; ABG91862

(first entry)

ABG91862

standard;

Protein;

98

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RESULT 9
AAY50952
ID AAY5
XX AAY5
XX AAY5
XX AAY5
XX Huma
XX Huma
XX Hem
XX HE
XX HEM

RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ś
                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has breasence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human anti-factor VIII antibody clone DP-14 protein which is used in the method
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Fig 4B; 61pp; English.
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                                                                                          AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                   QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                                        QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                          AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
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                                                                                                                                                                                                                                     diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS) ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-27739P.
25-MAY-2001; 2001US-293499P.
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88; Conservative
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                 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                          OVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                           QVQLLQSAAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
AOKLOGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
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                                                                                                                       Score 463; DB 23; Pred. No. 1.1e-39; 3; Mismatches 7
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                                                                                                        Query Match
Best Local S
Matches 87
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17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 2476-2477; 3148pp; English.
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(CAMB-) CAMBRIDGE ANTIBODY TO
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                                                                                                        1 Similarity
87; Conser
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                                                          QVQLLQSATEVKKPGASMKVSCMASGYPPTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                         QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTHY
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                                                                                                        Conservative
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                                                                                                     Score 463; DB 23;
Pred. No. 1.1e-39;
3; Mismatches 8
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immune disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
  19-AUG-2002
                                                    ABP45105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                     standard;
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entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 469; DB 21;
Pred. No. 9.4e-41;
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BLy8; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                       16-JUN-2000; 2000US-212210P.
17-CCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                               15-JUN-2001; 2001WO-US19110
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                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLyS binding
                                                                                                                                                                                                                                                                           CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                         Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCFV SEQ ID 1116.
                                                                                                                                                                                                                                                         Choi GH,
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                                                                                                                                                                                                                                                         Hilbert
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Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -

WPI; 2002-114799/15

Claim 1; Page 1734-1735; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to CC B Lymphocyte Stimulator (BLyS) polypoptides. BLyS is a member of the CC tumour necrosis factor (TNP) super family and induces B cell cumour necrosis factor (TNP) super family and induces B cell correct the invention and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC antibit the expression and activity of BLyS. The antibodies bind to BLyS in the company of the invention and activity of BLyS. The antibodies bind to BLyS in CC biological samples and may be used in this way to diagnose disease CC associated with aberrant expression of BLyS. They may also be associated with aberrant expression of BLyS. They may also be communicated to treat diseases associated with aberrant BLyS expression CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and CC common variable immunodeficiency (CVID) and ccurred immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent CC of the antibodies and fragments of the antibodies described in the method invention.

Sequence 247 \$

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ABP45549
ID ABP455
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                                                                                                                                                                  Similarity
                                                                                                         QVQLLQSAAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                     AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                      Conservative
                                                                                                                                                               88.9%;
                                                                                                                                                   Score 463; DB zz;
Pred. No. 1.1e-39;
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ABP45549 standard; Protein; 250

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RESULT 2
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hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human anti-factor VIII antibody VH IT-2 protein which is used in the method
                                                                                                                                                                                 New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
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                                                                                                                                                                                                                                                                            Voorberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hemophilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human;
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                                                                                                                                                        Example
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                                                                                                                        invention describes a novel polynucleotide (I) (and complements and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-factor VIII antibody VH protein VH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain; antibody; factor VIII; hemostatic;
; VH protein.
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Pred. No. 4.5e-45;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human anti-factor VIII antibody
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2; Mismatches 2
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1. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT;*
2. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT;*
3. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT;*
4. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT;*
6. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT;*
6. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT;*
7. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT;*
9. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT;*
9. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT;*
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11. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT;*
12. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT;*
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14. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT;*
15. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT;*
16. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT;*
17. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT;*
18. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT;*
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        98.1
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Copyright (c) 1993 - 2003 Compugen Ltd
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493.415 Million cell updates/sec
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ide and antibody usefilbodies against factorients with these anti-		l, Turenhout EAM;	BLOEDVOORZIENING.						factor VIII; hemosta	dy VH protein VH EL-			8 AA.	ALIGNMENTS	AAY64688 ABP45181	AAR22569	ABP45767	AAU02549	ABP45725 ABP45858	ABP44919 ABP44919	ABP45599	ABP45866 AAY50951	ABP45953	ABP45544	ABP45859 ABP45568	ABP45575	ABP45867	ABP45550 ABP45582	ABP45462 ABP45414	ABP45345	ABP45910 ABP45179	ABP45861	ABP45461	ABB40538 AAR66311	ABG55895	ABG91862 ABG78171
useful for diagnosing the actor VIII and for antibodies -									:atic;	5.					5' E	-		Anti-adipocyte mon						Human BLys binding						Human BLyS binding		Human BLys binding	BLyS bindin		Human liver pentid	antibody

New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US108 PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US108 PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US108 PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US108 PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US108 PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

15	14	13	12	11	10	9	80	7	ტ	v	4	w	2	1	Result No.
456	456	456	456	456	456	456	456	456	456	456	460	463	463	463	Score
87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	88.3	88.9	88.9	88.9	Query
125	125	117	104	98	98	98	98	98	98	98	250	251	250	247	Query Match Length DB
12	12	12	9	15	12	12	12	12	12	12	11	11	11	11	. DB
US-10-041-860-207	US-10-041-860-42	US-10-041-860-206	US-09-864-761-47285	US-10-194-975-4	US-10-308-817-44	US-10-041-860-356	US-10-041-860-355	US-10-041-860-326	US-10-041-860-324	US-10-041-860-2	US-09-880-748-1595	US-09-880-748-1738	US-09-880-748-1560	US-09-880-748-1116	ID
Sequence 207, App	Sequence 42, Appl	Sequence 206, App	Sequence 47285, A	Sequence 4, Appli	Sequence 44, Appl	Sequence 356, App	Sequence 355, App	Sequence 326, App		Sequence 2, Appli	Sequence 1595, Ap	Sequence 1738, Ap	Sequence 1560, Ap	Sequence 1116, Ap	Description

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	10
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ALIGNMENTS

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; SEQ ID NO 1116
; LENGTH: 247
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-880-748-1116
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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US-09-880-748-1116
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                                                                                                                                                                 Matches
                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                      Local
61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                   88;
                                                                                                                                                            h 88.9%; Score 463; DB 11; Length 247;
Similarity 89.8%; Pred. No. 6.9e-40;
88; Conservative 3; Mismatches 7; Indels
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AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

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APPLICATI: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
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                                                   ; ORGANISM: Homo sapiens US-09-880-748-1738
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PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR TILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER: 05/283,499
PRIOR FILING DATE: 2001-05-25
NUMBER: 05/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER: 05/283,499
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Best Local S
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Query Match
                                                                                                                                                              SEQ ID NO 1738
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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                                                                                                      LENGTH: 25
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                                                                                                                                  251
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nilarity 89.8%;
Conservative
88.9%;
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Pred. No. 7e-40;
3; Mismatches
Score 463;
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11;
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Length 251;
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; ORGANISM: Homo sapiens
US-09-880-748-1595
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APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
Gadi
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PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1595
LENGTH: 250
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Publication No. US20
GENERAL INFORMATION:
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
                                                                             APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REFERENCE: ABGENIX.051A
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                 CURRENT APPLICATION NUMBER: US/10/041,860 CURRENT FILING DATE: 2002-01-07 NUMBER OF SEQ ID NOS: 377
                                                                                                                                                                                                                                                                                    APPLICANT: Corvalan, Jose R.F.
SOFTWARE: FastSEQ for Windows Version 4.0
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3; Mismatches
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APPLICANT: CORVALAN, JOSE R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEG ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEG ID NO 324
             Sequence 326, Application US/1004
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES D
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LENGTH: 98
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ORGANISM: homo sapiens
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CANT: Bezabeh, Binyam
OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
OF INVENTION: THEREOF
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Similarity 87.8%;
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Pred. No. 1.3e-39;
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Pred. No. 1.3e-39;
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APPLICANT: APPLICANT: APPLICANT:

Jia, Xiao-Chi

Feng, Xiao Yang, Xiao-Chen, Franc

Xiao-Dong

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; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-326
US-10-041-860-356
Sequence 356, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
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US-10-041-860-355
                                                                                              RESULT 9
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APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 355
LENGTH: 98
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Best Local
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Best Local Similarity
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APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
                                                                                                                                              61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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Pred. No. 1.3e-39;
4; Mismatches 8
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Pred. No. 1.3e-39;
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APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO F
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGINIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 356
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-356
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US-10-308-817-44
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Best Local S
Matches 86
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SEQ ID NO 44
LENGTH: 98
TYPE: PRT
ORGANISM: human
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Publication No. US20030219861A1
GENERAL INFORMATION:
                                                            Sequence 4, Application US/10194975
Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: FOOLE, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
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CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
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APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
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Pred. No. 1.3e-39;
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Pred. No. 1.3e-39;
4; Mismatches 8;
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US-09-864-761-47285
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
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SOFTWARE: PatentIn version
SEQ ID NO 4
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Best Local Similarity
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APPLICANT: Rank, David R.
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
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                                       PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
FILING DATE: 2001-01-30
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
APPLICATION NUMBER: PCT/US01/00666
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
                                                                                                                     APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00662
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                                         2001-01-29
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Pred. No. 1.3e-39;
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  vers.
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RESULT 14
US-10-041-860-42
; Sequence 42, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
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FEATURE:

OTHER INFORMATION: MAP TO AB019440.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.42

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8

OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39

OTHER INFORMATION: EST_HUMAN HIT: AW403728.1, EVALUE 4.00e-45

US-09-864-761-47285
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US-10-041-860-206
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APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi APPLICANT: Feng, Xiao APPLICANT: Yang, Xiao-Dong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
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Local Similarity 87.8%;
hes 86; Conservative
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Yang, Xiao-Dong
Chen, Francine
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Pred. No. 1.6e-39;
4; Mismatches 8
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Pred. No. 1.4e-39;
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Sequence 207, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Yang, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEG ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 207
LENGTH: 126
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 42
LENGTH: 125
TYPE: PRT
ORGANISM: homo sapiens
Search completed: December 30, Job time : 21.0171 secs
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APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
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                                                                                                                                                                                                                                           Match 87.5%;
Local Similarity 87.8%;
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                                                                                                      AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                                                                       AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                  QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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87.8%;
               2003, 11:45:22
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Pred. No. 1.7e-39;
4; Mismatches 8;
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Pred. No. 1.7e-39;
4; Mismatches 8;
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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Match Length
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Copyright (c) 1993 - 2003 Compugen Ltd.
       DB
US-08-545-809A-105
US-08-264-093-3
US-08-264-090-22
US-08-964-690-22
US-08-561-521-45
US-08-555-539A-76
US-08-561-521-19-16
US-08-561-521-11
PCT-US95-01219-16
US-09-025-769B-29
US-09-025-769B-29
US-09-025-769B-59
US-09-025-769B-59
US-09-025-769B-59
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US-09-025-769B-59
US-09-025-769B-59
US-08-652-816A-19
US-08-652-816A-19
US-08-652-816A-19
US-08-137-117D-102
US-08-436-717-112
US-08-436-717-110
US-08-436-717-110
US-08-436-717-110
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                                                                  Sequence 105, Applisequence 2, Applisequence 2, Applisequence 45, Applisequence 45, Applisequence 10, Applisequence 10, Applisequence 10, Applisequence 10, Applisequence 11, Applisequence 13, Applisequence 14, Applisequence 14, Applisequence 17, Applisequence 17, Applisequence 17, Applisequence 17, Applisequence 17, Applisequence 10, Applisequence 11, Applisequence 11, Applisequence 11, Applisequence 12, Applisequence 11, Applisequence 12, Applisequence 11, Applisequence 11, Applisequence 11, Applisequence 12, Applisequence 13, Applisequence 12, Applisequence 13, Applisequence 14, Applisequence 15, Applisequence 16, Applisequence 16, Applisequence 17, Applisequence 17, Applisequence 18, 
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	atch cal Simí 86;	CITY: BOSTON STATE: MA COUNTRY: US ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: Window SOFTWARE: FASTEGO for Wi. CURRENT APPLICATION DATA: APPLICATION NUMBER: US/O FILING DATE: 27-MAR-1996 PRIOR APPLICATION NUMBER: PCT/- FILING DATE: 10-MAY-1993 ATTORNEY/AGENT INFORMATION: NAME: FREEMALD/DOCKET NUMBER: 29, REFERENCE/DOCKET NUMBER: 29, REFERENCE/DOCKET NUMBER: 10-MAY-1993 ATTORNEY/AGENT INFORMATION: NEGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER: 10-MAY-1993 ATTORNEY/AGENT INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION TELECOMMUNICATION TELECOMMUNICATION INFORMATION TELECOMMUNICATION TOMATION TOMATIO	109A-1 105, 106, 107 107 107 10 07 10 07 10 07 10 07 10 07 10 10 10 10 10 10 10 10 10 10 10 10 10	391 75 391 75 391 75 391 75 389 74 388 74 388 74 387 74 387 74 385 73 381 73 381 73 380 72
	larity (BOSTON MA MA MA MA Z2110-2804 Z2110-2804 ZYPE: Diskette R: IEM Compatible R: IEM Compatible RS YSTEM: Window E: FastSEQ for win E: FastSEQ for Window CICATION UNMBER: US/0 DATE: 27-MAR-1996 LICATION UNMBER: PCT// DATE: 10-MAY-1993 AGENT INFORMATION: Freeman, John W. ATION NUMBER: 29, CE/DOCKET NUMBER: POR SEQ ID NO: 1 CHARACTERISTICS: 117 Amino acids W: linear TYPE: protein -105	licat B ION: ION: TION TION TION TION TION TION TION TION	5.0 110 5.0 117 5.0 119 6.0 119 6.1 108 8.5 135 8.3 123 8.3
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	red. No. Mismat	vs Versi 15,809A 1/00603	5809A UNOGLOBU AND DNA	09-899-08-561-08-561-08-561-09-899-09-899-08-477-08-836-836-836-836-836-836-836-836-836-83
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US-08-264-093-3
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                                                                                                       Sequence
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Best Local
                                                                                            Patent No.
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                                                             GENERAL INFORMATION:
APPLICANT: CHESNU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lake, James R.
REGISTATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 ir
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDENNESS: not applic
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TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CYCLE-INDEPENDENT GLIOMA SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: No. 5639863 applicable ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US
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                 APPLICANT:
   APPLICANT:
                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Canada
ZIP: M5H 2J7
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                                                                                                          22, Application US/08202047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 117
                                                                                                                                                                                      AQKFQGRVSMTTDTSTSTAYMEVRSLRSDDTAVYYCAR 98
 CHESNUT Rober...
POLLEY, Margaret J.
PAULSON, James C.
TONES, S. Tarran
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         not applicable
                                                                                                                                                                                                                                                                                                              83.7%; Score 436; DB 1;
82.7%; Pred. No. 6.6e-40;
ative 9; Mismatches 8
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RESULT 4
US-08-964-690-22
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; OTHER INFORMATION:
US-08-202-047-22
                                                                                                                                                                                                                                                                                     Sequence 22, Appli
Patent No. 6033667
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
CLASSIFICATION: 424
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MEDIUM TYPE: Ploppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
COMPUTER READABLE FORM:
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TITLE OF INVENTION: Antibodies to P-Selectin
NUMBER OF SEQUENCES: 45
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                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94105
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                                                 CITY: San Francisco
STATE: California
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                               COUNTRY:
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                   94105
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One Market Plaza, Steuart Tower, Suite 2000
                                                                                   E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 20
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JONES, S. Tarran
SALDANHA, Jose W.
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                                   USA
                                                                                                                                                                                                                                     CHESNUT, Robert W. POLLEY, Margaret J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 5.4e-38;
8; Mismatches 10
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                                                                                    Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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RESULT 5
US-08-561-521-45
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OTHER INFORMATION: /label= HUMAN_I
US-08-964-690-22
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Patent No.
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: |
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPOSIBLE
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,690
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                    CLASSIFICATION:
                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: II
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SSIFICATION: 424
APPLICATION DATA
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80; Conserv
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linear
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IBM PC compatible
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80.8%; Pred. No. 5.4
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GENERAL INFORMATION:
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Best Local Similarity
Matches 80; Conserv
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Veri
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.
TELECOMMUNICATION INFORMATION:
TELECHHONE: (415) 813-5600
TELEFAX: (415) 494-0792
           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
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FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAMB: Smith, William L.
REGISTRATION NUMBER: 30,22
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DO COUTO, FERNANDO (APPLICANT: CERLANI, ROBERTO L. APPLICANT: PETERSON, JERRY A. TITLE OF INVENTION: RECOMBINANT TITLE OF INVENTION: MC3 ANTI-BJTITLE OF INVENTION: METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
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                                                                                            TELEFAX: 706141
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STATE: CA
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linear
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECOMBINANT PEPTIDES DERIVED FROM THE MC3 ANTI-BA46 ANTIBODY, METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FERNANDO J.R.
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Pred. No. 5.5e-38;
                                                                                                                                                                                                                                                                                                                                       Version #1.30
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RESULT 7
PCT-US95-01219-45
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                                                                                                                      Query Match
Best Local Similarity 80.8
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Best Local Similarity 80.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
                                                                                                                                                                                                                        TOPOLOGY: 1
MOLECULE TYPE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/186,269 FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/01219 FILING DATE: 25-JAN-1995
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                                                                                                                                                                                                                                                        STRANDEDNESS:
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YAQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                    QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAY-NGNTH 59
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                                                                   QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNGDTN
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                                                                                                                                                                                                                                                      single
                                                                                                                                                  80.3%;
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Pred. No. 5.5e-38;
                                                                                                                                                    Score 418.5; DB 5
Pred. No. 5.5e-38;
                                                                                                                                       Mismatches
                                                                                                                                                                      DB 5;
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US-09-025-769B-22
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US-08-545-809A-96
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APPLICATION NUMBER: US FEB-1998
FILING DATE: 18 FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18 AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
NAME: James F. Haley, Jr., Esq.
                                              Sequence 96, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/09025769B
Patent No. 6300064
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SEQUENCE CHARACTERISTICS:
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APPLICANT: I
APPLICANT: 1
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REFERENCE/DOCKET NUMBER: MO
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                  NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Plueckthun, Andreas
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 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                          61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                  79;
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                                                                                                                                                                                                                                                                                                                           QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGNTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 amino acide
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Ilag, Vic
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Fish & Richardson,
                    ADDRESS:
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80.6%;
                                                    SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
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                                     145
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 416; DB 4;
Pred. No. 9.1e-38;
 P.C.
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RESULT 10
US-08-561-521-10
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Patent No. 5840299
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                             APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
TOPOLOGY: lin-
(OLECHIP
                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
                                                                                                                                                                                                            CITY: :
STATE:
CLASSIFICATION:
                                                                                                                                                                                      COUNTRY:
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TELEX: 20015
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REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06
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CITY: Boston
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77; Conservative
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424
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78.6%;
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APPLICANT: HONG, Hyo Jeong
APPLICANT: PARK, Sung Sup
APPLICANT: KANG, Young Jun
APPLICANT: KANG, Chang-Yuil
APPLICANT: KANG, Chang-Yuil
APPLICANT: YOON, Sung Kwan
TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AN
TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AN
TITLE OF INVENTION: HAMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AN
CURRENT APPLICATION NUMBER: US/09/438,954
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEG ID NOS: 49
SOFTWARE: Patentin Ver: 2.1
SEG ID NO 41
                                                                                                                                                                                                                                                       ; ORGANISM: Artificial Sequence; FEATURE; OTHER INFORMATION: Description of Artificial Sequence: Variable; OTHER INFORMATION: region of heavy chain of human antibody (M17750) US-09-438-954-41
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                                                                                                                                                                        Matches
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Best Local :
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US/08/
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,22
                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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LENGTH: 119 amino acids
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                                                                                                                                                                                        Local
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STRANDEDNESS: sir
TOPOLOGY: linear
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es 77; Conserv
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                                                                                                       1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEMVGWISAYNGNTHY 60
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l Similarity 78.6%;
77; Conservative
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                          AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
SOKFOGRVTITRDTSASTAYMELSSLRSEDTAVYYCAR 98
                                                                                   QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60
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78.6%;
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                                                                                                                                                                   Score 407; DB 4;
Pred. No. 8.7e-37;
8; Mismatches 13
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Pred. No. 8.7e-37;
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RESULT 12 PCT-US95-01219-10

New York

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US-09-025-769B-36
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                          Sequence 36, Application US/09025769B Patent No. 6300064
                                                                                                                            GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Pecer
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
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FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                   APPLICANT: Moroney, S
APPLICANT: Plueckthun
TITLE OF INVENTION: P
NUMBER OF SEQUENCES:
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APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/
FILING DATE: 25-JAN-1995
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 amino acids
3: James F. Haley, Jr., Esq. c/o Fish & Neave
1251 Avenue of the Americas
                                       PlueOthun, Andreas
|VENTION: Protein/(Poly)peptide libraries
|SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                          Ge, Liming
Moroney, Simon
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78.6%;
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Pred. No. 8.7e-37;
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RESULT 14
US-09-025-769B-59
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APPLICANT: Pack, Peter
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 59, Application US/09025769B
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FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INPORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 18-FEB-1998
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
PRIOR APPLICATION DATA:
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                                                                                    SOFTWARE: PatentIn Release #1.0,
                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                             COUNTRY: USA
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77; Conservative
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78.6%;
                                          US/09/025,769B
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                                                                                    Version #1.30 (EPO)
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RESULT 15
US-08-652-816A-19
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SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAX-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAX-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 21-SEP-1993
PRICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United Stat
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: MO
TELECOMMUNICATION INFORMATION:
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FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 27,794
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78.6%;
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TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                          Query Match 77.8%;
Best Local Similarity 80.4%;
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/244,597

FILING DATE: 01-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: David W. Clough

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 28111/3330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 02-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                      60 AQKFQGRVTMTTDTSTSTAYMELRSLRSEDTAVYYCA 96
                                                                                                          61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCA 97
                                                                                                                                                                      1 QVTLQQSGAEVKKPGPSVKVSCKASGYTFTAYGFNWVRQAPGQGLEWM-WISAYSGNTKY 59
                                                                                                                                                                                                1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEWVGWISAYNGNTHY
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Maximum Match 100%
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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     of hits satisfying chosen parameters:
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1: pir1:*
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   GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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Ig heavy chain V r
anti-PR2 erythrocy
Ig heavy chain V r
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J. Mol. Biol. 227, 77
A;Title: The repertoi
A;Reference number: S
A;Accession: $26919
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C;Date: 22-Nov-1993 #
C;Accession: $26919
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C;Superfamily: immunc
C;Keywords: heterotet
F;15-98/Domain: immun
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A;Molecule type: DNA
A;Residues: 1-98 <TO
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ALIGNMENTS

1 QVQLLQS l Similari 87; Cons AQKFQGF QVQLVQS AQKLQGE Cons TTDTSRRTAYMELRSLRSDDTAVYYCAR 98 /ative .:212316; NID:g32855; FIDN:CAA78186.1; FID:g32856 bblin V region; immunoglobulin homology ner; immunoglobulin cobulin homology <IMM> :r, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G. 798, 1992
of human germline V(H) sequences reveals about fifty groups 85; MUID:93021117; PMID:1404388 puence_revision 10-Nov-1995 #text_change 23-Jul-1999 HTTDTSTSTAYMELRSLRSDDTAVYYCAR 98 :VRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY (DP-14) - human (fragment) (man) 89.1%; 4 Score 460; DB 2; L Pred. No. 1.5e-38; Length 98; Indels 0 Gaps 60 60

of.

R.Griffiths, A.D.; Ma EMBO J. 12, 725-734, A;Title: Human anti-e A;Reference number: S A;Accession: S36260 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-129 <GR Ig heavy chain V regi C;Species: Homo sapie C;Date: 03-Feb-1994 # C;Accession: S36260 (clone alpha-CEA4-8A) - human (fragment)

A;Cross-references: E C;Superfamily: immuno C;Keywords: heterotet F;15-98/Domain: immun

[Vist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty,)3 [uence_revision 03-Feb-1994 #text_change 23-Jul-1999 nucleic acid sequence not shown antibodies with high specificity from phage display libraries. 56; MUID:93178448; PMID:7679990

.:Z18851; NID:g33124; PIDN:CAA79303.1; PID:g939903
bulin V region; immunoglobulin homology
er; immunoglobulin
obulin homology <IMM> 88.6%; Score 457; BB 2 Length 129

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A; Note: the diff
C; Superfamily: in
C; Keywords: hete
F; 15-98/Domain:
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36271
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7678990
A;Accession: S36271
A;Accession: S36271
A;Cross-references: EMBL: Z18832; NID:933115; PIDN:CAA79284.1; PID:g939895
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (alpha-phOx15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C;Date: 28-Oct65; S24442
C;Accession: S1965; S24442
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. McCafferty, J. McCafferty, J.; Griffiths, A.D.; Winter, J. McCafferty, J. Mc
                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-40, 'GLSGWDGSALTMVTQSILDK', 61-118,'T', 120-124 <JON>
A;Residues: 1-40, 'GLSGWDGSALTMVTQSILDK', 61-118,'T', 120-124 <JON>
A;Cross-references: EMBL:X61647; NID:g37667; PIDN:CAA43828.1; PID:g1335368
A;Cross-reference for residues 41-60 results from misplacement of 10 l
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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submitted to the EMBL Data Library,
A;Reference number: S24442
A;Accession: S24442
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A; Residues: 1-124 < MAR>
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                                                                                                      immunoglobulin homology
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88.7%;
  88.0%; Score 454; DB 2;
87.8%; Pred. No. 7.6e-38;
tive 3; Mismatches 9
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Pred. No. 6e-38;
4; Mismatches
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                         October 1991
                                                                                                      <MM>
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                                                   Length 124;
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C;Species: Homo sapi.
C;Date: 20-Feb-1995
C;Accession: S21924;
R;Friedman, D.F.
                                                                                                                                                         F;34-117/Domain: imm
F;49-54/Region: comp
F;69-84/Region: comp
F;118-131/Domain: D
F;132-144/Domain: J
F;145-160/Domain: C
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A;Accession: S21924
A;Actus: preliminar
A;Molecule type: DNA
A;Residues: 1-131 <F
A;Cross;references:
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A; Residues: 1-160 <S
A; Note: the authors
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J. Exp. Med. 169, 16
A;Title: Relationshi
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C; Keywords: autoanti
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C;Accession: PL0105
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                                                     vative
                                                                                                                                                                                                          ion <DRG>
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     EVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                                                                                            ion <CRG>
                                                                                                                                                                                       gment
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Pred. No. 7.8e-37;
                                                                              Score 443; DB 2;
Pred. No. 1.2e-36;
                                                        Mismatches
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is one of the cold agglutining that preferentially obulin V region; immunoglobulin homology by; hemagglutinin
                                                                                                                                                                                                                                                                                                                              Twin, S.; Carmack, C.E.
1643, 1989

f variable region genes expressed
106; MUID:89235583; PMID:2541221
                                                                                                                                                                                                                                                                                                                                                                                                                                                            coantibody heavy chain precursor -
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                                  Length 160
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A;Cross-references: EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID:g32858 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388

A;Accession: S26918
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S21925
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A; Residues: 1-98 < TOM>
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A; Residues: 1-111 <FRI>
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A; Accession: S21925
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Homo sapiens (man)

Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999;

Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                   Matches
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Best Local (
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                                                                                                                                     QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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                                                         AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR 98
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                    82.0%;
82.7%;
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Pred. No. 6.8e-35;
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Pred. No. 6.2e-35;
                                                                                                                                                                                                                   Mismatches
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              C;Species: Homo Bapi,
C;Date: 03-Mar-1994,
C;Accession: S31680
R;Cuistnier, A.M.; G,
Submitted to the EMBI
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  A; Description: Mechar
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A; Note: the nucleotic
C; Superfamily: immun
C; Keywords: heterote:
F; 15-98/Domain: immu
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C;Date: 22-Nov-193
C;Accession: S31600
R;Cuisinter, A.M.; G
Bubmitted to the EMB
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C;Superfamily: immun.
C;Keywords: heterote.
F;34-117/Domain: imm
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R;Tomlinson, I.M.; W
J. Mol. Biol. 227, 7
A;Title: The reperto
                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-98 <TO
A;Cross-references:
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A; Accession: S26938
A; Status: preliminar
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A; Residues: 1-136 <C
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Best Local
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AQKFQG
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bulin V region; immunoglobulin homology
ner; immunoglobulin
jlobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ns that generate human immunoglobulin diversity operate 385
                                                                                                                                                                                                                             7:214071; NID:932969; PIDN:CAA78451.1; PID:932970 sequence was submitted to the EMBL Data Library, July 1992 bullin V region; immunoglobulin homology ner; immunoglobulin

    127, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
    198, 1992
    of human germline V(H) sequences reveals about fifty groups
    185; MUID:93021117; PMID:1404388

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                                                                   VKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60
                                                                                         VRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                                                                                                                                             cobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                    nucleic acid sequence not shown; translation not
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TRDTSISTAYMELSRLRSDDTAVYYCAR
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81.6%;
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Pred. No. 3.3e-34;
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Pred. No. 1.9e-34;
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is that generate human immunoglobulin diversity operate

ta Library, June 1992

(man)

ier, L.; Boubli, L.; Fougereau, M.; Tonnelle, puence_revision 10-Nov-1995 #text_change 23-Jul-1999

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from

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A;Reference number: S3158
A;Accession: S31680
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <CUI>
A;Cross - references: EMBL:
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglob
C;Keywords: heterotetrame
F;34-117/Domain: immunogl
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18551; S23625
R;Shin, E.K.; Matsuda, F: Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: S18551; MUID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X62106; NID:g37831; PIDN:CAAA4016.1; PID:g37832 R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, J. Exp. Med. 175, 831-842, 1992 A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors A;Reference number: S23623; MUID:92136804; PMID:1740665 A;Accession: S23625
                                                              RESULT
S49530
                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG> F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted F;34-117/Domain: immunoglobulin homology <IMM>
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C; Superfamily: :
C; Keywords: hete
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anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) -
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995
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A; Residues: 1-117 <OLE>
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A; Residues: 1-117 <SI
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                                                                                                                                               AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAR 117
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Pred. No. 4e-34;
5; Mismatches 13; Indels
    12-May-1995 #text_change
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S34014
Ig heavy chain V rec
C.Species: Homo sap.
C.C.Date: 02-Dec-1993
C.Accession: S34014
R.Mariette, X., Tsaj
Eur. J. Immunol. 23
A.Title: Nucleotidia
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A; Status: prelimina;
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A; Residues: 1-127 <
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          A;Cross-references:
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quence_revision 10-Nov-1995

#text_change 16-Aug-1996

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A.; Brouet, J.C.

.6-851, 1993 quence analysis of the variable domains 1001; MUID:93209281; PMID:7681398

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R;Griffiths, A.D.; b
EMBO J. 12, 725-734,
A;Title: Human anti-
A;Reference number:
A;Accession: 836265
A;Sratus.
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Bubmitted to the EMF
A; Description: Molec
A; Reference number:
A; Accession: $49530
A; Status: prelimina:
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C;Date: 03-Feb-1994
C;Accession: S36265
R;Griffiths, A.D.; N
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S36265
Ig heavy chain V rec
C; Species: Homo sapi
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C; Keywords: heterote
F; 15-98/Domain: immu
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A;Molecule type: mRb
A;Residues: 1-118 <
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C;Superfamily: immun
F;34-117/Domain: imn
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A; Residues: 1-135 < N
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                                                             .EVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                                                                                                  flobulin homology <IMM>
                                                                                                                                                                              obulin V region; immur.mer; immunoglobulin
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.93
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MTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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HV1C HUMAN
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Immunoglobulin V region; Signal
SIGNAL
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15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-I region V35 precurse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MADLINE=88296408; PubMed=2841108; Matsuda F., Lee K.H., Nakai S., Sato T., Ohno H., Fukuhara S., Honjo T.; "Dispersed localization of D segments in "Day-chain locus."; Proy-chain locus."
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P23083;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; 1.
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SIMILARITY: Contains 1 immunoglobulin-like domain.
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S00476; HVHU35.
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Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606; [1] SEQUENCE. HVIA_HUMAN STANDARD; PRT; 1 P01742; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence up 15-SEP-2003 (Rel. 42, Last annotation Ig heavy chain V-I region EU.

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GO; GO:0005576; C:extracellular; NAS.
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GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
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Eukaryota; Metazoa;
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SMART; SM00406; IGv; 1.
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MEDLINE=83065234; PubMed=6815656;
Kenten J.H., Molgaard H.V., Houghton
Bell L.O., Gould H.J.;
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ps50835; IG_LIKE;
bbulin_V region; Si
                                        QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY
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                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                   unrearranged VH gene segments."; Cell 40:271-281(1985).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Cunningham B.A., Rutish
Waxdal M.J., Edelman G.
                                                                                                                                                                                                                Yancopoulos G.D., Alt F.W.; "Developmentally controlled and tissue-specific
                                                                                                                                                                                                                                   MEDLINE=85099340; PubMed=2578321; Yancopoulos G.D., Alt F.W.;
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Immunoglobulin V region; Pyrrolidone carboxylic
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-JUL-1999 (Rel. 38, Last annotation update)
heavy chain V region VH558 Al/A4 precursor
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GO:0003823; F:antigen binding activity; NAS.
GO:0006955; P:immune response; NAS.
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hemistry 9:3161-3170(1970).
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117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 06,
(Rel. 06,
(Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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  a license agreement
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71.1%;
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8; Mismatches
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  noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1e-32;
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Best Local
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                                                                                                                                                                                                                                                                                                                 21-JUL-1986
21-JUL-1986
15-SEP-2003
                                                                                                                                                     Capra J.D., Nisonoff A.;
Capra J.D., Nisonoff A.;
Structural studies on induced antibodies with defined idiotypic specificities. VII. The complete amino acid sequence of the heavy chain variable region of anti-p-azophenylarsenate antibodies from mice bearing a cross-reactive idiotype.";

J. Immunol. 123:279-284(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V region (Anti-arsonate antibody).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                      MOUSE
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          DOMAIN
                                                                                            PIR; A02022; G1MSAA.
HSSP; P01772; 2FB4.
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                                                                                                                                                                                                                                             SEQUENCE
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SMART; SM00406; IGv;
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                                          Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
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          PROSITE; PS50835; IG_LIKE; Immunoglobulin V region.
                                                                        InterPro;
                                                                                   InterPro;
                                                                                                                -!- SIMILARITY: Contains 1 immunoglobulin-like domain
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THE IGG1 SUBCLASS. THERE
                                                                                                                          REGION SEQUENCE
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: PS50835;
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                                                                                                                                                                                                                                                                                                                                                                                                              NEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR 117
                                                             IPR003006;
IPR003596;
                                                                                IPR007110;
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117 AA;
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68
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117
115
                                                          Ig-like.
Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                          Rodentia;
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WAS NO HETERO
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Pred. No. 1.3e-32
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REMANORK-1.

COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-2.

FRAMEWORK-3.

BY SIMILARITY.
           IG-LIKE
                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RESULT
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RESULT 8
HV03_MOUSE
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Best Local S
Matches 63
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Best Local
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                                                                                                                                                                                                                                                                                                                     DISULFID
NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Sign
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Cell 24:625-637(1981)
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                                                                                                       AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                  NEKFKSKATLTVDTSSSTÄYMQLHSLTSEDSÄVYYCAR
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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Rodentia;
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                                                                                                                                                              VKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                            IG HEAVY CHAIN V REGION 186-1. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2. COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3. BY SIMILARITY.
                                                                                                                                                                                                                                    Score 330; UD -,
Pred. No. 4.1e-31;
Pred. No. 4.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 339; DB 1;
Pred. No. 3.7e-32;
4; Mismatches 17
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Sciurognathi; Muridae; Murinae; Mus
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           Query Match
Best Local S
Matches 61
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Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region 36-65.
Mus musculus (Mouse)
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma.
DOMAIN 1 111 IG-LII
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V region 93G7 precursor
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InterPro; IPR007110;
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Eur. J. Immunol. 12:1023-1032(1982).
FROM ANALYSIS OF THE SIZES OF
DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS C
CONCLUDE THAT ALL OF THESE V REGIONS HAVE REA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                             "Somatic mutation in genes for the immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the sw
                                                                                                                                                                                          Sims J., Rabbitts
                                                                                                                                                                                                               MEDLINE=82152818;
                                                                                                                                                                                                                               STRAIN=A/J
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P01746;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                        -!- SIMILARITY: Contains 1 immunoglobulin-like
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SIMILARITY: C
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T.H., Estess P.
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Rodentia;
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Pred. No. 5.6e-31;
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RESULT 10
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Best Local (
MGD; P01810; 2FBJ-VJ558.
MGD; MGI: 96486; IJh-VJ558.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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21-JUL-1986
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                                                                                                                                                    EMBL; J00488; AAA38519.1; PIR; A02041; HVMS8A.
                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents the statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-81245215; PubMed=6789211;
Givol D., Zakut R., Effron K., Rechavi
"Diversity of germ-line immunoglobulin
Nature 292:426-430(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
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P01758;
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InterPro; IPR003006; Ig_MHC.
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61.2%;
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Last annotation update)
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Pred. No. 1.1e
20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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RESULT 11
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Best Local S
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P01750;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835
Immunoglobulin V
SIGNAL 1
CHAIN 20
DOMAIN 20
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SEQUENCE 117
                                                                                                                                                                                            DOMAIN
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DOMAIN
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SIGNAL
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SMART; SM00406; IGv; 1.
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HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Heavy chain variable region contribution antibodies: somatic mutation evident in a Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=81234548; PubMed=6788376; Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - ! - MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RELATED GENES THAT
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                                                                                                                    62; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   PS50835; IG_LIKE;
bbulin V region; S:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSHGKSLEWIGYIYPYNGGTGY
  QKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCA
                                       VQLQQPGAELVKPGASVKVSCKASGYTFTSYWMHWVKQRPGQGLEWIGRIHPSDSDTNYN
                                                            VQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDYA
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117 AA;
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Pred. No. 1.2e-30;
                                                                                                                 Score 321; DB 1; 1
Pred. No. 4.5e-30;
2; Mismatches 22;
                                                                                                                                                                                                                                                        FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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                                                                                                                                                       Length 117;
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RESULT 12
HV04_MOUSE
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HV07_MOUSI
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Best Local S
Matches 61
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21-JUL-1986
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                            CHAIN
DOMAIN
                                          HV07_MOUSE STANDARD; PRT; 139 AA.
P01751; P01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last amoutation update)
15 heavy chain V region B1-8/186-2 precursor.
                                                                                                                                                                                                                                                                                             DISULFID
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HSSP; P01810; 2FBJ.
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Cell 24:625-637(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=81234548; PubMed=6788376; Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P01748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HV04_MOUSE
                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Heavy chain variable region antibodies: somatic mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                          mmunoglobulin
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RELATED GENES THAT COULD
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                                                                                                                                                                                                                   QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                                                                                         NEKFKSKVTLTVDKSSSTAYTQLSSLTSEDSAVYYCAR 117
                                                                                                                                                                                                   QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNINPGNGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                      PS50835;
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(Rel. 38, Last annotation
ain V region 23 precursor.
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larity 62.2%;
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5; IG LIKE;
7 region; Si
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annotation update)
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                                                                                                                                                                                                                                          Score 319; DB 1;
Pred. No. 7.7e-30;
5; Mismatches 22
                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION 23.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENCODE
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                   Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                     C530F829C906F69B
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ODE V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M., Imanishi-Kari T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGIONS
                    Vertebrata;
thi; Muridae;
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2a variable region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A SET OF CLOSELY NPB ANTIBODIES.
                                                                                                                                                                                                                                             Indels
                    Euteleostomi; 
; Murinae; Mus
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Best Local S
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                                             Ig heavy chain V regi
Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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                                                                                    DOMAIN
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DOMAIN
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See l
                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibodies: somatic n
Cell 24:625-637(1981)
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STRAIN=C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1A6U; 27-MAY-98.

PDB; 1A6W; 15-UUL-98.

InterPro; IPR007110; Ig-1ike.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Heavy chain variable region antibodies: somatic mutation
                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00529; AAA38170.1; -.
                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                    ROSITE; PS50835; IG LIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDON MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A90809; MHMS18
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                                                                                                                                                                            QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
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                                                Rodentia;
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Pred. No. 1.
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COMPLEMENTARITY-DETERMINING-2
FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                               IG HEAVY CHAIN V REGION B1-8/1 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                             205.12.
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                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                  1B57DD4FD0C9F465
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                                                Murinae; Mus.
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SEQUENCE.
MEDLINE=84182519; PubMed=6201162;
Dildrop R., Bovens J., Siekevitz

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Beyreuther

<u>~</u>

Rajewsky K.;

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RESULT 15
HV12_MOUSE
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P01756;

P01756;

21-JUL-1986 (Rel. 01, Created)

15-SEP-2003 (Rel. 42, Last amoutation update)

15-SEP-2003 (Rel. 42, Last amoutation update)

15 Je heavy chain v region MOPC 104E.

16 Mus musculus (Mouse)

17 Mus musculus (Mouse)

18 Mus musculus (Mouse)

19 Mus musculus (Mouse)

10 Eukaryota; Metazoa; Chordata; Craniata; Vertebra C Eukaryota; Metazoa; Rodentia; Sciurognathi; Muri
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Matches 59; Conserv
Query Match
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Immunoglobulin V region.
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SEQUENCE
118 AA; 12934 MW;
                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Glycop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete amino acid sequence of a mouse mu chain: homology heavy chain constant region domains.";
Biochemistry 21:5415-5424 (1982).
-!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS I PROTEIN HAS ALSO BEEN DETERMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
                                                                                                                                            SEQÜENCE
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-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02039; MHMS4E.
HSSP; P01789; 1MCP.
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Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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IG-LIKE.
BY SIMILARITY.
N-LINKED (GLCNAC. .
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Pred. No. 2.
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
     Score 313; DB 1;
Pred. No. 3.8e-29;
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                                                                                                                                            3CF8ACE4BE447E41 CRC64;
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                                             Length 117;
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AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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Search completed: December 30, 2003, 10:55:50 Job time: 5.25426 secs

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Maximum DB seq
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 2000000000
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378
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516
1 QVQLLQSAAEVRKPG
                                                                                                                                                                                                                                                                                                                            5:
6:
7:
9:
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1: sp_archea:*
2: sp_bacteria
                                                                                                                                                                   Query
Match
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      830525 segs, 258052604 residues
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_phage:*
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                   BB
Q9UL92
Q96GA6
Q8WY24
Q96QS0
Q9GYZ2
Q9UL92
Q9US98
Q925S3
Q9Y298
Q8VCX7
Q8VCX7
Q8VCX7
Q8VCX7
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Q9UL94
Q9BRV0
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                           Q8wy24 homo sapien
Q96q80 homo sapien
Q99y22 schistosoma
Q9ul89 homo sapien
Q992563 mus musculu
Q9y298 homo sapien
Q8vcx7 mus musculu
Q914t1 mus musculu
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Q9u194
Q9brv0
Q9bry0
Q9u192
Q96ga6
Q8wy24
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Q99LA6	Q924R5	Q925S2	Q924Q8	Q924Q3	Q924R8	Q924R4	Q924R1	Q924Q7	Q924R3	Q924Q9	Q924Q6	Q924R0	Q924Q5	Q924Q4	Q924R2	Q924R6	Q9JL75	Q91V67	Q924Q0	Q9Z1C4	Q924Q1	Q924Q2	Q8VDC9	Q920E8	Q921A6	Q8VIJ1	Q924P9	095978
Q991a6 mus musculu	Q924r5 mus musculu	ana	24 q 8 mus	24q3 mus	ana	Q924r4 mus musculu	4r1 mus	ana	Bnw	Bru	Bum	Q924r0 mus musculu	Bum	8nm	2 11118	anu 8	5 mus	mus	Bnm 0	mus	Bum	Q924q2 mus musculu	Brum 6	8 mus	8 mm8	Q8vij1 mus musculu	9 mus	095978 homo sapien

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RESULT 1
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Q9UL95;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF035019; AAI
HSSP; P01810; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                           76;
Similarity
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125 AA;
                                                                                                           Conservative
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                                                                                                                                                                                                                125
13516 MW; 0D3CD5C232488EAC CRC64;
                                                                                                                                        77.5%;
77.6%;
                                                                                                        Score 400; DB 4; Length 125;
Pred. No. 1e-37;
8; Mismatches 14; Indels
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Q9BRV0
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Matches 76
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Q9UL94;
01-MAY-2000
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MEDLINE=98277139; PubMed=9614934;
Van der Merwe P.L.,
                      TISSUE=Prostate;
Strausberg R.;
Submitted (APR-2001) to the
EMBL; BC005951; AAH05951.1;
HSSP; P01789; IMCP.
                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1
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01-MAR-2003
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                        Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BRV0
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HSSP; P01810; 2FBJ
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Mammalia; Eutheria;
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                        NCBI_TaxID=9606;
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119 AA;
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(TrEMBLrel. 13, Last sequence update)
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tive immunoglobulin heavy chain variable
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PRELIMINARY;

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RESULT 4
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Best Local S
Matches 76
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Best Local (
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 500 AA; 54154 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9UL92;
Q9UL92;
01-MAY-2000
01-MAY-2000
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NON_TER
SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                        Clin. Immunol. Imm
EMBL; AF035022; AAI
HSSP; P01772; 2FB4
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ul-may-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation updat Myosin-reactive immunoglobulin heavy chain variab
                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SPROSITE; PS50835; IG_LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                               fetus."
                                                                                                                                                                                                                                                                                                                         "Myosin-reactive autoantibodies in rheumatic
                                                                                                                                                                                                                                                                                                                                    Wu X., Liu B., Van Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Fragment).
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             AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                        QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEMMGWISIYSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKKFQGRVTLTTDTSTSTVYMELRSLRSDDTAVYYCAR
AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
                                                                                                                                                     124
124 AA;
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                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                        13580 MW;
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HW_bi
                                                                                                               75.8%;
76.5%;
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                                                                                                   Score 391; DB Pred. No. 1.1e-9; Mismatches
                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 398;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                        1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Best Local :
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Q8WY24;
Q8WY24;
Q1-MAR-2002 (TrEMBLrel. 2
Q1-MAR-2002 (TrEMBLrel. 2
Q1-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009851; AAH09851.1; -.
InterPro; IPR000005; HTHAraC.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_wHC.
InterPro; IPR003006; Ig_v.
Ffam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
"Identification and characterization of SNC66, a Ig-like
down-regulated in colorectal cancer.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF283666; AAL36987.1; -.
InterPro; IPR00710; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003106; Ig_WHC.
                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 4.

SMART; SM004406; IGv; 1.

PROSITE; PS50035; IG_LIKE; 4.

PROSITE; PS00250; IG_MIC; 1.

SEQUENCE 497 AA; 53665 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Zheng S., Shao X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNC66 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 614 AA; 67921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                   69;
                                                                                                                                                                                      Similarity
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OBQLEQSGAEVTKPGASVKVSCKASGYTFIAYDINWVRQAPGQGLEWMGWMNPQTGNTEF
                                                        QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QMQLVQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMGWITPFNGNTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKFQDRVTITRDRSMNTAYMELSSLRSEDTAMYYCAR 117
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                   72.78;
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23,
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Last
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 378; DB 4;
Pred. No. 2.3e-34;
2; Mismatches 15
                                                                                                                                                                                   Score 375;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                         F24D08DFA5A663E5 CRC64;
                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fang Y., Dong Q.;
n of SNC66, a Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497
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                                                                                                                                                                               DB 4;
.9e-34;
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                                                                                                                                                                                                               Length 497;
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Matches 71
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
SEQUENCE 159 AA; 17497 MW; !
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Q96QS0;
01-DEC-2001
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative matrix cell adhesion molecule-3.
                                                                                                                                                                                   Schistosoma japonicum.";
Submitted (JUN-2000) to the
EMBL; AF282622; AAG01452.1;
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                         Song X.T., Feng Z.Q., Guan X.H.;
"Amplification, cloning and sequence
"Amplification gene of monoclonal an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TYEMBLrel. 16, Created)
01-MAR-2001 (TYEMBLrel. 16, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GYZ2;
01-MAR-2001
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"Homo sapiens putative microfibrillar protein with Ig-like mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9GYZ2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
InterPro; IPR007110; Ig-like InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6182;
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                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
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anti-idiotypic
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Schistosoma.
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Q9UL89;
01-MAY-2000
Q925S3;
Q925S3;
Q925S3;
Q925S3;
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01-DEC-2001
01-MAR-2003
MRP3.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                      QGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCA 97
                                                                                                                                                                                                                                                                                                   VQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANYAQKF
                                                                                                                                                                                                                                                                                                                            LQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDYAQKF
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119 p
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116 AA;
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75.3%;
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Pred. No. 2.1e-32;
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RESULT 11
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EMBL; AP240166; AAK43731.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
SEQUENCE 147 AA; 16274 MW;
Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cui D., Zeng G., Yan X., Li X., Su C.; "Cloning of mouse genes related to repairing of the irradiated mice by treatment with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mechanism of exogenous nucleic acids and
the repair of intestinal epithelium after
World J. Gastroenterol. 6:709-717(2000).
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PubMed=11819679;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Su C.
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGG VH.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BALB/c
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                                                              Pfam; PF00047; ig;
SMART; SM00406; IGv
                                                                                                                                                                    Blood 92:496-506(1998).
EMBL; AJ224083; CAA11829.1;
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                              Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and kinetics of factor VIII
IgG4 monclonal antibody derived from a
inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9Y298;
01-NOV-1999
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                                          PROSITE;
                                                                                                      InterPro;
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                                          PS50835;
                                                                                                   IPR007110; Ig-like
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                                IGV;
                                     IG_LIKE;
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Rodentia;
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Pred. No. 3.
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hes 21;
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RESULT 13
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Q8VCX7;
Q8VCX7;
Q8VCX7;
Q8VCX7;
Q1-MAR-2002 (TrEMBLrel. 20, Cr
1 01-MAR-2002 (TrEMBLrel. 20, La
T 01-MAR-2003 (TrEMBLrel. 23, La
T 01-MAR-2003 (TrEMBLrel. 23, La
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InterPro; IPR0077110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50835; IG_LIKE; 5.
                                                     Q91WT1
Q91WT1;
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Q91WT1;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.1 kDa protein.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmanalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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  SEQUENCE
                                       NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                             NEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                           AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVQLQQSGAELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCA 97
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150 A
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613 AA; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67855 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.7%; Score 339; DB 11; 65.3%; Pred. No. 6.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 342;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41A9384DD4C22862 CRC64;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Glesi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Glesi C., King B., Kochiwa H.,
RA Schriml L.M., Stabbi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Stabbi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Stabbi F., Suzuki R., Tomita M., Gariboldi M.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boitelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashiraki Y., Soshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashiraki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                           Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -.
HSSP; P01842; 7PAB.
MGD; MGI:96443; Igh-1.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013490; AAH13490.1; -.
                 InterPro; IPR003596; Pfam; PF00047; ig; 4. SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9D8L4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                  Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGH-1 OR 1810060009RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Colon;
 PROSITE;
                                                                                                                                                                 "Functional annotation of a full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
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   PS50835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.5%;
nilarity 65.3%;
Conservative 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel 17, (TrEMBLrel 17, (TrEMBLrel 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                 IGv; 1.
                                                                                                                                  BAB25349.1; -.
IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52105 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11,
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Last annotation update)
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Pred. No. 6.1e-30;
1; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
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                                                                                                                                                                 mouse
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                                                                                                                                                                   CDNA
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                                                                                                                                                                   collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481;
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RESULT 15
OBKOZ4

ID Q8KOZ4

AC Q8KOZ
AC Q8KOZ
AC Q8KOZ
DT 01-OC
DT 01-MU
DE Simi:
OS Mus
OC Euka
OC Mamm
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OC IIS
RP SEQI
RP SEQI
RP SEQI
RP SEQI
RO IIIS
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Search completed: December 30, Job time: 24.883 secs
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P SEQUENCE FROM N.A.

C TISSUE-Breast tumor;

A Strausberg R.;

A Strausberg R.;

A Strausberg R.;

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

I Interpro; IPR003599; Ig.,

I Interpro; IPR003597; Ig. Cl.

R Interpro; IPR00306; Ig_MHC.

R Interpro; IPR003596; Ig_W.

R Pfam; PF00047; IG; 3.

RR SMART; SM00409; IG; 3.

RR SMART; SM00409; IGC1; 3.

RR SMART; SM00406; IGC1; 1.

RR SMART; PS50835; IG_HHC; 2.

RR PROSITE; PS50835; IG_MHC; 2.

RR PROSITE; PS00939; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.1%; Score 336; DB 11; Length 473; Best Local Similarity 65.3%; Pred. No. 1e-29; Matches 64; Conservative 14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to expressed sequence AI893585.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8K0Z4
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SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
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                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                     65.1%; Score 336; DB 11; Length 480; 62.2%; Pred. No. 1e-29; tive 17; Mismatches 20; Indels
                                  2003, 11:01:03
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               A Geneseq 19Jun03:*

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2. /SIDS1/gcgdata/ger
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516
1 QVQLLQSAAEVRKPG
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 summaries
// SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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460	460	464	467	467	471	491	500	504	Score
89.1	89.1	89.9	90.5	90.5	91.3	95.2	96.9	97.7	Query Match
98	98	250	250	247	98	132	132	9.6	Query Match Length DB
23	21	23	23	23	21	21	21	21	BB
ABG91862	AAY50952	ABP45584	ABP45549	ABP45105	AAY50954	AAY50950	AAY50953	AAY50955	ID
Human antibody fra	Human anti-factor	Human BLyS binding	Human BLyS binding	Human BLyS binding	Human anti-factor	Human anti-factor	Human anti-factor	Human anti-factor	Description

New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -

45	44	43	42	41	40	39	38	37	36	35	3 4	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
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259	253	121	251	251	251	259	257	247	98	246	248	253	254	251	257	248	251	251	248	251	250	250	249	247	251	259	255	251	251	251	248	117	104	104	98
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544	ABP45625	AAU02549	ABP45858	ABP45725	ABP44919	ABP44962	ABP45599	ABP45715	AAY50951	ABP45181	ABP45866	ABP45953	ABP45394	ABP45544	ABP45568	76	ABP45859	ABP45575	ABP45860	ABP45867	ABP45582	ABP45550	ABP45414	ABP45862	ABP45727	ın	ABP45179	ABP45910	ABP45861	ABP45551	ABP45461	AAR66311	ABB40538	ABG55895	ABG78171
BLyS	BLyS bind	a	BLyS	BLyS	BLyS	BLyS	BLyS-			BLyS	Human BLyS binding			BLyS	BLyS		BLyS		BLyS				BLyS		Human BLyS binding	Ē	Peptide #8044 enco	٠.	Human Fv molecule						

ALIGNMENTS

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RESULT 1
AAY50955
AAY50955
AAY50955
AAY50955
AC AAY5
AC AAY5
AC AAY5
AC Huma
A
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                                                                                                                                                                                     WPI; 2000-053102/04
                                                                                                                                                                                                                                                                    Voorberg JJ,
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                                                                                                                                                                                                                                                                                                                                                            (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chain; antibody; factor VIII; hemostatic;
; VH protein.
                                                                                                                                                                                                                                                                    Van Den Brink EN,
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RESULT 2
AAYS0953
ID AAYS
XX AAYS
XX AAYS
XX AYS
XX Huma
XX Huma
XX Hemc
XX Hemc
XX Homc
XX New
PT Pre
PT Fre
PX New
PT Pre
PX New
PT Pre
PX New
PT Pre
PX New
PT Fre
XX New
PT Fre
CC Thib
CC hyb
CC G pre
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Best Local S
Matches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilla A patients. This sequence represents the human anti-factor VIII antibody VH EL-25 protein which is used in the method
This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human anti-factor VIII antibody VH IT-2 protein which is used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         нuman; heavy
hemophilia А;
                                                                                                                                                                                                                    New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY50953 standard; Protein; 132
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                                                                                                                                                                                                                                                                                                                                 Voorberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-factor VIII antibody VH protein VH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chain; antibody; factor VIII; hemostatic;
; VH protein.
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                                                                                                                                                                                                                                                                                                                                 Van Den
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                                                                                                                                                                                   4B; 61pp; English.
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RESULT 3
AAY5090
ID AAY50
XX AAY50
XX AAY50
XX AAY50
XX Huma
XX Huma
XX Home
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                                                                                                                                                                                                                                                                       This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human anti-factor VIII antibody clone IT-2 protein which is used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY50950 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human anti-factor VIII antibody VH clone IT-2 encoded protein.
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                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Fig 4A; 61pp; English.
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QVQLLQSATEVKKPGASMKVSCMASGYPETSYDISMVRQAPGQGLEWMGWISIYSGNTDY
                             QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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\; VH gene.
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                                                                                                                            95.2%;
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Pred. No.
                                                                                                                          Score 491; DB 21;
Pred. No. 2.3e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; heavy chain; antibody; factor VIII; hemostatic;
hemophilia A; VH protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human anti-factor
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  19-AUG-2002
                                                                                                                                                                                                                                                                         Sequence
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                         ABP45105;
                                                   ABP45105 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Fig 4B; 61pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SANQ-)
                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                    the invention.
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                                                                                                                                AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                    QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                                                                                                                   QVQLVLSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
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                                                                                                                 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
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  (first
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 entry)
                                                                                                                                                                                                                                   91.3%;
89.8%;
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                                                                                                                                                                                                                                  Score 471; DB 21; Pred. No. 1.7e-39;
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 RESULT 6
ABP45549
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Best Local :
                                                                                                                                                                                                                                             cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (vTD) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUN-2000; 2000US-212210P.
17-CCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; antinhomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
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                                                                                                                                                                                                                                 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 1734-1735; 3148pp; English.
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                                                                                                                                          Similarity
                                                                    QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                 QVQLLQSAAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                                                                                                             247 AA;
                                                                                                                       Conservative
                                                                                                                                      90.5%;
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                                                                                                                   Score 467; DB 23;
Pred. No. 1.1e-38;
3; Mismatches 6;
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ABP45549 standard; Protein; 250

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AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

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                                                                                                                                                                                                                                                                                                                                                                                                                         CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TWP) super family and induces B cell crown recrosis factor (TWP) super family and induces B cell crown in the control of the invention have CC proliferation and differentiation. The antibodies of the invention have CC continuation, immunospirate, immunostimulant, immunomodulatory, CC antirheumatic and antiAIDS activity of BLyS. The antibodies bind to BLyS cand so may be used to detect and quantitate the presence of BLyS in CC biological samples and may be used in this way to diagnose disease CC administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (CUID) and CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC the antibodies and fragments of the antibodies described in the method control of the antibodies and fragments of the antibodies described in the method control of the invention.
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Best Local
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21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
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                                                                                                                                                                                                                                                                                                                                                   Sequence
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17-OCT-2000;
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51
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                                                                                                                                                                                                                                   89;
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                                                                                                                                                                                                                                                                                                                                                                                                             invention.
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CAMBRIDGE ANT
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                              QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEMMGWISIYSGNTDY
                              AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                             QVQLLQSAAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
   AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barash SC,
                                                                                                                                                                                                                                                                                                                                                   250 AA;
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2000US-240816P.
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                                                                                                                                                                                                                                Score 467; DB 23;
Pred. No. 1.1e-38;
3; Mismatches 6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP45584 standard; Protein; 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibodies against B Lymphocyte Stimulating the diagnosis and treatment of cancers and i
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17-OCT-2000; 2000US-240B16P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
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                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel antibodies that immunospecifically bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                    antibodies and fragments of the antibodies described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Page 2306-2307; 3148pp; English
             61
                                                                                                                         88;
                                                                                                                                                                                                                                   invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                        Similarity
AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                       QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                                                                                                                                 250 AA;
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-293499P
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                                                                                                                                          89.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choi GH,
                                                                                                                       Score 464; DB 23;
Pred. No. 2.2e-38;
4; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides, useful for immune disorders -
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                                                                                                                                                         Length 250;
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RESULT 9
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           Human antibody fragment #46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                         ABG91862 standard; Protein;
                                                                                                                                                                                                                                                                                                                                               of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-053102/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hemophilia A;
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                                                                                                                                                                                                                                                                l Similarity 88.8
87; Conservative
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                                                                                                                                                                                                                             QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                                                                                                                              AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
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                                                                                                                                                         AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                                                      98 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain; antibody;
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                                                                                                                                                                                                                                                              Score 460; DB 21;
Pred. No. 2.1e-38;
4; Mismatches 7;
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Matches 87; Conserv
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                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated epitope present on cancer cells and important physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardic diseases, and cancer
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29-DEC-2000;
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Szanthon E, Richter T,
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                                                                                                                     QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                           AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                           QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                                                                                                                                             98
                                                                                                                                                                                                                                                                                                                                             the invention.
                                                                                                                                                                                            Conservative
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2000US-0751181.
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Amit B, Kooperman L,
                                                                                                                                                                                            4.
                                                                                                                                                                                                                Score 460; DB 23;
Pred. No. 2.1e-38;
                                                                                                                                                                                            Mismatches
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Peretz T,
98
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ABG78171 standard;

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RESULT 11
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   BXCXCXB
                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a peptide or polypeptide comprising an Fv comblecule, a construct of fragments or a construct of a fragment with cenhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, cell empeloid leukaemia cell). The peptide is also useful for preparing a cutte myeloid leukaemia cell): The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region contact of the invention.
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favour of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-DEC-2001; 2001WO-US49440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200259264-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human
Human liver peptide,
                               25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Page 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plaksin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BIOT-) BIO-TECHNOLOGY GEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-DEC-2000; 2000US-0751181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-2002
                                                                                            ABG55895 standard; Peptide; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-619166/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fv molecule hypervariable region related peptide
                                                                                                                                                                           19
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                                                                                                                                                                                                                                                                                                   l Similarity
87; Conserv
                                                                                                                                                                                                                                                        QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISMVRQAPGQGLEWMGWISIYSGNTDY
                                                                                                                                                                                                                                      QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60
                                                                                                                                                                         AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                           AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                                                                                                                                                                                                                                                                                                                                                                  98
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                                                                                                                                                                                                                                                                                                     Conservative
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                  ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232pp;
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SEQ ID No 34543
                                                                                                                                                                                                                                                                                                                  89.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                  Score 460; DB 23;
Pred. No. 2.1e-38;
4; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipschitz O,
                                                                                                                                                                                                                                                                                                                                   23;
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                                                                                                                                                                                                                                                                                                                                 Length
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RESULT 12
ABB40538
ID ABB40
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AC ABB40
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XY
O1-FE
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Pepti
XX
XW
Human
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Matches
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26-MAY-2000; 2000US-0508408.
30-JUN-2000; 2000US-0532366.
23-AUG-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                      stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genc
analysing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00664
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hypercholesterolaemia; coronary heart disease.
              Human; foetal liver; gene expression; single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
                                             Peptide #8044
                                                                             04-FEB-2002
                                                                                                                                        ABB40538 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-)
                                                                                                            ABB40538
                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome-derived single exon nucleic acid probes useful for sing gene expression in human adult liver -
                                                                                                                                                                                                                                                                                                                                                al Similarity
87; Conserv
                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                    19
                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                    1 QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                   AOKLOGRVIMTIDISTSTAYMELRSLRSDDTAVYYCAR 101
                                                                                                                                                                                                                                       AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                   QVQLVQSGAEVKXPGASVKVSCKASGYTPTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID No 34543; 658pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                               104 AA;
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                           (first entry)
                                             encoded by
                                                                                                                                                                                                                                                                                                                                                             89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W, Rank DR;
                                             human foetal liver single exon
                                                                                                                                             104
                                                                                                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                                                                                                                                                                              Score 460; DB 22;
Pred. No. 2.2e-38;
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                                                                                                                                                                                                                                                                                                                                                                               Length 104;
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60 63

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RESULT 13
AAR66311
ID AAR66
XX AAR66
XX
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Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exc nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
03-AUG-1995
                                                   24-NOV-1994.
                                                                                                                                                                                                                                                                                         Human immunoglobulin variable heavy chain #17.
                                                                                                                                                                                                                                                                                                                                                                                                                            AAR66311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR66311 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000;
27-SEP-2000;
10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483447/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                          placenta; vector;
                                                                                                                                                                                                                                     PCR; amplify; human; immunoglobulin; variable; heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLVQSGAEVKXPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 33173; 639pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 AA;
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2000US-0608408.
2000US-0632366.
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2000US-0236359.
2000GB-0024263.
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(first entry)
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  93WO-JP00603
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                                                                                                                                                                                                          pJB81; E.coli; mammalian.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 460; DB 22;
Pred. No. 2.2e-38;
4; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank DR;
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RESULT 14
ABP45461
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Chain sequences encoded by novel isolated genes. The genes
Constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR
Constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR
Constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR
Constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR
Constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR
Constructs: The PNA was partially digested with TaqI restriction enzyme.
Constructs: The PNA was partially digested with TaqI restriction enzyme.
Constructs: The PNA was partially digested with TaqI restriction enzyme.
Constructs: The PNA was partially digested with ClaI-digested cosmid vector pJB81. The fragments were ligated with ClaI-digested cosmid vector pJB81. The ligation products were in vitro packed and infected that E.coli 490A. The fragments were then subcloned by colony the phybridisation. The Vn genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts.
Constructs: Y202; Y20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                           BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunosetimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                Ното варіелв.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human BLyS binding scrv SEQ ID 1472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP45461 standard; Protein; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                           WO200202641-A1
                                                                                                                                                                                                                                                                           common variable immunodeficiency; acquired immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA fragment comprising human immunoglobulin Vh genes production of human immunoglobulin in mammalian hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein sequences (AAR66295-51) are novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ78956.
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Pred. No. 2.5e-38;
4; Mismatches 7;
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16-JUN-2000; 2000US-212210P 17-OCT-2000; 2000US-240816P

15-JUN-2001; 2001WO-US19110

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RESULT 15
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                                                                                                                                                    BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficies systemic lupus erythematosus; rheumatoid arthritis; CVID; ALDS;
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21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 2159-2160; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
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15-JUN-2001; 2001WO-US19110
                                  10-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                ABP45551
                                                                                                                                       common variable immunodeficiency; acquired immunodeficiency syndrome
                                                                    WO200202641-A1
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Pred. No. 5.5e-38;
4; Mismatches 7;
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17-OCT-2000; 2000US-240816F.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                    diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of tumour necrosis factor (TNF) super family and induces B cell
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                     61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                                                                                                                                                                        Similarity
                                                                          QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
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Pred. No. 5.6e-38;
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Perfect score:
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Published Applications AA:*

1: /cgn2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

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12: /cgn2 6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

13: /cgn2 6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

14: /cgn2 6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

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16: /cgn2 6/ptodata/2/pubpaa/US00 NEW PUB.pep:*

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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15	14	13	12	11	10	9	8	7	6	S	.4	ω	2	ب	Result
460	460	460	460	460	460	460	460	460	460	460	460	464	467	467	Score
89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.9	90.5	90.5	Query
125	125	125	117	104	98	98	98	98	98	86	98	250	250	247	Query Match Length DB
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US-10-269-805-45	US-10-041-860-207	US-10-041-860-42	US-10-041-860-206	US-09-864-761-47285	US-10-194-975-4	US-10-308-817-44	US-10-041-860-356	US-10-041-860-355	US-10-041-860-326	US-10-041-860-324	US-10-041-860-2	US-09-880-748-1595	US-09-880-748-1560	US-09-880-748-1116	ID
Sequence 45, Appl		Sequence 42, Appl	Sequence 206, App	Sequence 47285, A	Sequence 4, Appli	Sequence 44, Appl	Sequence 356, App	Sequence 355, App	Sequence 326, App	Sequence 324, App	Sequence 2, Appli	Sequence 1595, Ap	Sequence 1560, Ap	Sequence 1116, Ap	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
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-09-880-748-9	9-880-748-16	-09-880-748-172	-09-880-748-11	9-880-7	-09-880-748-196	-09-880-748-140	-09-880-748-	7	-09-880-748-177	0-748-187	80-748-15	-09-880-748-187	-09-880-748-187	US-09-880-748-1593	-09-880-748-156	8-142	US-09-880-748-1873		US-09-880-748-1738	US-09-880-748-1356	0-748-119	US-09-880-748-1921	87	48-15	-09-880-748-147	1-860-	-10-041-860-24	-10-041-860-	
973	161	172	119	-	15	Sequence 140	15	15	17	Sequence 187	15	16	16	15	e 15	14	Seguence 187	S	Sequence 173	13	_	19	equence 18	e 15	14	w	4	w	
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ALIGNMENTS

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FILLE OF INVESTIGATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1116
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Sequence 1116, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                           LENGTH: 247
TYPE: PRT
                                                                                                                                                        Docal Similarity 90.5%;
es 89; Conservation
61 AQKFQGRVIMTIDISRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                             1 QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISMVRQAPGQGLEMMGWISIYSGNTDY 60
                                                                    QVQLLQSAAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEMMGWISAYNGNTNY 60
                                                                                                                                                               Score 467; DB 11; Length 247; Pred. No. 1.8e-40; 3; Mismatches 6; Indels
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AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

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                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1595
                                                                                                                                                                                                             FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-880-748-1560
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
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Best Local Similarity
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                                                                                                                    SEQ ID NO 1595
LENGTH: 250
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  Query Match
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 3239 SOFTWARE: PatentIn Ver. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 3239
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                                                                                                                                                                       PatentIn Ver.
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  89.9%;
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Pred. No. 1.9e-40;
  Score 464;
  BB
  11;
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Length 250;
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APPLICANT: Feng, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
APPLICANT: Bezabeh, Binyam
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Matches 88; Conserv
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SEQ ID NO 2
LENGTH: 98
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CURRENT APPLICATION NUMBER: US/10/041,860 CURRENT FILING DATE: 2002-01-07 NUMBER OF SEQ ID NOS: 377 SOFTWARE: FRASTSEQ for Windows Version 4.0 SEQ ID NO 324 LENGTH: 98
                                                                                                                                                                                                                                            APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi APPLICANT: Peng, Xiao APPLICANT: Yang, Xiao-Dong
                                                                                                             APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.1%;
1 Similarity 88.8%;
87; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
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Yang, Xiao-Dong
Chen, Francine
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Pred. No. 3.6e-40;
4; Mismatches 7
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Sequence 355, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX, 051A
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
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                                                                                                                                                                                                                                                                                                                   RESULT 7
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 326
LENGTH: 98
TYPE: PRT
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/041,860
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ORGANISM: homo sapiens
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88.8%;
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Pred. No. 3.6e-40;
4; Mismatches 7;
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                                                         PDGFD AND USES
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APPLICANT: Yang, Xiao Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit. Gazit
                                                                                                                              Sequence 44, Application US/10308817 Publication No. US20030219861A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 356
LENGTH: 98
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NUMBER OF SEQ ID NOS: 377
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 355
LENGTH: 98
TYPE: PRT
ORGANISM: homo sapiens
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Best Local 9
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              APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
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APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
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NUMBER OF SEQ ID NOS: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: homo sapiens
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88.8%;
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Pred. No. 3.6e-40;
4; Mismatches 7
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Pred. No. 3.6e-40;
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LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-44
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US-10-194-975-4
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Matches
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Publication No. US20030039649A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 87; Conserv
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PRIOR PILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOPTWARD NOS: 122
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CURRENT FILING DATE: 2002-10-10
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                                                                                                                                   APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                       FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                 APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                              PRIOR
                                           PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
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Pred. No. 3.6e-40;
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Sequence 206, Application US/1004
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
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US-10-041-860-206
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PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00661
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Best Local
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
               APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED
TITLE OF INVENTION: THEREOF
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.42
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8
OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39
OTHER INFORMATION: EST_HUMAN HIT: AM403728.1, EVALUE 4.00e-45
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                                                                                                                                                                                                                                                                                                                           Application US/10041860
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ABGENIX.051A
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Pred. No. 3.8e-40;
4; Mismatches 7
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                                                     PDGFD AND
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APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Yang, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Chen, Francine
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Hezabeh Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-041-860-207
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US-10-041-860-42
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                                                                                       ; Sequence 207, Application US/10041860 ; Publication No. US20030157109A1 ; GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 206
SEQ ID NO 206
SEQ ID RO 206
ORGANISM: homo sapiens
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Best Local :
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Matches
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                                           APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi APPLICANT: Feng, Xiao
                               APPLICANT:
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ORGANISM: homo
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Local Similarity 88.8%;
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87; Conserv
Jia, Xiao-Chi
Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
Gazit, Gadi
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Pred. No. 4.4e-40;
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RESULT 15

US-10-269-805-45

US-10-269-805-45

Sequence 45, Application US/10269805

Publication No. US20030124129A1

GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BII
FILE REFERENCE: A-722

CURRENT FAPPLICATION NUMBER: US/10/269,805

CURRENT FAPPLICATION NUMBER: US/0/328,604

PRIOR APPLICATION NUMBER: US 60/328,604

PRIOR APPLICATION NUMBER: US 60/328,604
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; TYPE: PRT
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CURRENT APPLICATION NUMB
CURRENT FILING DATE: 20
NUMBER OF SEQ ID NOS: 37
SOPTWARE: FBSTSEQ for Wi
SEQ ID NO 207
LENGTH: 125
                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 45
                                                                                                                                Best Local Similarity Matches 87; Conserv
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                    61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                                                                                   QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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Pred. No. 4.7e-40;
4; Mismatches 7;
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Pred. No. 4.7e-40;
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Search completed: December 30, 2003, 11:45:23 Job time: 22.0171 secs

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Maximum Match 100%
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
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    DB
US-08-545-809A-105
US-08-264-093-3
US-09-025-769B-22
US-08-964-690-22
US-08-964-690-22
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US-08-561-521-10
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US-08-61-77-8078-94
US-08-477-281A-94
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1 QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60

US-08-545-809A-105

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

TELEX: 200154
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid

Query Match
Best Local Similarity
Matches 87; Conserv

89.1%; ilarity 88.8%; Conservative

Score 460; DB 3; Length 117; Pred. No. 1.2e-41; 4; Mismatches 7; Indels

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Gaps

RESULT 1 US-08-545-809A-105 (Sequence 105, Application US/08545809A) Patent No. 6096878 GENERAL INFORMATION: APPLICANT: HONJO, TASUKU APPLICANT: HONJO, TASUKU APPLICANT: HONJO: FUNDAN IMMUNOGLOBULIN VH GENE TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTA NUMBER OF SEQUENCES: 145 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street CITY: Boston STATE: MA COUNTRY: US ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER READABLE FORM: COMPUTER READABLE FORM: DERATING SYSTEM: Windows95 SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION NATA: APPLICATION NUMBER: US/08/545,809A FILING DATE: 27-MAR-1996 PRIOR APPLICATION NUMBER: PCT/JP93/00603 FILING DATE: 10-MAY-1993 ATTORNEY/AGENT INFORMATION: NAME: Freeman, John W. REGISTRATION NUMBER: 29,066 REFERENCE/DOCKET NUMBER: 06501/004001 FILEFAX: 617-542-5070 TELEFAX: 617-542-8906	28 401 77.7 108 4 US-09-899-896-3 29 401 77.7 117 3 US-08-255-809A-128 30 397 76.9 121 1 US-08-202-047-23 31 397 76.9 121 3 US-08-94-690-23 32 397 76.9 135 1 US-08-137-1170-100 34 396 76.7 135 1 US-08-137-1170-112 35 396 76.7 135 2 US-08-436-717-112 36 396 76.7 135 2 US-08-436-717-112 37 395 76.6 119 3 US-08-933-983-21 38 395 76.6 119 2 US-08-545-809A-91 39 395 76.6 119 2 US-08-253-877C-19 41 395 76.6 139 3 US-08-253-877C-19 41 395 76.6 139 2 US-08-253-877C-19 42 395 76.6 139 2 US-08-253-877C-19 43 395 76.6 139 2 US-08-63-024-18 44 393 76.2 138 4 US-08-450-809-14 45 393 76.2 236 3 US-09-049-672A-13 45 393 76.2 236 3 US-09-049-672A-13
CONTAINING THE SAME	Sequence 3, Appli Sequence 128, Appl Sequence 23, Appl Sequence 100, App Sequence 100, App Sequence 110, App Sequence 112, Appl Sequence 112, Appl Sequence 11, Appl Sequence 13, Appl Sequence 13, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appli Sequence 11, Appli Sequence 13, Appli

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                                                                                                                                                RESULT 3
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                                             Sequence 22, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5639863
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: No. 563
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION UNUBER: 31081
REFERENCE/DOCKET NUMBER: NOVO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 3:
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TITLE OF INVENTION: I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS 6.00 SOFTWARE: ASCII Editor CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/264, FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
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                    APPLICANT:
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STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY. -----
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: Canada
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                                                                                                                                                                                                AQKFQGRVSMTTDTSTSTAYMEVRSLRSDDTAVYYCAR 98
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (416) 868-1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette -
                                                                                                                                                                                                                                                                                                                                                                                                                             not applicable
                                                                                                                                                                                                                                                                                                                                               85.3%;
83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO CELL CYCLE-INDEPENDENT GLIOMA SURFACE ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/264,093
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                                                                                                                                                                                                                                                                                                                              Score 440; DB 1; L
Pred. No. 1.7e-39;
                                                                                                                                                                                                                                                                                                                                                              Length 121;
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RESULT 4
US-08-202-047-22
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COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-198
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: CHESNUT
APPLICANT: POLLEY,
APPLICANT: PAULSON
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Best Local S
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                            APPLICANT: BENDIG, Mary M.

TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREST: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MO
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                      STREET: One Maine. .
CITY: San Francisco
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                                                                               COUNTRY:
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                                                           94105
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                                                                                                  California
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1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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(212)596-9090
                                                                                                                                                                                                                                                       JONES, S. Tarran
SALDANHA, Jose W.
                                                                                                                                                                                                                                                                                              POLLEY, Margaret J. PAULSON, James C.
                                                                                                                                                                                                                                                                                                                                     CHESNUT, Robert W.
IBM PC compatible
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US-08-964-690-22
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OTHER INFORMATION: /label= HUMAN_I
US-08-202-047-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.5%;
Best Local Similarity 82.8%;
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TELEPHONE: 415-226-2400
TELEPAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,690
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,2
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: PAULSON, James C.
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, Jose W.
APPLICANT: BENDIG, Mary M.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
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CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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CLASSIFICATION: 424
                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82;
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                                                                                                                                                                                                                                                                                        USA
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n Release #1.0,
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Pred. No. 6.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Mismatches
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US-08-561-521-45
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                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-OOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION LOATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: SMith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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Best Local Similarity
Matches 82; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                  TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-77
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Leger, Olivier J
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein LOCATION: 1..128 OTHER INFORMATION: /label= HUMAN_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino actu
STRANDEDNESS: single
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                                                                                             TELEPHONE: 415-543-9600
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                    ENGTH:
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amino acid
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                  129 amino acids
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Leger, Olivier J.
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82.8%;
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Pred. No. 6.2e-38;
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US-08-525-539A-77
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APPLICANT: DO COUTO, FERNANDO J
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT
TITLE OF INVENTION: METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 630963
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                                                                                                                                             Query Match
Best Local
                                                                                                                              Matches
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NAME: DYLAN, TYLER
REGISTRATION UNMBER: 37,612
REFERENCE/DOCKET NUMBER: 2763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                        TELEFAX: (415) 494-079
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: line
MOLECULE TYPE: |
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
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TOPOLOGY: li
                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                          ENGTH:
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                60 YAQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNGDTN 60
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linear
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82.8%;
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82.8%;
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                                                                                                                                             Score 425.5; DB of Pred. No. 6.2e-38
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Pred. No. 6.2e-38;
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RESULT 8
PCT-US95-01219-45
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                                                                                                                                                    Sequence 96, Application US/08545809A Patent No. 6096878
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Monjo, Tasuku
APPLICANT: Motsuda, Fumihiko
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,22
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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ADDRESSEE:
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Fish & Richardson,
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P.C.
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225 Franklin Street

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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36, Application US/09025769B Patent No. 6300064
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INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/545,809A FILING DATE: 27-MAR-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/JP93/00603 FILING DATE: 10-MAY-1993 ATTORNEY/AGENT INFORMATION:
             SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Win
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                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                      CITY: New York
STATE: New York
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TOPOLOGY: linear
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 FILING DATE:
                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                            E: James F. Haley, Jr., Esq. c/o Fish & Neave
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 amino acids
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Ilag, Vic
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18-FEB-1998
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82.7%; Pred. No. 1e-37;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                            APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                            APPLICATION NUMBER: US/09/025,769B FILING DATE: 18-FEB-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                      TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1251 Ave
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 10021
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                                        TELEFAX:
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1251 Avenue of the Americas
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Moroney, Simon
Plueckthun, Andreas
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                                      (212)596-9090
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Ilag, Vic
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82.7%;
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US-08-652-816A-19
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                                                                                                                                                                                                               APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
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                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GE
FILING DATE: 02-DCC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
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APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: CFILING DATE: 24-MAR-PRIOR APPLICATION DATA:
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APPLICATION NUMBER: GB 9
FILING DATE: 02-DEC-1991
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APPLICATION NUMBER:
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 02-DEC-1991
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5872215
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82.7%;
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                                                                                                                                US 08/244,597
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Pred. No. 1.7e-37
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RESULT 13
US-09-199-149-3
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APPLICANT: Jonak, Zdenka L.
APPLICANT: Taylor, Alexander H.
APPLICANT: Trulli Jr., Stephen H.
APPLICANT: Johanson, Kyung O.
TITLE OF INVENTION: Humanized Monoclonal Antibodies
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Patent No. 6096878
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 37
                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Honjo, Tabuku
APPLICANT: Matsuda, Fumihiko
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: P50860
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TYPE: PRT
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                           STREET: 225 F
CITY: Boston
STATE: MA
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TOPOLOGY:
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Local Similarity 83.5%;
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                             COUNTRY: US
ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWIN-PGGDTNY
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                                                                                                                                                                                                                                                       Application US/08545809A
                                                                                           225 Franklin Street
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Diskette
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RESULT 15
US-08-561-521-10
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TELEX: 200154
INFORMATION FOR SEO ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08561521 Patent No. 5840299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                STATE: C
                                                                                                                                                                                                                                                                                                                                                                                     STREET: One Market F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Freeman, John W. REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                              FILING DATE:
REFERENCE/DOCKET NUMBER: 15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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Leger, Olivier J.
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                                                                                                                                      Pest Local Similarity 79.7%;
Matches 78; Conservative
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TELEPHONE: 415-543-9600
TELEPAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
61 SQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAR 98
                     61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                             1 QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60
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                                                                                                                                                Score 411; DB 2; Length 119; Pred. No. 2e-36; 8; Mismatches 12; Indels
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Search completed: December 30, 2003, 11:05:32 Job time : 10.0346 secs

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Minimum
Maximum
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5.5
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length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Maximum Match 100%
Listing first 45 s
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
                                                         F84247
A98339
AI2943
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T12741
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S43507
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A49171
                                         T44142
T23612
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F90708
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36.7	36.7	37.1	37.1	37.1	37.1	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5
239	147	644	275	76	76	1756	1472	1175	555	395	383	376	302	255	255
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T16159	H71016	AD3471	B49394	G64663	C71852	T02599	A84470	D85089	T45351	T43892	B87579	G95949	JQ1878	H97360	AI2578
_	hypothetical prote	adenylyl-sulfate k	translation elonga	ribosomal protein	ribosomal protein		hypothetical prote	hypothetical prote	ferredoxin [import	translation elonga	hypothetical prote	probable oligopept	hypothetical 33.4K	hypothetical prote	conserved hypothet

ALIGNMENTS

RESULT JE0110

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A;Molecule type: mRNA
A;Residues: 369-593,'K', 595-1000 <WAM>
A;Cross-references: EMBL:ALL800158
A;Experimental source: adult testis; clone DKFZp434L194
C;Comment: This protein enhances a temporarium.
                                                                                                                      C;Species: Tetrahymena pyriformis
C;Date: 21-Jan-1994 #sequence_revision 15-Oct-1994 #text_change 02-Feb-2001
C;Accession: A49171 B49171
R;Kurasawa, Y.; Numata, O.; Katoh, M.; Hirano, H.; Chiba, J.; Watanabe, Y.
Exp. Cell Res. 203, 251-258, 1992
A;Title: Identification of Tetrahymena 14-nm filament-associated protein as elongation A;Reference number: A49171; MUID:93049915; PMID:1385189
A;Accession: A49171
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
A49171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitotic control protein dis3 homolog - human

C;Species: Homo sapiens (man)

C;Date: 22-May-1998 #sequence revision 29-May-1998 #text_change 02-Nov-2001

C;Accession: JE0110; T12542

R;Shiomi, T.; Fukushima, K.; Suzuki, N.; Nakashima, N.; Noguchi, E.; Nishimoto, T.
J. Biochem. 123, 883-890, 1998

A;Title: Human Dis3p, which binds to either GTP- or GDP-Ran, complements Saccharomyces A;Reference number: JE0110; MUID:98230695; PMID:9562621

A;Accession: JE0110
A;Molecule type: mRNA
A;Residues: 1-435 <KUR>
A;Residues: 1-435 <KUR>
A;Cross-references: GB:D11083; NID:g217407; PIDN:BAA01856.1; PID:g217408
A;Note: sequence extracted from NCBI backbone (NCBIN:117509, NCBIP:117510)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Note: DKFZp434L194.1
C;Superfamily: mitotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-1000 <SHI>
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann,
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17524
A;Accession: T12542
                                                                                                                                                                                                                                                                                                                                                                   translation elongation factor eEF-1 alpha chain - Tetrahymena pyriformis N; Alternate names: 14-nm filament-associated protein
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Comment: This protein enhances a temperature-sensitive mutant RCC1-stimulated nucleot
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Pred. No. 11;
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A;Accession: B49171
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 2-21 <KU2>
C;Genetics:
A;Genetics:
A;Genetic code: SGC5
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homo
C;Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis
F;2-435/Product: translation elongation factor EBF-1 alpha chain #status experimental
F;9-157/Domain: translation elongation factor Tu homology <ETU>
F;15-22/Region: nucleotide-binding motif A (P-loop)
F;15-98/Region: GTP binding #status predicted
F;154-157/Region: GTP binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, submitted to the EMBL Data Library, July 1999
A;Reference number: Z21598
A;Accession: T37174
                                                                                                                                                                                                                                                                                                                         micofilarial sheath protein, major component -
C;Species: Brugia pahangi
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1
C;Accession: S26854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-164 <SEE>
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                                                                                                                                                                                                                              A;Reference number: S26854
A;Accession: S26854
A;Status: preliminary
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                                                                                                                                                                                                                                                                                       submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                           R;Selkirk, M.
                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-205 <SEL>
                                                           Query Match
Best Local S
Matches 9
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Best Local (
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QNGGWYEGPLLEPRPDA 18
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                                                           Score 50; DB Pred. No. 3.7; Mismatches
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Pred. No. 6.1;
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                                                                                             Length 205;
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J. Biol. Chem. 266, 11002-11008, 1991
A;Title: A proline-rich structural protein of the surface sheath of larval Brugia fila A;Reference number: A40525; MUID:91250404; PMID:1710216
A;Servico.
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A; Molecule type: DNA
A; Residues: 1-403 < KAW>
A; Cross-references: DDBJ: AP000061;
A; Cross-references: DDBJ: AP000061;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
A40525
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                                    R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proline-rich sheath protein Mf22 precursor - nematode (Brugia pahangi)
C;Species: Brugia pahangi
C;Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 27-Jan-1995
C;Accession: A40525; S18744
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DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Kawarabayasi,
                                                                                                                                                                                  probable dehydrogenase YPO1556 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
                   A; Reference number: AB0001; A; Accession: AG0189
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A; Residues: 1-205 <SEL>
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A;Status: preliminary
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ya, M.; Masuda, S.; Funahashi, T.; Tanaka,
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Pred. No.
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T.; Kudoh, Y.; Yamazaki,
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A/Gene: EF-La; aEF-lalpha
C/Superfamily: translation elongation factor Tu; translation elongation factor Tu
C/Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis
F;7-155/Domain: translation elongation factor Tu homology <ETU>
F;13-20/Region: nucleotide-binding motif A (P-loop)
F;152-155/Region: GTP-binding NKXD motif
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A;Title: Organization of a Sulfolobus solfataricus gene cluster homologous to A;Reference number: Z17331; MUID:95078778; PMID:7527264
A;Accession: T11747
                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X76767; NID:g510206; PID:g510209
A;EXperimental source: ATCC 49255 / MT-4
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A; Residues: 1-435 < IAN>
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A;Note: this sequence has been revised in reference $37631
R;Arcari, P.; Gallo, M.; Ianniciello, G.; dello Russo, A.; Bocchini, Nucleic Acids Res. 21, 3920, 1993
A;Reference number: $37631
A;Concents: erratum
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A;Title: Primary structure of the elongation factor 1-alpha in Sulfolobus A;Reference number: S33718; MUID:93241951; PMID:8369039
A;Accession: S33719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 02-Feb-2001 C;Accession: S43507; S33719; S37631; T11747 R;Arcari, P.; Gallo, M.; Ianniciello, G.; Russo, A.D.; Bocchini, V. Biochim. Biophys. Acta 1217, 333-337, 1994 A;Title: The nucleotide sequence of the gene coding for the elongation factor 1-alpha A;Reference number: S43507; MUID:94198299; PMID:8148382
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 'H', 2-13,'Q', 15-435 <ARC2>
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A; Residues: 1-13, 'Q', 15-435 < ARC1>
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A; Residues: 1-435 <ARC>
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A;Cross-references: GB:AL590842; PIDN:CAC90378.1; PID:g15979597; GSPDB C;Generics:
A;Gener YPO1556
A;Gene: YPO1556
C;Superfamily: glycerol dehydrogenase; lactaldehyde reductase homology
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                   ENMKWYNGPTLEEYLDQLEL 224
                                                               ONGGWYEGPLLEPRPDALDI 21
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s: GB:AL590842; PIDN:CAC90378.1; PID:g15979597; GSPDB:GN00175
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V
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                                                                                                           Pred. No. 12;
3; Mismatches
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hypothetical protein 25 - Methanobacterium phage psiM2
C;Species: Methanobacterium phage psiM2
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A;Cross references: GB.AL591985; PIDN:CAC48799.1; PID:g15140272; GSPDB:GN00167 A;Experimental source: strain 1021, megaplasmid pSymb R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barll pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisl Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C. hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
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[95893]

hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSym

Cyspecies: Sinorhizobium meliloti

Cyspecies: """ 2001 #secuence revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                A;Gene: SMb20413
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A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: G95891
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A;Molecule type: DNA
A;Residues: 1-435 <KUR>
A;Cross-references: GB:AE006641; NID:gl3813351; PIDN:AAK40559.1;
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A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: H90162
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                                                                                          Query Match
Best Local Similarity
Matches 11; Conserv
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C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 05-May-2000 C;Accession: T12741
R;Pfister, P.; Wasserfallen, A.; Stettler, R.; Leisinger, T. submitted to the EMBL Data Library, May 1998
A;Pescription: Archaeophage PsiM2 complete genomic DNA.
A;Reference number: Z17578
A;Accession: T12741
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-354 <PFI>A;Residues: 1-354 <PFI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                glycerol dehydrogenase (EC 1.1.1.6) ybdH - Escherichia coli (strain K-12) C;Species: Escherichia coli (c;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002 C;Accession: E64793 C;Accession: E64793 V - Parra N T -
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A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-362 <BLATY A;Cross-references: GB:AEO00165; GB:U00096; NID:g1786808; PIDN:AAC7370 A;Experimental source: strain K-12, substrain MG1655 C;Genetics: C;Genetics: A;Gene: ybdH C;Superfamily: glycerol dehydrogenase; lactaldehyde reductase homology
                                                                                                                                                                                                                                                             R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; E.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64793
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A;Molecule type: DNA
A;Residues: 1-362 <HAY>
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C;Keywords: oxidoreductase; transmembrane protein F;9-354/Domain: lactaldehyde reductase homology <LAR>F;109-125/Domain: transmembrane #status predicted <TMM>
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DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: B85559
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable oxidoreductase ybdH [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli (C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Date: B6-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 #text_change 1
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                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE005174; NID:g12513492; PIDN:AAG54934.1; GSPDB:GN00145; UWGP:?
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551
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Shiba, T.;
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M.; Shinagawa,
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O9y211 homo sapien
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O08046 giardia lam
P09128 escherichia
P37702 arabidopsis
P10686 rattus norv
O92349 schizosacch
P11919 manduca sex
O07440 mus musculu
P12159 oryza sativ
P59270 mus musculu
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SEQUENCE OF 297-928 FROM N.A. TISSUE=Testis; Wambutt R., Heubner D., Mewes HW., Gassenh Submitted (JUN-1999) to the EMBL/GenBank/DDB -!- FUNCTION: COMPONENT OF THE EXOSOME 3->5	SEQUENCE FROM N.A. TISSUE=Brain, and Peripheral blood leukocytes; MEDLINE=21932550; PubMed=11935316; MEDLINE=21932550; PubMed=11935316; Rozenblum E., Vahteristo P., Sandberg T., Bergthorsse, Syrjakoski K., Weaver D., Haraldsson K., Johannsdott; Syrjakoski K., Weaver D., Haraldsson K., Johannsdott; Vehmanen P., Nigam S., Golberger N., Robbins C., Pak Gillander E., Stephan D.A., Bailey-Wilson J., Juo S., Gillander E., Stephan D.A., Bailey-Wilson J., Juo S., Arason A., Barkardottir R.B., Nevanlinna H., Borg A., Kallioniemi OP., Kallioniemi OP., Kallioniemi of a 6-Mb region at 13q21-q22 implicat development: identification and characterization of c Hum. Genet. 110:111-121(2002).	SEQUENCE FROM N.A. TISSUE=Brain; MEDLINE=99246063; PubMed=10231032; MEDLINE=99246063; PubMed=10231032; Miyajima N., Tishikawa KI., Suyama M., Kikuno R., Hin Nagase T., Ishikawa KI., Suyama M., Nomura N., Obara "Prediction of the coding sequences of unidentified The complete sequences of 100 new cDNA clones from b for large proteins in vitro."; DNA Res. 6:63-70(1999).	Shiomi T., Fukushima K., Suzuki N., Nakashima N., Nos Nishimoto T.; "Human dis3p, which binds to either GTP- or GDP-Ran, Saccharomyces cerevisiae dis3."; J. Biochem. 123:883-890(1998). [2] ERRATUM. Shiomi T., Fukushima K., Suzuki N., Nakashima N., Nos Nishimoto T.; J. Biochem. 124:250-250(1998).	TANDARD; PRT; 928 AA. Q9UG36; 39, Created) 39, Last sequence update) 42, Last annotation update) exonuclease RRP44 (EC 3.1.13) (Riboso in 44) (DIS3 protein homolog). KIAA1008. Man) oa; Chordata; Craniata; Vertebrata; Eutia; Primates; Catarrhini; Hominidae; Ho	34 42 35.0 324 1 B3G2_RAT 35 42 35.0 419 1 GLPB_ECOLI 36 42 35.0 420 1 EFIA_HALMA 37 42 35.0 457 1 GALB_KLULA 38 42 35.0 530 1 FUSA_BURCE 39 42 35.0 814 1 FADE_ECOS7 40 42 35.0 814 1 FADE_SALTI 41 42 35.0 814 1 FADE_SALTY 42 35.0 814 1 FADE_SALTY 43 42 35.0 814 1 FADE_SALTY 44 42 35.0 824 1 JBP2_HUMAN 44 42 35.0 888 1 YGB4_YEAST 45 42 35.0 1550 1 GLTB_SYNY3 ALIGNMENTS ALIGNMENTS
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InterPro; IPR004539; EFI alpha.
InterPro; IPR004795; EF GTPbind.
InterPro; IPR004160; EFTU Cterm.
InterPro; IPR004161; EFTU D2.
Pfam; PF00009; GTP EFTU, 1.
Pfam; PF03144; GTP EFTU D3; 1.
Pfam; PF03144; GTP EFTU D3; 1.
TIGRFAMS; TIGR00483; EF-1 alpha; 1.
PROSITE; PS00301; EFACTOR GTP; 1.
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NP_BIND
SEQUENCE
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                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 49255 / DSM 5833 / MT
MEDLINE-93241951; PubMed-8369039;
Arcari P., Gallo M., Ianniciello (
"Primary structure of the elongat:
solfataricus.";
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MEDLINE=94198299; PubMed=8148382; Arcari P., Gallo M., Ianniciello G., Dello Russo A., Bocchini V.; "The nucleotide sequence of the gene coding for the elongation far 1 alpha in Sulfolobus solfataricus. Homology of the product with
                                                                   STRAIN=ATCC 49255
MEDLINE=94198299;
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SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
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FUNCTION: This protein promotes the GTP-de aminoacyl-tRNA to the A-site of ribosomes
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-i- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN PROMOTEIN PROMOTES DURING PROTEIN
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Biochim. Biophys. Av
[3]
                                                                                                      CONFLICT
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Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGATNFCT.
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InterPro; IPR004539; EF1 alpha.
InterPro; IPR004795; EF GTPbind.
InterPro; IPR004160; EFTU Cterm.
InterPro; IPR004161; EFTU_D2.
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EMBL; X76767; CAA54162.1; -.
EMBL; AJ312397; CAC42886.1; -.
EMBL; AE006658; AAK40559.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as modified and this statement is not removed. It entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
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MEDLINE=21332296; PubMed=11427726;
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"The nucleotide sequence of the gene encoding the elongation factor lalpha from the archaeon Sulfolobus solfatarious isolate MT3.";
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION
EF-TU/EF-1A SUBFAMILY.
Similarity
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HAMAP; MF 00118; -; 1.

InterPro; IPR004539; EFI alpha.

InterPro; IPR004539; EF GTPbind.

InterPro; IPR000795; EF GTPbind.

InterPro; IPR004160; EFTU Cterm.

InterPro; IPR004161; EFTU D2;

Pfam; PF00009; GTP EFTU; 1.

Pfam; PF03144; GTP EFTU D2; 1.

Pfam; PF03143; GTP EFTU D2; 1.

PFAM; PF03143; GTP EFTU D3; 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X52382; CAA36608.1; -. PIR; S12818; EFUC1A. HSSP; P07157; 1AIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN-ATCC 33909 / NCIB 11770 / DSM 639;

Auer J. Spicker G., Mayerhofer L., Puehler G., Boeck A.;

"Organisation and nucleotide sequence of a gene cluster comprising the translation elongation factor 1-alpha from the extreme thermophilic archaebacterium Sulfolobus acidocaldarius: phylogenetic implications.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EF1A SUI
P17196;
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Sulfolobus acidocaldarius.
Sulfolobus acidocaldarius.
Sulfolobales; Sulfolobaceae;
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01-AUG-1990 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. Appl. Microbiol. 14:14-22(1991).

FUNCTION: THIS PROTEIN PROMOTES THE GTP-DI
AMINOACYL-THNA TO THE A-SITE OF RIBOSOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: C
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9; Conserv
                                                                                                                                  WYNGPTLEELLDQLEI
                                                                                                                                                                                 WYEGPLLEPRPDALDI
                                                                                                                                                                                                                                                                                                              factor; Protein biosynthesis;
13 20 GTP (BY SIM)
90 94 GTP (BY SIM)
152 155 GTP (BY SIM)
435 AA; 48200 MW; A012AF5646
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                          STANDARD;
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15, Last sequence update;
41, Last annotation updat
1-alpha (EF-1-alpha) (EIc
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THE GTP-BINDING ELONGATION
                                                                                                                                                                                                                       Score 48; DB
Pred. No. 8.9;
1; Mismatches
                                                                                                                                                                                                                                                                                                            A012AF564624803F CRC64;
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8.9;
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OSOMES DURING F
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EMBL; AE000165; AAC73700.1; -.
EMBL; U82598; AAB40800.1; -.
EMBL; D90701; BAA35229.1; -.
EMBL; X52904; -; NOT_ANNOTATED_C
PIR; E64793; E64793.
ECOGene; EG12692; ybdH.
InterPro; IPR001670; Fe-ADH.
                                                                                                                This SWISS-PROT entry is copyright. It is produced through a cubetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatics requires a license agreement (See http://www.isb-sib.cr send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  "Detection of new genes in a bacterial genome using three gene classes."; Nucleic Acids Res. 23:3554-3562(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Iaba T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
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                                                                                                                                                                                                                                                                                                                                              MEDLINE=96032851; PubMed=7567469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yano M., Horiuchi T.,
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage me DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-K12 / MG1655;
Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
Pederspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                Borodovsky M., McIninch
                                                                                                                                                                                                                                                                                                                                                                                    J. Mol. Biol. 218:129-140(1991).
                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular and functional characterization gene of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           Schultz J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91162636; PubMed=1848300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 282-362
STRAIN=K12;
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01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                    DENTIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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Enterobacteriaceae; Escherichia.
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FAMILY. STRONG, TO BACTERIAL GLYCEROL DEHYDROGENASE.
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fuctase ybdH (EC 1.1.-.-).
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Matches
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                                                                                                                                                                                                                                                     InterPro; IPR004539; EFT alpha.
InterPro; IPR000795; EF GTPbind.
InterPro; IPR004160; EFTU Cterm.
InterPro; IPR004161; EFTU D2.
Pfam; PF00009; GTP EFTU D2; 1.
Pfam; PF03143; GTP EFTU D3; 1.
PFAM; PF03143; GTP EFTU D3; 1.
PRINTS; PR00315; ELONGATNECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produce between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as impodified and this statement is not removed. Use entities requires a license agreement (See http or send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
Elongation factor 1-alpha C (EF-1-alpha).
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PROSITE; PS00913; ADH_IRON_1; 1.

PROSITE; PS00060; ADH_IRON_2; FALSE_NEG.

Hypothetical protein; Oxidoreductase; Complete proteome Hypothetical protein; Oxidoreductase; Complete proteome SEQUENCE 362 AA; 39091 MW; C28BBBB4F8F247AE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu Q.Y., Baldauf S.L., Reith M.E.;
"Elongation factor 1 alpha genes of the red alga Porphyra
"Elongation factor 1 alpha genes of the red alga Porphyra
include a novel, developmentally specialized variant.";
Plant Mol. Biol. 31:77-85(1996).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BIND
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Avonport;
MEDLINE=96309386; PubMed=8704161;
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                                                                       SEQUENCE
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HSSP; P07157;
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Eukaryota; Rhodophyta;
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01-OCT-1996
                                                                                                                                                                                TIGRAMS; TIGR00483; EF-1 alpha; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
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DEVELOPMENTAL STAGE: EXPRESSED IN BOTH SPOROPHYTE AND GAMETOPHYTE PHASES OF THE LIFE CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY. EF-TU/EF-1A SUBFAMILY.
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Similarity
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95
156
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43.8%;
    38
52
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Pred. No.
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                                                                                             Y SIMILARITY).
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                      Length 449;
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RESULT 10
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                                                                             PEAM; PROUGLY; LELY,
PRINTS; PRO0354; 7FEBSFRDOXIN.
PRINTS; PRO0419; ADXRDTASE.
PRINTS; PR00368; FADPUR.
PROSITE; PR00198; 4FE4S; FERREDOXIN; 1.
Oxidoreductase; Flavoprotein; NADP; FAD;
Iron-sulfur; 4Fe-4S; Complete proteome.
Iron-sulfur; 4Fe-4S; FERREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mingall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Feltwell T., Fraser A., Hamlin N.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream R., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Probable ferredoxin/ferredoxin--NADP reduct
FPRB OR ML2134 OR MLCB57.39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-I- CATALYTIC ACTIVITY: Reduced ferredoxin + N
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                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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Bacteria; Actinobacteria;
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                                                                                                                                                                                           InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR000131; 7Fe ferredoxin.
InterPro; IPR000759; Adrīdx_reductase.
InterPro; IPR001327; FAD_pyr_redox.
Pfam; PF00037; fer4; 2.
                                                                                                                                                                                                                                                                                                                          EMBL; Z99494; CAB16679.1; -. EMBL; AL583924; CAC31089.1;
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                                                                                                                                                                                                                                                                       Leproma; ML2134; -
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SIMILARITY: IN THE C-TERMINAL,
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an email to license@isb-sib.ch
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PERREDOXIN--NADP REDUCTASE:
IRON-SULFUR 1 (BY SIMILARITY).
IRON-SULFUR 1 (BY SIMILARITY).
IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY)
IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY)
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O THE BACTERIAL
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                                                                                                                   transport;
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RESULT RE
RESULT 12
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ID RS16_H
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                                                                                                                                                                                                                                                                                                                EMBL; AE001535; AAD06658.1; --
PIR; C71852; C71852.
HSSP; P80379; 1EMW.
HAMAP; MF 00385; -; 1.
InterPro; TPR000307; Ribosomal S16; T.
ProDom; PP00886; Ribosomal S16; T.
ProDom; PD003791; Ribosomal S16; 1.
TIGRPAMS; TIGR00002; S16; 1.
PROSITE; PS00732; RIBOSOMAL S16; 1.
Ribosomal Protein; Complete Proteome.
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Best Local
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., I Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G. Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Iv Tummino P.J., Marberg D., Mills S.D., Jiang Q., Taylor D.E.,
  RS16_HELPY
P56023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way encified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gastrance sequence comparison of two unrelated isolates of the human Nature 39:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9ZK63;
30-MAY-2000
30-MAY-2000
28-FEB-2003
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SEQUENCE
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NCBI_TaxID=85963;
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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                                                                                                                             27
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                                                                                                                   RRDGGWIESIGYYNPLSEPKDVRID
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(Rel. 39, Last sequence up
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al protein S16.
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8985 MW; FC0FB21B58E230C8 CRC64;
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Pred. No. 4.6;
5; Mismatches
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             PRT;
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IRON-SULFUR 1 (BY S)
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Pred. No. 33;
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                                                       Hypothetical 14.7 kDa pr
114D OR FRD.2.
Bacteriophage T4.
Viruses; dsDNA viruses,
T4-like viruses.
                                                                                                                                                                                                                                                                                                                                                                       TIGR, HP1151;
HAMAP: MF_00385; -; 1.
InterPro; IPR000307; Ribosomal_S16; T.
Probom; PF00886; Ribosomal_S16; T.
Probom; PF003791; Ribosomal_S16; 1.
TIGRFAMS; TIGR00002; S16; 1.
PROSITE; PS00732; RIBOSOMAL_S16; 1.
Ribosomal protein; Complete proteome.
    SEQUENCE FROM N.A. Poglazov A.B., Mes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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STRAIN=26695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A. Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Nelson K., Richardson D., Dodson R., Khalak H.G., Glodek A., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., Loftus B., Kichardson D., Dodson R., Khalak H.G., Hickey E.K., McKenney K., FitzGetald L.M., Lee N., Adams M.D., Hickey E.K., McKenney E.K., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M. Cotton M.D., Weidman J.M., Fujii C., Bownan C., Watthey L., Wallin Cotton M.D., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pylori.";
Nature 388:539-547(1997).
-1- SIMILARITY: BELONGS TO
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TIGR; HP1151; -.
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PIR; G64663; G64663.
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
30S ribosomal protein S16.
RPSP OR HP1151.
Helicobacter pylori (Campylobacter pylori).
Bacteria, Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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36.0%;
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Kutter E.M
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                                                               Caudovirales, Myoviridae;
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15-JUL-1999 (Rel. 3
16-OCT-2001 (Rel. 4
Hypothetical 14.8 k
FRD: 2 OR FRD2.
                                                                                                                 Pfam; PF03197; FRD2; 1.
Hypothetical protein.
SEQUENCE 128 AA; 14768 MW;
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                                                                                                                                                                                                                                                                                                                                      Poglazov A.B., Porter D., Kutter E.M., Mesyanzhinov V.V.; "DNA Sequences of the frd region in T4-related bacteriophages."; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  EMBL; L46846; AAA74669.1; -. InterPro; IPR004885; Frd2.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses,
T4-like viruses.
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15-JUL-1999
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Pfam; PF03197; FRD2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10666;
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 9.6;
2; Mismatches
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R PROSITE; PS00843; DALA DALA LIGASE 1; 1.

R PROSITE; PS00844; DALA DALA LIGASE 2; 1.

R PROSITE; PS00844; DALA DALA LIGASE 2; 1.

R PROSITE; PS00844; DALA DALA LIGASE 2; 1.

SEQUENCE 358 AA; 40128 MW; 225CF998A0A979F1 CRC64;
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J. Mol. Evol. 42.706-712(1996)
-i- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
-i- CURALYTIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an
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01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
D-alanine-D-alanine ligase (EC 6.3.2.4) (D-a. (D-Ala-D-Ala ligase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the D-alanine--D-alanine ligase
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MEDLINE=96270057; PubMed=8662022;
Canadewall B., Charles M., Dutka-Malen S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus hirae.
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
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1: sp_archea:*
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sp_phage:*
sp_plant:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_invertebrate:*
sp_mammal:*
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sp_bacteria:*
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Q9FOM685
Q9H685
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Q96SF5
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096979 paranophrys
0968f5 homo sapien
Q8kbc1 chlorobium
000032 brugia paha
090032 brugia paha
090033 brugia paha
090033 brugia paha
090033 enterococcu
09f0m3 enterococcu
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09zfw9 yersinia pe
08zfw9 yersinia pe
08zfw9 yersinia pe
08zfw9 refiania pe
08de8c5 shewanella
080215 methanobact
099f00 rhizobium 1
080215 methanobact
099f183 rattus norv
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ĸ	9		Q8x6c1 escherichia		Ň	Q94sd1 dactylopten	homo		a	Q9pwx1 human herpe	Q8mxn3 dictyosteli	Q9w9g4 human herpe		1		Q8ub66 agrobacteri	Q9hr12 halobacteri	92	-				ס		Q8xbu7 escherichia	Q8z8k6 salmonella	Q8zr27 salmonella	Q9fgx4 arabidopsis	

ALIGNMENTS

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OSSO79:

ID OSSO79:

PRELIMINARY; PRT; 408 AA.

AC OSSO79;

OI -MAY-1999 (TEMBLrel. 10, Created)

DT 01-MAY-1999 (TEMBLrel. 11, Last sequence update)

DT 01-MAY-1999 (TEMBLrel. 21, Last annotation update)

DT 01-MAY-1999 (TEMBLrel. 21, Last annotation update)

DT 01-MAY-1999 (TEMBLrel. 21, Last annotation update)

DE Translation elongation factor 1-alpha (Fragment).

GR PATHOPHYS CARTHIVOTA.

OC ENKATYOTA; Alveolata; Ciliophora; Oligohymenophorea; Scuticociliatia;

OC Philasterida, Orchitophryidae; Paranophrys.

OX NCBL_TAXID=85900;

RN [1]

RN SEQUENCE FROM N.A.

RY SEQUENCE FROM N.A.

RY MEDLINE-99152616; Pubmed=10028290;

RN MIDLINE-99152616; Pubmed=10028290;

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RESULT OR RESULT OF REAL PROPERTY OF REA
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01-DEC-2001
01-OCT-2002
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                                                                                                                                                                            Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M., Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H., Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F., Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey I Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune I Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.; Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.; Wenter Genome sequence of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium."; Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-OCT-2002 (TrEMBLrel. 22, Last annotation
BA555G22.1 (Hypothetical protein KIAA1008) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2001) to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=TLS / ATCC 49652 / DSM 12025;
MEDLINE=22103685; PubMed=12093901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002
01-OCT-2002
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01-OCT-2002
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                                                                                              SEQUENCE 1
                                                                                                                                                            TIGR; CT1868; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1097;
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                                                                                       al protein;
175 AA; 19
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? (TrEMBLrel. 22, I)
? (TrEMBLrel. 22, I)
al protein CT1868.
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Primates;
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19661 MW; 3C87FFF6C5A7E930
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-91250404; PubMed=1710216;
Selkirk M., Yazdanbakhsh M., Free
Jenkins R.E., Willams S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2002 (TrEMBLrel. 22, Major protein component of the comp
                                                                                                                                                                                                                                                                                              Luo Y., Pfister P., Leisinger T., Wasserfallen A.; "The Genome of Archaeal Prophage PsiM100 Encodes the Lytic Enzyme Responsible for Autolysis of Methanothermobacter wolfeil."; J. Bacteriol. 183:5788-5792(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 38 6 kDa protein.
Methanobacterium wolfei.
Archaea; Euryarchaeota; Methanobacteria; Methanobac
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Onchocercidae; Brugia.
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                                                                                                                              Submitted (AUG-2000) to the EMBL/Gen
EMBL; AF301375; AAG39973.1; -.
InterPro; IPR001993; Mitoch carrier.
PROSITE; PS00215; MITOCH_CARRIER; 1.
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NCBI_TaxID=145261;
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                                                                                                                  Hypothetical
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1674
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US-09-880-748-1674
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RESULT 7
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PRIOR FILING DATE: 2000-10-17
PRIOR PELICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 325
LENGTH: 127
TYPE: PRT
ORGANISM: homo sapiens
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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78.0%;
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78.9%;
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Pred. No. 1.4e-42;
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; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-973
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US-09-880-748-1921
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
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PRIOR APPLICATION NUMBER: 60/277,379
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PRIOR FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR PELICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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                                                                                                    SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 973
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 251
TYPE: PRT
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Local Similarity 74.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR-----DGGGGAYEDVWSGEYP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
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Pred. No. 4e-42;
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Query Match

73.3%;

Score 521.5;

DB 11;

Length 259;

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GENERAL INFORMATION: Antibodies that Immunospecifically Bind BLyS
ITITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOPTMARDE: DATE: 2001-05-25
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US-09-880-748-1778
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US-09-880-748-1777
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US-09-880-748-1777
Sequence 1778, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                               AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                                                                                                                                                                                                                                                                                                                                   VWGQGTMVTVSS 130
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8; Mismatches 18
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Matches
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PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR PPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR PPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 1778
                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-880-748-1610
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US-09-880-748-1610
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR PRIOR PRIOR DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3339
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3339
SOCTURARE: Patentin Ver: 2.0
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; ORGANISM: Homo sapiens
US-09-880-748-1778
                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1610
LENGTH: 257
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind FILE REFERENCE: PF523
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TYPE: PRT
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les 100; Conserv
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                           AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEVPE---YY 117
                                                                                       OVOLOOSGAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGOGLEWMGWISAYNGNTKY 60
                                                                                                                    QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
AQELQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDTLG---YDILTG-YPPPPYYYY 116
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                                                                                                                                                                                        72.4%; ilarity 77.0%; Conservative
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75.8%;
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Pred. No. 2.7e-41;
6; Mismatches 18
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Pred. No. 2.6e-41;
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US-09-880-748-1576
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US-09-880-748-1425
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
                                            PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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SEQ ID NO 1425
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                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ruben et al. TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS FILE REFERENCE: PF523
SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1576
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 MDVWGQGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLVESGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60
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76.9%;
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RESULT 15
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US-09-880-748-1562
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US-09-880-748-1562
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR PPLICATION NUMBER: 60/240,816
PRIOR PLICHE DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
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SEQ ID NO 1562
LENGTH: 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.1%;
Best Local Similarity 75.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ruben et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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Local Similarity 76.5%;
les 101; Conservative
                                                                                                                      121 VWGQGTTVTVSS 132
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                                                                                           114 YWGQGTTVTVSS 125
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                                                                                                                                                                                                                                                                                                         QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEMMGWISIYSGNTDY 60
                                                                                                                                                                                     AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR-----MEYDILTGYYGGYF--D 113
                                                                                                                                                                                                                  AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                                                                                                                                                                                                              QVQLVQSGAEVKKPGASVKVSCKASGYTETSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                                                                                                                                                                                                                                                                                        Score 510.5; DB 11; Length 251; Pred. No. 6.2e-41; 7; Mismatches 17; Indels 7;
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Pred. No. 4.1e-41;
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Sequence 1452, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:

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FILE REFERENCE: P523
FILE REFERENCE: P523
CURRENT APPLICATION NUMBER: US/09/880.748
CURRENT APPLICATION NUMBER: 2001-66-15
PRIOR APPLICATION NUMBER: 60/215.210
PRIOR APPLICATION NUMBER: 60/215.210
PRIOR APPLICATION NUMBER: 60/276.248
PRIOR FILING DATE: 2000-66-15
PRIOR APPLICATION NUMBER: 60/276.248
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-03-25
PRIOR PILING DATE: 2001-03-26
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Result
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Maximum Match 100%
Listing first 45 summaries
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1 : /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2 : /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3 : /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4 : /cgn2_6/ptodata/1/iaa/AB_COMB.pep:*
5 : /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5 : /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-025-769B-59
US-09-025-769B-22
US-08-264-093-3
US-08-561-521-45
US-08-565-539A-77
PCT-US95-01219-45
US-08-964-690-22
US-08-964-690-22
US-08-964-690-22
US-08-964-890-105
US-08-852-186A-19
US-08-852-186A-19
US-08-652-186A-19
US-08-652-186A-19
US-08-652-186A-19
US-08-652-186A-19
US-08-652-186A-19
US-08-565-216A-19
US-08-565-216A-13
US-08-652-155-155
US-09-025-769B-35
US-09-025-769B-37
US-09-025-769B-37
US-09-025-769B-37
US-09-025-769B-37
US-09-025-769B-37
US-09-025-769B-37
US-09-025-769B-57
US-08-899-575-155
US-08-899-575-155
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                         sequence
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36, Appl
25, Appl
3, Appli
45, Appl
45, Appl
45, Appl
22, Appl
22, Appl
22, Appl
23, Appl
26, Appl
19, Appl
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Query Match Best Local Similarity Matches 96; Conservat	RESULT 1 US-09-025-769B-36 Sequence 36, Application Sequence 36, Application Patent No. 6300064 GENERAL INFORMATION: APPLICANT: Ilag, Vic APPLICANT: Ilag, Vic APPLICANT: Pack, Pet APPLICANT: Plueckthu TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES ADDRESSEE: James F STREET: 1251 Avenu CITY: New York COUNTRY: USA ZIP: 10021 COMPUTER: READABLE FOR MEDIUM TYPE: Plopp COMPUTER: IBM PC C OPERATING SYSTEM: SOFTWARE: Patentin CURRENT APPLICATION NUMBER: FILING DATE: 18-AU APPLICATION NUMBER: FILING DATE: 18-AU ATTORNEY/AGENT INFORM NAME: James F. Hal REGISTRATION FOR SEQ ID SEQUENCE CHARACTERIST LENGTH: 120 amino TYPE: amino acid STRANDEDNESS: TOPOLOGY: linear MOLECULE TYPE: prote US-09-025-769B-36	28 438 61.6 1 29 438 61.6 1 30 438 61.6 1 31 436.5 61.4 1 33 436.5 61.4 1 34 436.5 61.3 1 35 435.5 61.3 1 36 435.5 61.3 1 37 434.5 61.1 1 39 434.5 61.1 1 39 434.5 61.0 1 40 433.5 61.0 1 41 433.5 61.0 1 42 433.5 61.0 1 43 434.5 61.0 1 44 433.5 61.0 1 47 433.5 61.0 1 48 433.5 61.0 1 49 434.5 61.0 1 40 433.5 61.0 1 41 433.5 61.0 1 42 433.6 60.9 1 43 433 60.9 1 44 433 60.9 1 45 432 60.8 1
2%; Score 485; DB 4; Length 7%; Pred. No. 5.3e-39; 7; Mismatches 17; Indel	;/09025769B iim ion Andreas tein/(Poly)peptide librarie ;3 if the Americas f the Americas is/09/025,769B pg8 pg 5 11 3021.0 pg 5 11 3021.0 pg 5 11 3021.0 gg 7, 794 R: MORPHO/5 ATION: ;000 36: ds ds	2 US-08-561-521-41 5 PCT-US95-01219-41 1 US-08-137-117D-102 2 US-08-36-717-102 1 US-08-30-366-65 3 US-08-931-645-65 5 PCT-US95-11235-65 5 PCT-US95-11235-65 2 US-08-561-521-12 5 PCT-US95-1219-12 1 US-08-477-8778-94 2 US-08-477-8978-94 2 US-08-477-9898-94 3 US-08-137-17D-100 1 US-08-137-117D-100 1 US-08-137-117D-112 2 US-08-137-117D-112 2 US-08-137-117D-112
h 120; lels 12; Gaps 1;	Neave	Sequence 41, Appl Sequence 102, App Sequence 102, App Sequence 65, Appl Sequence 65, Appl Sequence 12, Appl Sequence 12, Appl Sequence 94, Appl Sequence 94, Appl Sequence 94, Appl Sequence 63, Appl Sequence 100, Appl Sequence 110, Appl Sequence 110, Appl Sequence 112, Appl Seque

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Best Local S
Matches 96
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APPLICANT: Knappik, Achi
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
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                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212)596-900
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Procein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                      TYPE: amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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STATE: New York
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STREET: 1251 Avenue of the Americas
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   VWGQGTTVTVSS 132
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Pred. No. 5.3e-39;
7; Mismatches 17; Indels
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STRANDEDNESS:
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US-09-025-769B-22
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       RESULT 4
US-08-264-093-3
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Patent No.
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Best Local :
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GENERAL INFORMATION:
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MEDIUM TYPE: Flop.
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CORRESPONDENCE ADDRE.
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INVENTION:
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ER: MORPHO/5
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Pred. No. 5.7e-39;
5; Mismatches 16;
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US-08-561-521-45
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                                                                                                                                                                                                                    Patent No. 5840299
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION DATA: NO. 563
ATTORNEY JAGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
                                                                                       APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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MEDIUM TYPE: Diskette -
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TITLE OF INVENTION:
                                                                      CORRESPONDENCE ADDRESS:
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STREET: 101 Richmond Street West
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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2300 Richmond-Adelaide Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.3%; Score 478.5; DB 1
72.0%; Pred. No. 2.2e-38;
tive 11; Mismatches 15
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RESULT 6
US-08-525-539A-77
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INFORMATION FOR SEQ ID :
SEQUENCE CHARACTERIST;
LERGTH: 129 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 630963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 77,
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Best Local Similarity
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APPLICANT: DO COUTO,
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PRIOR APPLICATION UMBER:
APPLICATION NUMBER:
FILING DATE: 25-JA|
ATTORNEY/AGENT INFORM/
NAME: Smith, Willi,
REGISTRATION NUMBER
REFERENCE/DOCKET NUMBER
RE
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COMPUTER READABLE FOR:
MEDIUM TYPE: Flopp;
COMPUTER: IBM PC C:
OPERATING SYSTEM: |
SOPTWARE: Patentin
CURRENT APPLICATION D.
APPLICATION NUMBER:
                                                    ZIP: 94304-1018
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy
COMPUTER: IBM PC CC
OPERATING SYSTEM: I
SOSTWARE: Patentin
CURRENT APPLICATION DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CERIANI, |
APPLICANT: PETERSON,
TITLE OF INVENTION: |
TITLE OF INVENTION: |
TITLE OF INVENTION: |
                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESSEE: MORRISO:
STREET: 755 Page Mi
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                                                                                                                                                                                                                                                                                                STREET: 755 Page
CITY: Palo Alto
STATE: CA
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APPLICATION NUMBER: FILING DATE: 14-SE
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                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 DVWGQGTTVTVS:
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DOS/MS-DOS
lease #1.0, Version #1.30
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S/08/525,539A
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US-08-525-539A-77
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PCT-US95-01219-45
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TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 77
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
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Best Local Similarity
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APPLICANT: Leger, Olivier J.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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                    TELEFAX: 415-543-5043
                                                     ATTORNEY AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-OOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
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ATTORNEY/AGENT INFORMATION:
SEQUENCE
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CITY: San Francisco
STATE: California
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                                                                                                                                                                            APPLICATION NUMBER: US 08/186,269 FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
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  CHARACTERISTICS:
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linear
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; LENGTH: 129 amino
; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: prote
PCT-US95-01219-45
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Patent No.
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Best Local Similarity
                                                                                                            TELECOMMUNICATION IN:
TELEPHONE: 415-326-
TELEFAX: 415-326-
INFORMATION FOR SEQ ID
SEQUENCE CHARACTERIS;
LENGTH: 128 amino
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                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COPERATING SYSTEM:
SOFTWARE: PatentI:
CURRENT APPLICATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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CITY: San Francisc
STATE: California
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CORRESPONDENCE ADDRES
                                                       STRANDEDNESS: sine TOPOLOGY: linear MOLECULE TYPE: prote
                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 25-FIGURE CLASSIFICATION: 4:
NAME/KEY: Protein LOCATION: 1..128 OTHER INFORMATION:
                                                                                                TYPE: amino acid
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                                                                                                                                                                                       MATION:
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                                                                                                                                                                                                                                                                                                                  elease #1.0, Version #1.25
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                                                                                                                                                                                                      14137-77
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Pred. No. 3.7e-38;
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US-08-964-690-22
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                Query Match
Best Local Similarity
Matches 95; Conserve
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GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                       TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       NAME: Smith, William M.
REGIZENT NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: One Plan.
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CHESNUT, Robert W.
APPLICANT: POLLEY, Margaret J.
APPLICANT: PAULSON, James C.
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, Jose W.
APPLICANT: BENDIG, Mary M.
APPLICANT: BENDIG, Mary M.
APPLICANT: BENDIG, Mary M.
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                   LOCATION: 1..128
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                     NAME/KEY: Protein LOCATION: 1..128
                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear
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          Conservative
                66.9%; Score 476; DB 3; Length 128; 71.4%; Pred. No. 4.1e-38; Itive 11; Mismatches 21; Indels
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71.4%; Pred. No. 4.1e-38;
tive 11; Mismatches 21; Indels
                                                                                                /label= HUMAN_I
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US-09-199-149-3
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                                                                                                                                                                                                                                                                                                           Patent No. 587221
                                                                                                                                                                                                                                                                                                                         Sequence 19, Application
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: Osbourn, J
APPLICANT: Allen, DJ
APPLICANT: McCafferty
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TYPE: PRT
              COMPUTER READABLE FORK MEDIUM TYPE: Floppy COMPUTER: IBM PC CC OPERATING SYSTEM: I
                                                                                                                                                   NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESSEE: Marshall
                                                                                                                                                                                                  TITLE OF INVENTION: S
                                                                                                   CITY: Chicago
STATE: Illinois
                                                                                                                                  STREET:
                                                                                       COUNTRY:
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es 96; Conserv
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Patent In
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                                                                                                                                   O'Toole,
wer, 233
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                                                                                 s of America
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lease #1.0, Version #1.25 (EPO)
                 DOS/MS-DOS
                                 atible
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South Wacker Drive
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US-08-933-983-21
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Best Local S
Matches 94
                                                                                                                                                                                              Sequence 21
          GENERAL INFORMATION:

APPLICANT: HEED, GUY L
APPLICANT: HARRIS, LINDA
APPLICANT: BAJORATH, JURGEN
APPLICANT: MATSUEDA, GARY
APPLICANT: MOVOTIN, JIRI
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING
TITLE OF INVENTION: FIBRINOLYSIS
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/GB92/02240
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APPLICATION NUMBER:
FILING DATE: 23-MAY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 120 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: GB 9206372.6 FILING DATE: 23-SEP-1992
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                          VWGQGTTVTVSS 132
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                                                                                                                                                                                                                                                                                                     VWGQGTMVTVSS 120
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STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
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23-MAY-1996
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US-08-545-809A-105
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                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                             Sequence 105, Application Patent No. 6096878
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                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Honjo, T
APPLICANT: Matsuda,
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INFORMATION FOR SEQ ID
SEQUENCE CHARACTERIST
LENGTH: 139 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
FILLING DATE: 19-SE
CLASSIFICATION: 53
PRIOR APPLICATION DAT
APPLICATION NUMBER:
FILLING DATE: 20-SE
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                   COMPUTER READABLE FOR MEDIUM TYPE: Disk: COMPUTER: IBM Componerating System:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: line
OLECTOR
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                                                                                                                 CORRESPONDENCE ADDRES
ADDRESSEE: Fish &
STREET: 225 Frankl
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SOFTWARE:
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                                                                                                                                                                TITLE OF INVENTION:
                                                                                          STREET: L. STREET: L. STREET: MA
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OPERATING SYSTEM:
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CLASSIFICATION:
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128 YWGQGTTVTVS:
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RESULT 14
US-08-253-877C-19
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Best Local Similarity 86.7%;
Matches 85; Conservative
                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
 TELEFAX: 201-831-3 INFORMATION FOR SEQ ID
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Syr
NUMBER OF SEQUENCES: 73
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REGISTION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
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FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 201-C-
TELEPHONE: 201-831-3305
                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 03-JU
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Hallett, William
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                                                                         32,368
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Pred. No. 1.1e-35;
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RESULT 15
US-08-452-164A-19
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Best Local Similarity
                                                                                                                   TELEFAX: 201-683-4
                                                                                                                                                                                                                          COMPUTER READABLE FORMEDIUM TYPE: Floppy
COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: Patentin SOFTWARE: Patentin CURRENT APPLICATION UNMBER: FILING DATE: 26-MA)
CLASSIFICATION : 53
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                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRES:
ADDRESSEE: America:
STREET: One Campus
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                                                                                                                                                                           ATTORNEY/AGENT INFORMATION NAME: Barnhard, Eli
REGISTRATION NUMBER
REFERENCE/DOCKET NUMBER
                                        TOPOLOGY: 1i
MOLECULE TYPE:
                                                                             SEQUENCE CHARACTERIST:
LENGTH: 139 amino a
TYPE: amino acid
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APPLICANT: Weiss, Mar
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                                                              STRANDEDNESS:
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STATE: New Jersey
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Ig heavy chain V r
anti-PRZ erythrocy
Ig heavy chain V r
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Query Match

86.9%;

Score 453;

DB 2:

Length 129

; Marks, J.D.; Llewelyn, M.B. germline V(H) sequences [UID:93021117; PMID:1404388] in V region; immunoglobulin ha immunoglobulin lin homology <imm> 7.5%; Score 456; DB 2; Leng 17.8%; Pred: No. 1.7e-39; IN e 4; Mismatches 8; In PGASMKVSCMASGYPFTSYDISWVRQAPGG </imm>	2 PH1668 2 S26915 2 S31698 ALIGNMENTS 4) - human (fragment) :_revision 10-Nov-1995 #text_ch	30 382 73.3 1 2 PH1666 Ig 31 381 73.1 1 2 A32483 Ig 32 380 72.9 1 2 S23623 Ig 33 379 72.7 2 PH0871 Ig 34 376 72.4 1 2 S31667 Ig 36 377 72.4 1 1 HVHU35 Ig 37 77.4 1 2 S3199 Ig 38 377 72.4 1 2 B32274 Ig 39 376 72.2 1 2 I44151 Ig 40 370 71.0 2 S26921 Ig 41 370 71.0 2 S26921 Ig 42 369 70.8 1 2 PH1665 Ig
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C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_C
C;Accession: S36271
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity
A;Reference number: S36256; MUID:93178448; PMID:7679990
                                                                                                                                RyReference number: S24442

A;Reference number: S24442

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A;Rocession: S24
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #Bequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C;Accession: S19665; S24442
C;Accession: S19665; S24442
B;Accession: S19665; S24442
D; Mol. Biol. 22, 581-597, 1991
J; Mol. Biol. 22, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on A;Reference number: S19663; MUID:92085276; PMID:1748994
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-122 < GRI>
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A;Status: preliminary; nucleic acid sequence not
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A; Residues: 1-124 < MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: X61647
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;Species: Homo sapiens (man)
;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
Query Match
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Matches 85
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   l Similarity
85; Conser
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86.7%;
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Score 450; DB 2;
Pred. No. 9.1e-39;
3; Mismatches 10
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3; Mismatches
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Pred. No. 7.1e-39;
4; Mismatches 8
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1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY

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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S21924; S21923
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C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990
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A; Residues: 1-131 <FRI>
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                                                                                                              P;49-54/Region: complementarity-determining F;69-84/Region: complementarity-determining F;118-131/Domain: D region <DRG>
                                                                                                                                                                       A;Residues: 1-160 <SIL>
A;Rote: the authors translated the codon GAC for residues 108 and 109 as C;Comment: The antibody is one of the cold agglutinins that preferentiall C;Comment: The antibody is one of the cold agglutinins that preferentiall C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: autoantibody; hemagglutinin F;1-19/Domain: signal sequence #status predicted <SIG>
F;1-19/Domain: immunoglobulin homology <AlMN>
F;34-117/Domain: immunoglobulin homology <AlMN>
                                                                                                                                                                                                                                                                                                                                                   R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1989

A;Title: Relationship of variable region genes expressed

A;Reference number: PL0106; MUID:89235583; PMID:2541221
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                                                                             F;145-160/Domain: C region <CRG>
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                                                                                                    132-144/Domain:
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82.7%;
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81.6%;
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    Score 428; DB Pred. No. 2.1e 6; Mismatches
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Pred. No. 6.5e-37;
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e 428; DB 2; we
l. No. 2.1e-36;
he 12;
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J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26918
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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C;Datc: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S21925
R;Friedman, D.F.
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                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-98 < TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26918
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A; Residues: 1-111 <FRI>
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RESULT
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                                                                            AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                  QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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78.6%;
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Pred. No. 1.7e-34;
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Pred. No. 9.1e-36;
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RESULT 10
831600
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul
C;Accession: S31600
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RiShin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: A;Reference number: S18551; MUID:92037524; PMID:1935893
A;Accession: S18553
                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG>F;20-117/Product: Ig heavy chain V region (VI-3b) #status predicted <WAT>F;34-117/Domain: immunoglobulin homology <IMM>
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R;Cross-references: EMBL:X62109
T, Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups
A;Reference number: S26885; MUID:93021117; PMID:1404388
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A; Residues: 1-136 < CUI>
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A; Accession: S31600
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A; Residues: 20-117 < TOM>
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Best Local Similarity
Matches 77; Conserv
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                              AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                                             QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                 QVQLVQSGAEVKKPGASVKVSCRASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR
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78.6%;
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78.6%;
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Pred. No. 2.4e-34;
9; Mismatches 12
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117
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Ig heavy chain V region - human (fragment)

N;Alternate names: anti-cytomegalovirus glycoprotein B antibody

C;Species: Homo sapiens (man)

C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000

C;Accession: S68170

R;Boeldicke, T.; Haase, B.; Boecher, M.; Lindenmaier, W.

Eur. J. Biochem. 234, 397-405, 1995

A;Title: Human monoclonal antibodies to cytomegalovirus. Characterization and reference number: S68170; MUID:96128166; PMID:8536681

A;Accession: S68170

A;Status: preliminary
A;Status: preliminary
A;Cross-references: GB:S80750; NID:g1246061; PIDN:AAB35861.1; PID:g1246062

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin homology <IMM>
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C;Superf
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: $26938
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: $26885; MUID:93021117; PMID:1404388
A;Accession: $26938
                                                                      RESULT
S31680
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F; 15-98/Domain:
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Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision
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Best Local S
Matches 76
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Best Local (
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76.5%;
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Pred. No. 3.5e-34;
9; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                 Score 401; DB 2;
Pred. No. 6.8e-34;
7; Mismatches 15
         10-Nov-1995
                                                                                                                                                                                                                                                                                                                                    15;
    #text_change
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <CUI>
A;Cross-references: EMBL
C;Genetics:
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A; Residues: 1-117 <SHI>
A; Residues: 1-117 <SHI>
A; Cross-references: EMBL:x62106; NID:g37831; PIDN:CAA44016.1; P
A; Close, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.;
J. Exp. Med. 175, 831-842; 1992
A; Title: Genetic analysis of 892
A; Reference number: S23623; MUID:92156804; PMID:1740665
A; Reference number: S23623; MUID:92156804; PMID:1740665
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S18551
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R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity A;Reference number: $31885
A;Accession: $31680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18551; S23625
C;Accession: S18551; S23625
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E. R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E. RMBO J. 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: A;Reference number: S18551; MUID:92037524; PMID:1935893
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; ommunoglobulin pomology <IMM>
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A; Residues: 1-117 < OLE >
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AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAR
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7; Mismatches 15
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R.W.; Deftos, M.; Kozin, F.;
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D.A.

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S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C;Species: Homo sapiens (man)
C;Species: Library
C;Accession: S49530
R;Mahmoudi; M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Cession: S49530
A;Reference number: S48797
A;Accession: S49530
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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521
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HV1F HUMAN
HV55_MOUSE
HV31 HUMAN
HV01_MOUSE
HV1H HUMAN
HV3P_HUMAN
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HV3P_HUMAN
HV3P_HUMAN
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HV52_MOUSE
HV1A_HUMAN
HV00_MOUSE
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QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY

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Similarity 4; Conserva	A02024; HVHUHG. A02024; HVHUHG. S0:0002576; C:ext C0:0003823; F:ant G0:000585; F:inm G0:0006955; F:inm G0:0006955; F:inm G1:0006955; F:inm G1:000695; F	IENCE FROM N.A. LINE=83144028; PubM LINE=83144028; PubM Lavi G., Ram D., Gl lutionary aspects gene subgroups."; SIMILARITY: Contain SWISS-PROT entry een the Swiss Ins European Bioinform by non-profit if fied and this stat ties requires a li end an email to li end an email to li	STAN (Rel. C (Rel. C (Rel. V-I ain V-I s (Human Metazoa; utheria; 9606;	55000000000000000000000000000000000000
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RESULT 2
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PROSITE; PS50835; IG LIKE; 1.
PROMINOGIODULIN V region; Signal.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1991 (Rel. 20, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding act
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EMBO J. 7:1047-1051(1988).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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  sequence update
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Pred. No. 5.1e-37;
7; Mismatches 18
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IG-LIKE.
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MEDLINE=83065234; PubMed=6815656;
MEDLINE=83065234; PubMed=6815656;
                                                                                                                  HV52 MOUSE
P06327;
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CHAIN
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InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kenten J.H., Molgaard H.V., Houghton M., Derbyshire Bell L.O., Gould H.J.; Bell L.O., Gould H.J.; Consing and sequence determination of the gene for immunoglobulin epsilon chain expressed in a myeloma proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
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Ig heavy chain V-I region
Homo sapiens (Human)
                                                                                                                                            MOUSE
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
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(In) Bach
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                  01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 heavy chain V region VH558 Al/A4 precursor.
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SEQUENCE
                 NCBI_TaxID=10090;
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MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
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                                                                                                                                                                                                                                           QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY
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ND precursor (Fragments)
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IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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Pred. No. 8.3e-35;
3; Mismatches 19
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PYRROLIDONE CARBOXYLIC ACID.
                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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21-JUL-1986
15-SEP-2003
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P01742;
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SEQUENCE
  MEDLINE=71064027; PubMed=4923144; Gall W.E., Edelman G.M.; "The covalent structure of a huma
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"The co
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                                                    "The covalent structure of a human gamma acid sequence of heavy-chain cyanogen bro siochemistry 9:3161-3170(1970).
                                                                                Cunningham B.A., Rutisnaus Waxdal M.J., Edelman G.M.;
                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unrearranged VH gene segments."; Cell 40:271-281(1985).
                                                                                                                      SEQUENCE
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21-JUL-1986 (Rel. 01, Last sec
15-SEP-2003 (Rel. 42, Last and
Ig heavy chain V-I region EU.
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                                                                                                         MEDLINE=71064024;
                                                                                                                                                                        Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch)
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                      PubMed=5489771;
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FRAMEWORK-1
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Pred. No. 1e-32;
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
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gamma
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G-immunoglobulin.
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21-JUL-1986
21-JUL-1986
15-SEP-2003
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"Structural studies on induced antibodies with defined idiotypic specificities. VII. The complete amino acid sequence of the heavy chain variable region of anti-p-azophenylarsenate antibodies from mice bearing a cross-reactive idiotype.";

J. Immunol. 123:279-284(1979).
                SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
DOMAIN 1 106
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
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IG-LIKE.
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Biochemistry 9:3188-3196(1970)
                                                                                     Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 immunoglobulin-like
PIR; A02022; GIMSAA.
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Mammalia; Eutheria;
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GO; GO:0003823; F:antigen binding activity; NAS
GO; GO:0006955; P:immune response; NAS.
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InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                                                                                                                    HSSP; P01772; 2FB4.
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HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003006; InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [nterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                         MISCELLANEOUS: ANTIBODY I
THE IGG1 SUBCLASS. THERE
                                                                                                                                                                                                                                                                      REGION SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66;
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117 AA;
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(Rel. 01, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                      Ig-like.
Ig_MHC.
Ig_v.
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Pred. No. 1.2e-3
                  IG-LIKE
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Best Local S
Matches 62
                                                                                                   Query Match
Best Local S
Matches 59
                                                                                                                                                                                                                                             MGD; MGI:96486; Igh-VJ558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986
21-JUL-1986
15-SEP-2003
Ig heavy chai
IGH-VJ558
                                                                                                                                                                  DOMAIN
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=81245215; PubMed=6789211; Givol D., Zakut R., Effron K., Rechavi G., "Diversity of germ-line immunoglobulin VH c Nature 292:426-430(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                 SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                          HSSP;
                                                                                                                                                                                                                                                                                                                                        EMBL; J00488; AAA38519.1; PIR; A02041; HVMS8A.

    -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                   mmunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -JUL-1986 (Rel. 01, Created)
-JUL-1986 (Rel. 01, Last sequence update)
-SEP-2003 (Rel. 42, Last annotation update)
heavy chain V region 108A precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                                                                                          P01810; 2FBJ
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                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVQLQQSGAELVKAGSSVKWSCKATGYTFSSYELYWVRQAPGQGLEDLGYISSSSAYPNY
                                                                          QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQKFQGRVTITADESTNTAYMELSSLRSEDTAVYFCA 97
NOKFKSKATLTVDNSSSTAYMELSSLTSEDSAVYYCAR
             AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                  EVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSHGKSLEWIGYIYPYNGGTGY
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20
20 >
117
117 AA;
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                                                                                                    Conservative
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                                                                                                                                                                               117
>117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                        12972 MW; 428CB44DF25D1BC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.6%;
63.9%;
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Pred. No. 4.4e-31;
                                                                                                   Score 326; DB 1;
Pred. No. 4.5e-31;
6; Mismatches 23
                                                                                                                                                                                IG HEAVY CHAIN V REGION 108A. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₿
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes.
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                                                                                                                          Length 117;
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                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 59
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P01747;
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
NON TER
SEQUENCE
antibodies: somatic mutation evident in a Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
1g heavy chain V region 23 precursor.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                          HV04 MOUSE
P01748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00406; IGv; 1.
PROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1023-1032(1982).
-i- mISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL
DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Siekevitz M., Gefter M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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21-JUL-1986 (Rel.
                                                                                   Baltimore D.;
                                                                                                         MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M.,
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marshak-Rothstein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=83131846; PubMed=6186498;
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21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V region 36-65.
                                                                                                                                                      STRAIN=C57BL/6;
                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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P; P01789; 1MCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F00047; 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OKFOGRVIMITDISRRIAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VOLQOSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contains 1 immunoglobulin-like domain
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13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                            Rodentia;
                                                                                                                                                                                                                                                                Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 326; DB 1;
Pred. No. 4.6e-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG-LIKE
                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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      BELONGS
                                                                                                              Imanishi-Kari T.,
                                                                                                                                                                                                                                                                                                                             update)
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                                                                                                              Rajewsky
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TO THE S
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RESULT 10
HV02_MOUSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986
21-JUL-1986
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                              HV02_MOI
P01746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
NON TER
SEQUENCE
                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
                                                     EMBL; J00493; AAA38128.1; -. PIR; A94264; HVMSG7. HSSP; P01810; 2FBJ.
                                                                                                   or send
                                                                                                                                                                                                   "Somatic mutation in genes for the variable immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                      Capra J
                                                                                                                                                                                                                                                           MEDLINE=82152818;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Loca1
                                                                                                                                                                                                                                                                                                                                                   heavy chain
                                                                                                                                                                                       SIMILARITY: Contains 1 immunoglobulin-like domain.
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A02030; HVMS
                                                                                                                                                                                                                                                                                                       TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61;
                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                Rabbitts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNINPGNGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEKFKSKVTLTVDKSSSTAYTQLSSLTSEDSAVYYCAR 117
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(Rel. 01, Las
(Rel. 42, Las
nain V region (
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n V region; Signa
1 19
20 117 I
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                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
IGv;
                                                                                                                                                                                                                                              PubMed=6801765;
T.H., Estess P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THAT COULD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
54
68
85
117
117
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                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
on 93G7 precursor.
                                                                                                                                                                                                                                               Estess P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
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Pred. No. 5.9e
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY-DETERMINING-2 FRAMEWORK-3.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG HEAVY CHAIN V REGION 23.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENCODE V REGIONS OF NPB ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C530F829C906F69B
                                                                                                                                                                                                                                               Slaughter C.,
                                                                                                                                                                                                                                                                                                                                                                                                           140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .9e-31;
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                                                                                                                                                                                                                                                Tucker P.W.,
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RESULT 11
HV09_MOUS
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                                                         Query Match
Best Local S
Matches 59
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Best Local
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SIGNAL 1
CHAIN 20
DOMAIN 20
NON TER 140
SEQÜENCE 140
                                                                                               DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region 186-1 precursor.
Mus musculus (Mouse)
                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                  Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                         antibodies: somatic m
Cell 24:625-637(1981)
                                                                                                                                       DOMAIN
                                                                                                                                                                    DOMAIN
                                                                                                                                                                            CHAIN
                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                    PIR; D90809; HVMS61.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                       Baltimore D.;
                                                                                                                                                                                                                                                                                                                                               MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV09 MOUSE
P01753; P11271
                                                                                                                             DOMAIN
                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                      InterPro; IPR003596;
                                                                                                                                                                                                                                               InterPro; IPR003006;
                                                                                                                                                                                                                                                          InterPro; IPR007110;
                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                             "Heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                [mmunoglobulin
                                                                                                                                                                                                                                                                                      RELATED GENES THAT COULD
 61
                    20
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59; Conservative
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 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS50835; IG_LIKE;
obulin V region; Hy
                   QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
                            QVQLLQSATEVKKPGASMKVSCMASGYPPTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                          PS50835;
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117 AA;
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                                                                                                                                                                                             ; IG_LIKE; 1. region; Signal.
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139
140
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54
68
85
117
117
                                                                                                                                                                                                                                    ; Ig-like.
; Ig_MHC.
; Ig_v.
                                                                                                                                                                                                                                                                                                                   mutation
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                                                                                                12890 MW;
                                                                 61.2%;
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59.2%;
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                                                          15;
                                                                                                                           IG HEAVY CHAIN V REGION 186-1.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                        Score 319; DB 1; 1
Pred. No. 2.9e-30;
5; Mismatches 24;
                                                                                                                                                                                                                                                                                                                   contribution evident in a
                                                                                                                                                                                                                                                                                                                                                 Reth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 324; DB 1;
Pred. No. 9.5e-31;
0; Mismatches 20
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                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                               16191A088CB17F5A CRC64;
                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                       REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                               Imanishi-Kari T., Rajewsky
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                                                                                                                                                                                                                                                                                                                   gamma
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                                                                           Length 117
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 98
                                                                                                                                                                                                                                                                                                                   2a variable region.";
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                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                          Murinae;
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RESULT
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밁
                                                                                                                                                                                             RESULT 13
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Best Local
                                                                                                               HV06 MUSE
SIANUL-1906 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
15-JUL-1999 (Rel. 38 annotation update)
15-JUL-1999 (Rel. 38 annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P06330;
01-JAN-1988
01-JAN-1988
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A V region determinant () lymphocytes is encoded by EMBO J. 3:517-523(1984). PIR; A02040; MHMS38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-84182519; PubMed=6201362,
Dildrop R., Bovens J., Siekevitz M.,
"A V region determinant (idiotope) e:
lymphocytes is encoded by a large se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                          MEDLINE=81234548;
Bothwell A.L.M., I
Baltimore D.;
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
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InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003596;
antibodies: somatic mu Cell 24:625-637(1981).
        "Heavy chain variable region antibodies: somatic mutation
                                                            SEQUENCE FROM N.A. STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                         ISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heavy chain V region AC38 205.12.
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                                     PubMed=6788376;
Paskind M., Reth
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Ig_MHC.
Ig_v.
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Pred. No. 8.7e-30;
6; Mismatches 24
        contribution to the evident in a gamma
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Sciurognathi; Muridae;
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D SEGMENT.
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BY SIMILARITY.
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Best Local S
Matches 59
                    Query Match
Best Local
Matches
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PIR; A02037; MHMS15.

HSSP; P01810; ZFBJ.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003056; Ig_v.
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RELATED GENES THAT
PIR; A02032; HVMS02.
HSSP; P01810; 2FBJ.
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MEDLINE=84182519; PubMed=6201362;

MEDLINE=84182519; PubMed=6201362;

Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

Take Median M
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01-JAN-1988 (Rel. 06, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig heavy chain V region AC38 15.3.
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DOMAIN 1
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Mammalia; Eutheria; Rodentia;
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MART; SM00406; IGv;
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ITE; PS50835; IG LIKE; 1.
noqlobulin V region; Sign
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                      Score 314;
Pred. No. 1
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Sciurognathi; Muridae; Murinae; Mus
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HV05_MOUSE
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P01749;
21-JUL-1986
                                                                                                                                                                                                  DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:96486; Igh-VJ558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baltimore D.;
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IGH-VJ558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P01810; 2FBJ.
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20
                                                                                                Similarity 58; Conserv
QVQLQQPGAELVRPGSSVKLSCKASGYTFTSYMMDWVKQRPGQGLEWIGNIYPSDSETHY 79
                                                 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEKFKSKATLTVDKSSSATYMQLSTPTSEDSAVYYCAR 98
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                                                                                                                                                                                                                                                                         49
54
68
85
117
                                                                                                                                                                                                     13016 MW;
                                                                                             60.1%; Score 313; DB 1; Length 117; 59.2%; Pred. No. 1.5e-29; tive 15; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                          IG HEAVY CHAIN V REGION 3.

FRAMEWORK-1.

COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.
                                                                                                                                                                                                                                                                         COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.
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                                                                                                                                                                                                  427C861C53975EDC CRC64;
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Search completed: December 30, 2003, 10:55:49 Job time : 5.25426 secs

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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length: 2000000000
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521
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_bacteria:*
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sp_plant:*
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Q96QS0
Q9GYZ2
Q8WY24
Q9UL89
Q9UB9
Q925S3
Q91WT1
Q9Y29B
Q9Y29B
Q8V1J1
Q9DBL4
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Q9UL92
Q96GA6
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Q9UL94
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Q96g0 homo
Q96g0 homo
Q96g36 homo
Q96g2 schis
Q8wy24 homo
Q9u195 homo
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Q9u186 mus
Q9y298 homo
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58.9	•	•	•	•	•	•	•	•	58.9	•	•	•	59.5	•	•	60.1	60.1	60.1	60.1	•		•	61.2		61.4	٠	62.8	
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Q924R8	Q924R4	Q924R1	Q924Q7	Q924R3	Q924Q9	Q924Q6	Q924R0	Q924Q5	Q924Q4	Q924R2	Q924R6	Q924Q2	Q924Q0	Q9Z1C4	Q925S2	QBVDC9	Q91V67	Q924P8	Q9QXF0	Q9QXE9	Q91WR1	Q921A6	095978	Q924P9	Q920E8	Q9JL75	Q8VCX7	Q924Q1
Q924r8 mus musculu	Bull	Bum	Q924q7 mus musculu	Q924r3 mus musculu	Q924q9 mus musculu	Q924q6 mus musculu	Q924r0 mus musculu	B nB	Q924q4 mus musculu	Q924r2 mus musculu	8 nm	Q924q2 mus musculu	Q924q0 mus musculu		Q925s2 mus musculu	Q8vdc9 mus musculu	Q91v67 mus musculu	Q924p8 mus musculu	Q9qxf0 mus musculu	Q9qxe9 mus musculu	Q91wr1 mus musculu	Bun	O95978 homo sapien	92	ยนต	Q9j175 mus musculu	Q8vcx7 mus musculu	Q924q1 mus musculu
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ALIGNMENTS

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Best Local Similarity
Matches 72; Conserva
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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SEQUENCE 125 AA; 13516 MW;
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O9UL95;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clin. Immunol. Immunopathol. 87:184-192(1998). 
EMBL; AF035019; AAD56255.1; -. 
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myosin-reactive autoantibodies in rheumatic carditis and normal
1 QVQLLQSATEVKKPGASMKVSCMASGYPPTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
                                                                                                                                                                                                                                                                                                 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
                                                                                                                          73.9%; Score 385; DB 4; Length 125; illarity 73.5%; Pred. No. 7.3e-35; Conservative 10; Mismatches 16; Indels
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    Query Match
Best Local S
Matches 72
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01-MAY-2000
01-MAY-2000
01-MAR-2003
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O9BRVO;
O1-JUN-2001 (TEMBLrel. 17,
01-JUN-2001 (TEMBLrel. 17,
01-MAR-2003 (TEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                  Submitted (APR-2001) to the EMBL; BC005951; AAH05951.1; HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                               Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UL94
                                                                                      TISSUE=Prostate;
Strausberg R.;
                                                                                                                                                             NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Upfar. Prof. 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF035020; AAD56256.1;
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fetus.";
Clin. Immunol. Immunopathol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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    InterPro;
                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 73.7%;
Similarity 73.5%;
72; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
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IPR007110;
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119 AA;
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Primates;
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Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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Last seq
Last ann
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Pred. No. 8.9e-35;
.0; Mismatches 16;
                                                                   EMBL/GenBank/DDBJ
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                                                                                                                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13E64F5345F4A16E CRC64;
                                                                                                                                                                                                                                                                                      sequence update) annotation updat
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PER SELLE SELECTION OF SELECTIO
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Q96GA6
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Best Local S
Matches 72
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Best Local Similarity
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Clin. Immunol. Immunopathol. 8.
CMBL; AF035022; AAD56258.1; -.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSSITE; PS50835; IG_LIKE; 1.
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MC; 1.

Hypothetical protein.

SEQUENCE 500 AA; 54154 MW;
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Q9UL92;
Q9UL92;
01-MAY-2000
Q96GA6;
Q96GA6;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1)
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu X., Liu B., Van der Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myosin-reactive
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InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies in
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                                                                                                                                                                                                                                                             1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                           Similarity
72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                                                                                                                                                   AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
                                                                                                                                                                                         AOKFOGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
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EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMG:
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124 AA;
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                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBLrel. 13, Last sequence update)
EMBLrel. 23, Last annotation update)
immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                             72.6%;
73.5%;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                 13580 MW;
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                                                                                                                                                                                                                                                                                                                                                 Score 378;
Pred. No. 4
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Pred. No. 8.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                   1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0A9BF43F2A3CC6D9
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 69
                                                                                                SMART; SM
PROSITE;
SEQUENCE
                                                                                                                   "Homo sapiens putative microfibrillar protein with Ig-like mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3)."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY039025; AAK82649.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR00710; Ig-like. InterPro; IPR003006; Ig-MHC. InterPro; IPR00396; Ig-MHC. InterPro; IPR00396; Ig-V. Pfam; PF00047; ig; 1. SMART; SM00406; IGy; 1.
                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                             Q96QS0;
                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence
01-MAR-2003 (TrEMBLrel. 23, Last annotati
Putative matrix cell adhesion molecule-3.
                                                                                                                                                                                                                               Tilson M.D
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 5.
SMART; SM00406; IGv; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00041; HTH ARAC FAMILY 1; PROSITE; PS50835; IG LIKE; 5. PROSITE; PS00290; IG MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-2001) to the E
EMBL; BC009851; AAH09851.1; -
InterPro; IPR000005; HTHARAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2001)
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Mammalia; Eutheria; Primates;
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01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FISSUE=B-cell;
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                                                    68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69; Conserv
                                                              Similarity
OVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY
                  QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEWVGWISAYNGNTHY
                                                                                              PS50835; IG_LIKE; 1.
159 AA; 17497 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                             AQKFQDRVTITRDRSMNTAYMELSSLRSEDTAMYYCAR
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                                                69.7%;
ilarity 69.4%;
Conservative 1:
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                                                                                                                                                                                                                                                                         Chordata;
Primates;
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70.4%;

    Created)
    Last sequence update)
    Last annotation update)

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23,
                                                 13;
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                                             Score 363; DB 4; L
Pred. No. 2.6e-32;
3; Mismatches 17;
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Last
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                                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 371;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                             5D29537E881FAF02 CRC64;
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1es 17;
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                                                                    Length 159;
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RESULT QUESTION OF THE PROPERTY OF THE PROPERT
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Best Local
      Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
"Identification and characterization of SNC66, a Ig-like
down-regulated in colorectal cancer.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF283666; AAL36987.1;
InterPro; IPR003101; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                          01-MAR-2002
01-MAR-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                     Q8WY24;
Q8WY24;
                                                                                                                                                                                                                                       Homo gapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9GYZ2
Q9GYZ2;
01-MAR-2001
                                                                                                                                                      SEQUENCE FROM N.A. Zheng S., Shao X.,
                                                                                                                                                                                                                                                                                                     SNC66 protein.
                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003596; Pfam; PF00047; ig; 1. SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schistosoma japonicum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF282622; AAGO1452.1; -.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Song X.T., Feng Z.Q., Gu
"Amplification, cloning
variable region gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
Monoclonal anti-idiotypic an
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InterPro; IPR003006;
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119 AA;
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(TrEMBLrel.)
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19: 4
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.; 13567 MW;
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Primates;
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Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.7%; Score 358; DB 5; L
68.4%; Pred. No. 6.7e-32;
Mismatches 17;
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g and sequence and monoclonal and
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20,
23,

    Last sequence update)
    Last annotation update)
    antibody NP30 heavy chain

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Last annotation updat
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                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BA893873FD5FA6AB CRC64;
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Schistosoma.
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Ig-like
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Best Local S
Matches 65
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Best Local
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Q9UL89;
01-MAY-2000
                                    Q925S3;
01-DEC-2001
01-DEC-2001
01-MAR-2003
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PROSITE; PS50835; IG_MIC; 1.
PROSITE; PS00290; IG_MIC; 1.
SEQUENCE 497 AA; 53665 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
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Mammalia; Eutheria;
                     MRP3
                                                                                                                      Q925S3
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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  Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment)
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musculus
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67; Conserv
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                                                                            (TrEMBLrel.
                                      (TrEMBLrel. (TrEMBLrel.
                                                                                                                      PRELIMINARY;
(Mouse)
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                                      Last sequence update)
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Pred. No. 4.7e-31;
4; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                          Score 340; DB 4;
Pred. No. 6.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C8F9131DE13EA898 CRC64;
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Best Local S
Matches 63
Query Match
Best Local S
Matches 62
                                                                             Straubberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ da
EMBL; BC013490; AAM13490.1; -.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS05085; IG_LIKE; 4.
PROSITE; PS05093; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Int. J. Radiat. Biol. Relat. St. EMBL; AF240166; AAK43731.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1. SEQUENCE 147 AA; 16274 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q91WT1;
Q91WT1;
01-DEC-2001 (
01-DEC-2001 (
01-MAR-2003 (
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the repair of intestinal
World J. Gastroenterol. 6
[2]
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Cui D., Zeng G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical 52.1 kD. Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of mouse genes
of the irradiated mice h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cui D., Zeng G., Yan X., Li
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the same strain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/c
                                                                                                                                                                                                                                                                                                                                            TISSUE=Colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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  l Similarity
62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.1 kDa protein.
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Rodentia;
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Pred. No. 1
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                        Pred.
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  ed. No. 1.2e-28;
Mismatches 23;
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RESULT 13
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ID Q8K0Z
AC Q8K0Z
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                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to expressed sequence AI893585.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Musmalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Q8K0Z4;
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SEQUENCE
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Strausberg
                       SEQUENCE FROM N.A.
TISSUE=Breast tumor;
                                                                                          NCBI_TaxID=10090;
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SMART; SM00406; IGv; 1.
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HSSP; P01772; 2FB4.
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Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and kinetics of factor VIII inactivation: study with an IgG4 monclonal antibody derived from a hemophilia A patient with
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR003596; Ig_v.
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67.0%;
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Pred. No. 4e-29;
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RESULT 14
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Best Local
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      QBVIJ1;
QBVIJ1;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2004 (Pragment).
                                                                                                                                                                                                                                                                  SEMPLEAGE FAVO. 1977 | Priser STRAIN=C91/HeJ-lpr/lpr;
STRAIN=C9409289; PubMed=8814271;
MIDCH M.K., Alexander A.L., Pippen A.M., Pisersky D.S., Gilkeson G.,
"Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
Fir. J. Immunol. 26:2225-2233(1996).
                                                                                                                                                                   NON_TER
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SMART; SM00409; IG; 3.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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PROSITE; PS00290; IG_MHC; 2.
SEQUENCE 480 AA; 51645 MW;
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                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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InterPro; IPR003006;
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SQKFKDKATLTVDKSSRTAYMQLNSLTSEDSAVYYCAR
                                                                        QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEWVGWISAYNGNTHY
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                        ACKFOGRVIMTIDISRRIAYMELRSLRSDDTAVYYCAR 98
                                                 EIQLQQSGTELVKPGASVKISCKASGYSPTGYNMNWVKQSHGKSLEWVGDINPYYGGTRY
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123 AA;
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Ig-like.
Ig_cl.
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Pred. No. 3.4e-28;
LB; Mismatches 21;
                                                                                                   Score 330; DB 11;
Pred. No. 8.6e-29;
9; Mismatches 20;
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RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubhi F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashina J., Mamazarelli J., Mombaerts P.,

RA Asasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Havashizaki Y.,
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Best Local S
Matches 60
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Q9D8L4;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1810060009Rik protein.
                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 4.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

SEQUENCE 473 AA; 51699 MW;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                       ch 63.3%; Score 330; DB 11; Length 473; Similarity 61.2%; Pred. No. 4.3e-28; 60; Conservative 17; Mismatches 21; Indels
                                                                            AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                  QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79
December 30, secs
                    2003, 11:01:02
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RESULT 14
Q94MR7
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ID Q934G
AC Q934G
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DT Q1-DE
DT Q1-DE
DT G1-DE
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OC G1OST
OC GNGC.
OS G10ST
GN GNC.
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Q94MR7;
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"Cloning and expression of the gene encoding GlcNAc-alpha-1,4-Gal-releasing endo-beta-galactosidase from Clostridium perfringens.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB05955; BAB69460.1; -.
CHAIN.

18 420 POTENTIAL.
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0934G8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01_CNAC-alpha-1,4-Gal-releasing endo-beta-galactosidass.
                                                                         Youderian P., Walthers D., Salmi D., Magrini V., Hartzell P.L.; "Genome organization of temperate Myxococcus phage Mx8."; Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AF396866; AAK94387.1; -.
SEQUENCE 536 AA; 56864 MW; 08BCA8810380E0BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Potential virulence determinants in terminal regions smallpox virus genome.";
Nature 366:748-751 (1993).
EMBL; L22579; AAA60931.1;
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC10543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1502;
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                                                                                                                                                                     NCBI_TaxID=49964;
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                                                                                                                                                                                       Viruses
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Local Similarity 46.2%;
hes 6; Conservation
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 GGGGAYE--
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1 (TrEMBLrel.
2 (TrEMBLrel.
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 -- DVWSGEY 15
                                      38.8%;
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19,
21,
                        Score 52; DB Pred. No. 78; Pred. No. 78; 2; Mismatches
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Last annotation update)
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Pred. No. 60;
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Search completed: December 30, Job time : 7.6052 secs

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                STRAIN=Columbia;
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                              Kaneko T., Katoh T., Asamizu E.,
Tabata S.;
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253
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72.7%;
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Q89192
ID Q8
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Q89192;
Q89192;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
B26R protein
B26R.
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Q89096;
01-NOV-1996
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Virology 221:291-300(1996). 
EMBL; U18341; AAA69465.1; -. 
SEQUENCE 1896 AA; 213552 MW; 70444AODAE289E37 CRC64;
                                                                                                                                                                                                                                                                   SPECIES-Variola virus; STRAIN-Garcia-1966;
Shchelkunov S.N., Blinov V.M., Totmenin A.V., Resenchuk S.M.,
Sandakhchiev L.S.;
"XhOI-I,P DNA fragments of variola minor virus strain Garcia-1966.";
                                                                                                                                                                                                                                                                                                                                                  SPECIES-Variola minor virus; STRAIN-GARCIA-1966; Shchelkunov S.N., Totmenin A.V., Gutorov V.V., Safronov P.F., Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M Esposito J.J., Sosnovtsev S.; "Analysis of the complete coding sequence of DNA of alastrim variola minor virus strain Garcia-1966.";
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                         EMBL; V18339; AAA69405.1; -. EMBL; Y16780; CAB54796.1; -. EMBL; X70841; CAA50189.1; -.
                                                                                                                                                                                                                                                            Submitted (JAN-1993) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=Variola virus; STRAIN=GARCIA-1966; Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Totmenin A.V., Shchalkunov S.N., Esposito J.J.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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D15R.
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01-NOV-1996
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MEDLINE-95159666; PubMed=7856312;

Mchelkunov S.N., Blinov V.M., Resenchuk S.M., Totmenin A.V.,

Shchelkunov S.N., Blinov V.M., Resenchuk S.M., Totmenin A.V.,

Olenina L.V., Chirikova G.B., Sandakhchiev L.S.;

"Analysis of the nucleotide sequence of 53 kbp from the right terminus of the genome of variola major virus strain India-1967.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93202281; PubMed=8384129;
Shchelkunov S.N., Blinov V.M., Sandakhchiev
"Genes of variola and vaccinia viruses neces
protective mechanisms.";
FEBS Lett. 319:80-83(1993).
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Blinov V.M.;
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Viruses; dsDNA viruses,
Orthopoxvirus.
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MEDLINE=95320969; PubMed=7597802;
Shchelkunov S.N., Totmenin A.V.;
"Two types of deletions in orthop
Virus Genes 9:231-245(1995).
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Massung R.F., Esposito J.J., Liu L., Qi J., Utterback
Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Lope
Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy
                                                                 STRAIN=Bangladesh-1975;
MEDLINE=94088747; PubMed=8264798;
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Viruses; dsDNA viruses,
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PRELIMINARY;
OBOPZ7;
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
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01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
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Viruses; dsDNA viru
Orthopoxvirus.
NCBI_TaxID=203174;
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Viruses, dsDNA viruses,
Orthopoxvirus.
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Dokl. Akad. Nauk SSSR 321:404-406(1991).
EMBL; X67117; CAA47538.1; -...
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Q8V2H2;
01-MAR-2002 (TrEMBLrel. 2
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"The sequence of camelpox virus shows it variola virus, the cause of smallpox.";
J. Gen. Virol. 83:855-872(2002).
SEQUENCE FROM N.A.
STRALN=Somalia-1977;
MEDILINE=96295428; PubMed=8661439;
Massung R.F., Loparev V.N., Knight J.C.
Chizhikov V.E., Parsons J.M., Safronov Shchelkunov S.N., Esposito J.J.;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP438165; AAL73914.1;
SEQUENCE 1869 AA; 210498 MW; 64ABEF98F88237A9 CRC64;
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Submitted (OCT-2000) to the EMBI
SMBL, AY009089; AAG337713.1; -
SEQUENCE 1869 AA; 210470 MW;
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PubMed=11907336;
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Pred. No. 2.2e+02;
5; Mismatches 2;
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Q8R3W5;
01-JUN-2002
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ data
SUBDL; BC024342; AAH24342.1; -.
SEQUENCE 168 AA; 18530 MW; 99D8E6E14C2FCAAO CR
    Q9BZQ5;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat Similar to RIKEN CDNA 5730449L18 gene.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat Mammalia; Eutheria; Rodentia; Sciurognathi; Murid
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
EMBL; BC022030; AAH22030.1; -.
Hypothetical protein.
SEQUENCE 171 AA; 18641 MW; E728BF39A89DDII
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Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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STRAIN-Nipponbare;
Spiegel L., de la Bastide M., Nascimento L., Kirchoff K., King L.,
Preston R., Vil M.D., Baker J., Bell M., Zutavern T., Santos L.,
Miller B., Kuit K., Rodriguez S., Cunnius D.M., Balija V., Shah
Bahret A., Bal H., O'Shaughnessy A., Dedhia N., McCombie W.R.;
"Genomic Sequence for Oryza sativa, Nipponbare strain, clone
OSJNBA0089015, from Chromosome 10, complete sequence.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE
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MEDLINE=21218927; PubMed=11318611;

Sood R., Bonner T.I., Malakowska I., Stephan D.A., Robbins
Connors T.D., Morgenbesser S.D., Su K., Faruque M.U., Pinke
Graham C., Baxevanis A.D., Klinger K.W., Landes G.M., Trent
                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
Oryza sativa (Rice)
Eukaryota; Viridiplantae;
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01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2002 (TrEMBLrel. 22,
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Bhrhartoideae; Oryzeae; Oryza.
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01-OCT-2002 (TrEMBLrel.
SEQUENCE FROM N.A.
STRALN=Nipponbare;
FRAME L.E., Spiegel L., de la Bastide M., Nascimento L., F
Palmer L.E., Spiegel L., de la Bastide M., Zutavern
King L., Preston R., Vil M.D., Baker J., Bell M., Zutavern
Santos L., Miller B., Kuit K., Rodriguez S., Cunnius D.M.,
Shah R., Bahret A., Bal H., O'Shaughnessy A., Dedhia N.,
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McCombie W.R.;
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Genomics 73:211-222(2001).
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ALIGNMENTS

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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
     "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK017650; BAB30855.1; -.
                                                                                                                                                                                                                       Q9CYI5
                                                                                                                                                                                  5730449L18RIK.
                                                                                                                                                                                        5730449L18Rik protein.
MGI:1913887; 5730449L18Rik
                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                               17,
17,
                                                                                                                                                                                               Last sequence update)
Last annotation update)
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CC
EMBL; AL627275; CAD02714.1; -.
DR EMBL; AE016835; AA068065.1; -.
DR HAMAP; MF_00378; -; 1.
DR InterPro; IPR003753; Exonuc_VII_L.
DR InterPro; IPR003753; Exonuc_VII_L; 1.
DR Pfam; PF02601; Exonuc_VII_L; 1.
DR Pfam; PF0136; EXNA, anti; 1.
DR TIGRFAM8; TIGR00237; xseA; 1.
KW Hydrolase; Nuclease; Exonuclease; Complete proteome.
SQ SEQUENCE 449 AA; 50720 MW; 511957DEC878F5D2 CCC64;

Query Match
Best Local Similarity 70.0%; Pred. No. 78;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGAYEDVWS 12
Db 206 GGGSUEDLWS 215

Search completed: December 30, 2003, 10:55:52

Job time: 2.23314 secs
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EX7L_RICCN
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Best Local (
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REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII large subunit
(Exonuclease VII large subunit).
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REPEAT
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EMBL; D00295; BAA00209.1; A:
EMBL; D00295; BAA00207.1; A:
EMBL; D00295; BAA00207.1; A:
HSSP; P25963; 1NFI.
                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                         "Mechanisms of evolution in Rickettsia conorii and R. Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                             Ogata H., Audic S.,
Samson D., Roux V.,
                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q92GU6;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
REPEAT
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                                                                                                                                                                                                                                                                                                       MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                                                                                                                                                                      STRAIN=Malish
                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                           XSEA OR RC1026.
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                        or send an email to license@isb-sib.ch).
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                                                                                                                                                                          FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides (By similarity). CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'- or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
                                                                                                                           SIMILARITY: BELONGS TO
                                                                                                                                                                SUBUNIT: Heterooligomer
                                                                                                                                        SUBCELLULAR LOCATION:
                                                                                                                                                     similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RICCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133
AE008654; AAL03564.1; ALT_INIT
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9; Conserv
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PS50297; ANK_REP_REGION;
ical protein; Repeat; ANK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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132
169
202
238
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Cossart P., Weissenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49194 MW;
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                                                                                                                          Cytoplasmic (By similarity).

THE XSEA FAMILY.
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ANK 3.

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ANK 6.

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ANK 8.
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Pred. No.
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repeat.
                                                                                                                                                               of large and
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                                      (See http://www.isb-sib.ch/announce/
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ch J., Claverie
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RESULT 15
EX7L_SALTI
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InterPro; IPR003753; EXONUC_VII
InterPro; IPR004365; tRNA_anti:
InterPro; IPR004365; tRNA_UII_L; 1.
Pfam; PP02601; EXONUC_VII_L; 1.
Pfam; PF01336; tRNA_anti; 1.
TIGRPAMB; TIGR00237; x8eA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CT18;

MEDLINE=21534947; PubMed=11677608;

Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.

Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.

Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,

Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,

Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
15-SEP-2003 (Rel. 42, Last ann
Probable exodeoxyribonuclease
(Exonuclease VII large subunit
                                                                                                                                                                                                                                                                       STRAIN=Ty2 / ATCC 700931;

MEDLINE=22531367; PubMed=12644504;

Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;

"Comparative genomics of Salmonella enterica serovar Typhi strains
                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                       (Exonuclease VII large subunit).
XSEA OR STY2753 OR T0345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Nuclease; SEQUENCE 444 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8Z4Q1;
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                                                                                       This
                                                                                                                                                                                                                                                              and CT18."
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                                                                                                                   SIMILARITY: BELONGS
                                                                                                                                  SUBCELLULAR LOCATION:
                                                                                                                                            Bimilarity)
                                                                                                                                                             SUBUNIT: Heterooligomer
                                                                       SWISS-PROT entry is copyright. It is produced through a centry the EMBL the Swiss Institute of Bioinformatics and the EMBL
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1. 41, Last sequence update)
1. 42, Last annotation update)
1. 42, Last annotation update)
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; Exonuclease; Complete proteome.
49886 MW; CAB0B6BB443F476B CRC64;
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                                                                                                                                Cytoplasmic (By similarity).
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Pred. No.
                                                                                                                   XSEA FAMILY.
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77;
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CIBA_PAEPP
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Best Local S
Matches 10
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                        CIBA PAEPP STANDARD; PRT; 675 AA. 157051; PRT; 675 AA. 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Parasporal crystal protein cry18Ba (Parasporal CryxVIIIB(a)) (Crystaline parasporal protoxin)
                                                                                                                                        PACCEARNA
CRY18BA OR CRYXVIIIB(A).
Paenibacillus popilliae (Bacillus
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DNA_BIND
DOMAIN
STRAIN=BP3;
Patel R., Yousten A.A., Rippere
"Detection of two new cry genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                              SEQUENCE FROM N.A.
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DOMAIN
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PROSITE; PS00036; BZIP_BASIC;
DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P34707; 15KN.
MGD; MGI:99421; Nfe211.
Interpro; IPR004827; TF_bZIP.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X78709; CAA55362.1; -. EMBL; AF015881; AAC40108.1; -.
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                                                                                                                      NCBI_TaxID=78057;
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TISUE SPECIFICITY: Widely expressed.
PTM: COULD BE DEPENDENT ON CKII PHOSPHORYLATION FOR BINDING.
SIMILARITY: Belongs to the bZIP family. CNC subfamily.
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SUBCELLULAR LOCATION: Nuclear (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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387
741 AA;
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414
467
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387 P
; 81545 MW;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASIC MOTIF (BY SIMILARITY).
LEUCINE-ZIPPER (BY SIMILARITY).
NUCLEAR LOCALIZATION SIGNAL (P
Missing (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation; Alternative splicing.
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
POLY-SER.
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     in K
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                                                                                                                                                popilliae).
Paenibacillaceae; Paenibacillus
  Paenibacillus popilliae.";
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(In isoform Short).
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                                                                                                                                                                                                                                             delta-endotoxin
(76 kDa crystal
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Matches
                                                                                                                                                                                   SEQUENCE OF 65-428 FROM N.A.
STRAIN=FP-9 / Isolate HP-438;
MEDILINE=88229622; PubMed=2836548;
MEDILINE=88229622; PubMed=2836548;
Tomley F., Binns M., Campbell J., Boursnell M.E.G.;
"Sequence analysis of an 11.2 kilobase, near-terminal, of fowlpox virus";
"Gen. Virol. 69:1025-1040(1988).
J. Gen. Virol. 69:1025-1040(1988).
-!- SIMILARITY: Contains 8 ANK repeats.
-!- CAUTION: Ref.2 sequence differs from that shown due in position 204, 219 and 237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V234_FOWPV STANDARD; PRT; 428 AA.
p14368; p14367; Q9J501;
01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative ankyrin-repeat protein FPV234 (BamHI-ORF12/ORF13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOMPV
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InterPro; IPR005638; endotoxin C.
InterPro; IPR005639; endotoxin N.
Pfam; PF03944; endotoxin C; 1.
Pfam; PF03945; endotoxin N; 1.
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DOMAIN 101
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8; Conservative
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204 Po
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                                                                                                                                                                                                                                                                                                            P34304;
01-FEB-1994
28-FEB-2003
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commet entities requires a license agreement (See http://www.isb-sib.ch/annou
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InterPro; IPR001015; Ferrochelatase.
Pfam; PF00762; Ferrochelatase; 1.
ProDom; PD002792; Ferrochelatase; 1.
TIGRPAMS; TIGR00109; hemH; 1.
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EMBL; AE008306; AAK89636.1; ALT_INIT
PIR; AG3020; AG3020.
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                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                           Hypothetical C06E1.9.
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks Bonfield J., Burton J., Connell M., Copsey T., Cooper
                                             MEDLINE=94150718; PubMed=7906398;
                                                                           STRAIN-Bristol N2;
                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                              Caenorhabditis elegans.
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PROSITE; PS00534; FERROCHELATASE; 1.
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L protein C06E1.9 in chromosome
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39472 MW;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPL1 MOUSE STANDARD; PRT; /41 AA. 061985; 070234; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Nuclear factor erythroid 2 related factor 1 (NF-E2 (NF-E2-related factor 1) (Nuclear factor, erythroid)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Prieschi E.E., Novotny V., Csonga R., Jaksche D., Elbe-Buerger A., Prieschi E.E., Novotny V., Csonga R., Jaksche D., Elbe-Buerger A., Thumb W., Auer M., Stingl G., Baumruker T.;

"A novel splice variant of the transcription factor Nrf1 interacts with the TNFalpha promoter and stimulates transcription.";

Nucleic Acids Res. 26:2297(1998).

-1- FUNCTION: THE SHORT ISOFORM INTERACTS WITH THE EXTENDED KAPPA 3 SITE OF THE TWF ALPHA PROMOTER AFTER FC GAMMA RIII STIMULATION IS PARTICIPATES IN THE INDUCTION OF THIS CYTOKINE. THE LONG ISOFORI IS EITHER INACTIVE OR REPRESSES THE TRANSCRIPTIONAL ACTIVATION.

-1- SUBUNIT: HETERODIMER (PROBABLE). IT MAY FORM A HETERODIMER WITH
                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical SEQUENCE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 368:32-38(1994).
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                                                                                                                                                                                                                                             TISSUE=Embryo;
MEDILINE=99278942; PubMed=7759107;
McKie J., Johnstone K., Mattei M.-G., Scambler
"Cloning and mapping of murine Nfe211.";
Genomics 25:716-719(1995).
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                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
MEDLINE=98248571; PubMed=9580677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFE2L1 OR NRF1
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB Pred. No. 83; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF83EBCFC880A10A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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074254;
15-JUL-1999
15-JUL-1999
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
                                                                                                                                                                                                                                                                                                                               InterPro; IPR000322; Glyco hydro 31.
Pfam; PF01055; Glyco hydro 31; 1.
PROSITE; P800129; GLYCOSYL HYDROL F31 1; 1.
PROSITE; PS00707; GLYCOSYL HYDROL F31 2; 1.
                                                                                                                                                                                                                                                                                                 Signal; Cell
SIGNAL
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(1,4-alpha-D-glucan
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                                                                                                                                                                                                                                                                                                                        Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         surface glucoamylase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sturtevant J., Dixon F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99451422; PubMed=10520161;
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                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5476;
                                                               Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucose residues successively from non-reducing ends of with release of beta-D-glucose.
SUBCELLULAR LOCATION: CELL WALL ASSOCIATED.
SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Mycol. 37:357-366(1999). CATALYTIC ACTIVITY: Hydrolysis of
                                         Similarity 9; Conser
                   GGGAYEDVWSGE-YPEYYAM
GSGKYMGHWGGDNYADYYMM
                                                                                                                                                                                                                                                                                                                       Glycosidase;
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(Rel. 38,
(Rel. 41,
                                                                                               Conservative
                                                                                     A
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                                                                                              8, Last sequence update)
1, Last annotation updat
ursor (EC 3.2.1.3) (Gluc
glucohydrolase).
                                                                                    105804
                                                  34.7%;
45.0%;
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GLUCOAMYLASE 1.
BY SIMILARITY.
SER/THR-RICH.
N-LINKED (GLCNA)
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                                                  Score
Pred.
636
                   21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                -LINKED (GLCNAC...
                                         Mismatches
                                                  No. 1
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(Glucan 1,4-alpha-glucosidase)
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CRC64;
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28-FEB-2003 (Rel. 41
28-FEB-2003 (Rel. 41
Ferrochelatase (EC 4
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T4-like viruses.
NCBI_TaxID=66711;
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28-FEB-2003
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SEQUENCE FROM N.A.
MEDLINE=20485545; PubMed=11029414;
Yu S.L., Ko K.L., Chen C.S., Chang Y.C., Syu W.J.;
"Characterization of the distal tail fiber locus and determination
"Characterization of the distal tail fiber locus and determination
"Characterization of the distal tail fiber locus and determination
"Characterization of the distal tail fiber locus and determination
MEDLINE-21608550; PubMed-11743193;
MEDLINE-21608550; PubMed-11743193;
Mood D.W., Setubal J.C., Kaul R., Mood G.E., Almeida N.F. Jr., Woo L.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                       HEMZ AGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
Fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 182:5962-5968(2000).

-i- FUNCTION: VGJ8 IS AT THE TIP OF THE LONG TAIL FIBERS AND AS THE PRACE RECOGNITION SITE FOR THE CELLULAR RECEPTOR.

-i- MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEIN OMPA
                                                                                                                                                                                                                   Agrobacterium tumefaciens (strain C58 / ATCC 33970)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhiz
Rhizobiaceae; Rhizobium/Agrobacterium group; Agroba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fiber protein;
SEQUENCE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriophage AR1.
Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                     HEMH OR ATU3771 OR AGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                NCBI_TaxID=176299;
                                                                                                                                                                   EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
8; Conserv
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003 (Rel. 41, Last sequence up
003 (Rel. 41, Last annotation
recognizing protein (Protein
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(Rel. 41, Last ann
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AA; 26277 MW; 042225B00128AE5B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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    41, Last sequence update)
    41, Last annotation update)
    C 4.99.1.1) (Protoheme ferro-lyase) (Heme

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Pred. No. 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          344
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(Gp38).
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                                                                                                                                                                                                                     a; Rhizobiales;
Agrobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=86176742; PubMed=2870470; MEDLINE=86176742; PubMed=2870470; Claassen I., Bakker D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1988 (Rel. 07, Created)
01-MAY-1991 (Rel. 18, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
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         EMBL; X03675; CAA27310.1; -.
EMBL; X56002; CAA39476.1; -.
EMBL; X56003; CAA39477.1; -.
PIR; S24931; MMECOF.
InterPro; IPR000015; Fimb_usher.
Pfam; PF00577; Usher; 1.
PROSITE; PS01151; FIMBRIAL USHER; 1.
Outer membrane; Transmembrane; Fimbria; Transport; Signal; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96020654; PubMed=8577257;
Valent Q.A., Zaal J., de Graaf F.K., Oudega B.
"Subcellular localization and topology of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Regulation and structure of an outer membrane protein involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                               enterotoxigenic Escherichia col
Mol. Microbiol. 5:875-886(1991)
                                                                                                                                                                                                                                                                                                                                              "Structure and function of periplasmic chaperone-like proteins involved in the biosynthesis of K88 and K99 fimbriae in enterotoxigenic Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pFM205
                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91312125; PubMed=1713284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-1990)
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                                                                                                                                                                                                                                                                                                                                                                                        kker D., Vader C.E.M., Roosendaal B., Graaf F.K.;
                                                                                                                                                                                                                                                                                     FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF SUBUNITS ACROSS THE OUTER MEMBRANE.
SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
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5; Mismatches
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Escherichia coli gene coding
in export of K88ab fimbrial
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15-JUL-1998
16-OCT-2001
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                                                                                                     ProDom: PD011569; DUF39; 1.

PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.

Hypothetical protein; Complete proteome.

SEQUENCE 431 AA; 46950 MW; 802FA39757194B8
                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Evthe European Bioinformatics Institute. There are no restr
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Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
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                                                                                                                                                                                                                                           EMBL; AE000926; AAB86156.1;
                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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InterPro; IPR002708; DUF39
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PROSITE; PS00030; RRM_RNP_1; RNA-binding; Nuclear protein;
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Pfam; PF00076; rrm; 2.
SMART; SM00360; RRM; 2
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GO; GO:0005717; C:Chromatin; IDA.
GO; GO:0016607; C:nuclear speck; IDA.
GO; GO:0005634; C:nucleus; IDA.
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or send a
                                                            SEQUENCE OF 318-393 FROM N.A. MEDLINE=94008528; PubMed=8404528; Whittaker C.A., Desimone D.W.;
                                                                                                                                                                     XENLA
                                                                                                                                                                                                                                                     Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
18-FBE-2003 (Rel. 41, Last annotation update)
Integrin alpha-5 precursor (Fibronectin recep
(Integrin alpha-F) (VLA-5).
Xenopus laevis (African clawed frog).
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                                               Whittaker C.A., "Integrin alpha
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                 Xenopus embryos.";
Development 117:1239-1249(1993)
                                                                                                                         "Integrin alpha 5 during early development of Xenopus laevis.";
Mech. Dev. 50:187-199(1995).
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BL; S62100; AAB26989.1; -
BL; S61875; AAB26989.1; J
BL; X62637; CAA44503.1; -
BL; X62638; CAA44504.1; -
R; A47369; A47369.
R; B41732; B41732.
R; B41732; B41732.
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   FUNCTION: INTEGRIN ALPHA-5/BETA-1
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TSSNYYQNKNNSQNYQQF (in isoform SqdA).
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This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR000413; Integrin_alpha.
Pfam; PF01839; FG-GAP; 4.
Pfam; PF00157; integrin A; 1.
PRINTS; PR01185; INTEGRINA.
SMART; SM00191; Int alpha; 5.
PROSITE; P800242; INTEGRIN_ALPHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U12683; AAA99668.1; -.
EMBL; L10191; AAA16249.1; -.
PIR; I51527; I51527.
HSSP; P06756; 1JV2.
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SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. TH
SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKE.
DISULFIDE BOND. ALPHA-5 ASSOCIATES WITH BETA-1.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
SIMILARITY: Contains 7 FG-GAP repeats.
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CYTOPLASMIC (POTENTIAL).

FG-GAP 1.

FG-GAP 2.

FG-GAP 3.

FG-GAP 4.

FG-GAP 5.

FG-GAP 6.

FG-GAP 7.

FG-GAP 7.

POTENTIAL.

BY SIMILARITY.

BY SIMILARITY.
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INTEGRIN ALPHA-5.
INTEGRIN ALPHA-5 HEAVY CHA.
INTEGRIN ALPHA-5 LIGHT CHA.
EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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(GLCNAC.
                                                                                                   (GLCNAC.
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LINKED
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BY A
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35.4%;

Score 47.5;

DB 1;

Length 1050; CRC64;

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RESULT 2
SYC1_MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C., III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cysteinyl-tRNA synthetase 1 (EC 6.1.1.16) (Cysteine--tRNA ligase 1)
                                                                                                                                                                                                                                                                                                                                                                                                             laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
-!- CATALYTIC ACTIVITY: ATP + L-cysteine + tRNA(Cys) = .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Kolonay J.F., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula Pickey R., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                               modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restude by non-profit institutions as long as its content
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                                                                                                                                                 EMBL; Z92774; CAB07154.1; -. EMBL; AE007169; AAK48044.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole genome comparison of Mycobacterium tuberculosis clinical
                 Pfam; PF01406; tRNA-synt_le; 1 PRINTS; PR00983; TRNASYNTHCYS.
                                              HAMAP; MF_00041; -; 1.
InterPro; IPR002308; Cys_tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
                                                                                                  TubercuList;
                                                                                                                  TIGR; MT3686;
                                                                                                                                  PIR; B70607; B70607.
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                                                                                                                                                                                                                                                                                                                                                  diphosphate + L-cysteinyl-tRNA(Cys).
SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
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TIGR00435; cysS;
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BINDING
CONFLICT
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01-FEB-1996
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00178; AA_TRNA_LIGASE_I;
Aminoacyl-tRNA_synthetase; Protein k
Complete proteome.
SITE 35 45 "HTCH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQD_DRON
Q08473;
                         between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                           Kelley R.L.; "Initial organization of the Drosophila dorsoventral an RNA-binding protein encoded by the squid gene."; Genes Dev. 7:948-960(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92112968; PubMed=1730754;
Matunis E.L., Matunis M.J., Dreyf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93279471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                     "Characterization of the major hnRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HNRNP 40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A
                                                                                                                                                                                                                           PUNCTION: THIS PROTEIN IS A COMPONENT OF RIBONUCLEOSOMES. COULD BE FUNCTION: THIS PROTEIN IS A COMPONENT OF RIBONUCLEOSOMES. COULD BE FUNCTION: THIS PROTEIN IS A CONCENTRATION GRADIENT OF A DORSALIZING MORPHOGEN (DM) ORIGINATING IN THE GERMINAL VESICLE. AT LEAST ONE OF THE ISOFORMS IS ESSENTIAL IN SOMATIC TISSUES.

SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC. IT IS POSSIBLE THAT SOME ISOFORMS ARE FOUND ONLY IN ONE OF THESE LOCATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DROME
 European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed
                                                                                       ISOId=Q08473-3; Sequence=VSP_005877; DISEASE: FEMALES WITH MUTATIONS IN SQD THAT DISPLAY ONLY DORSAL STRUCTURES.
                                                                                                                                         Name=SqdA; Synonyms=HRP40.1;
IsoId=Q08473-2; Sequence=V
                                                                            SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
                                                                                                                                                                 Name=SqdS; Synonyms=HRP40.2;
IsoId=Q08473-1; Sequence=Displayed;
                                                                                                                                                                                          Event=Alternative splicing; Named : Comment=Additional isoforms seem
                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS:
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                                    SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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(Rel. 33, Last sequence update)
(Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $
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D -> E (IN REF. 2).
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Pred. No.
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biosynthesis;
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             ormatics and the EMBL outst
There are no restrictions
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                                           EMBL outstation
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                                           a collaboration -
MBL outstation -
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Query Match Best Local Similarity

36.9**%**; 42.3**%**;

Score 49.5; DB 1; Pred. No. 9.1;

Length 220;

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C;Species: Drosophila melanogaster
C;Apate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_ch
C;Accession: B41732
R;Matunis, E.L.; Matunis, M.J.; Dreyfuss, G.
J. Cell Biol. 116, 257-269, 1992
A;Title: Characterization of the major hnRNP proteins from A;Reference number: A41732; MUID:92112968; PMID:1730754
A;Accession: B41732
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F;137-203/Domain: ribonucleoprotein repeat homology <RRM2>
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A;Note: sequence extracted from NCBI backbone (NCBIN:132997, NCBIP:133000)
R;Matunis, E.L.; Matunis, M.J.; Dreyfuss, G.
J. Cell Biol. 116, 257-269, 1992
J. Cell Biol. 116, 257-269, 1992
A;Title: Characterization of the major hnRNP proteins from Drosophila melanogaster.
A;Reference number: A41732; MUID:92112968; PMID:1730754
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C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
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C;Superfamily: unassigned ribonucleoprotein repeat-containing
F;57-123/Domain: ribonucleoprotein repeat homology <RRM1>
F;137-203/Domain: ribonucleoprotein repeat homology <RRM2>
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A;Residues: 1-168,'F',170-321 <MAT>
A;Residues: 1-168,'F',170-321 <MAT>
A;Cross-references: CB:X62637; GB:S76630; NID:g11037; PIDN:CAA44503.1; PID:g11038
A;Note: sequence extracted from NCBI backbone (NCBIN:76630, NCBIP:76631)
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A;Cross-references: FlyBase:FBgn0003498
C;Superfamily: helix-destabilizing protein; ribonucleoprotein repeat
F;57-123/Domain: ribonucleoprotein repeat homology <RRM1>
F;137-203/Domain: ribonucleoprotein repeat homology <RRM2>
Search completed: December 30, Job time: 4.20471 secs
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A; Introns: 37/3;
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                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-558 < WOO>
                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z21943
A; Accession: T40651
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R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hamlin,
submitted to the EMBL Data Library, February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pre-mrna splicing factor, WD repeat protein - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe
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Pred. No. 4
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Pred. No. 84;
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RESULT 9
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R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, E.F.; Kerlavage, J; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: E64169
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: H96940 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng. O.; Gib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaev, White, O.; Salzey, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87389
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                                                                  hypothetical protein CAC0334 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum
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A; Residues: 1-509 <STO>
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C;Species: Caulobacter crescentus
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A; Residues: 1-220 <T
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1; Mismatches
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Pred. No. 16;
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  K.S.; Zeng, Q.; Gibson,
                                                                                                                                                                                                                                                                                                                                                                                                          GSPDB: GN00148
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C;Superf
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A; Residues: 1-308 < KEL>
A; Cross-references: GB: S62100
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    A; Gene: FlyBase: sqd
A; Cross-references:
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A; Residues: 1-166 < KI
                                              C;Genetics:
                                                               A; Note: sequence extracted
                                                                                                                                                   A;Status: preliminary
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    FlyBase:FBgn0003498
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70607
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
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A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: H96940

A;Status: preliminary
                                                                                                                                                                                                                                                                          RNA-binding protein (alternatively spliced) SqdB - fruit fly (Drosophila me C;Species: Drosophila melanogaster C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999 C;Accession: B47369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: strain H37Rv C;Genetics:
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jull-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: B70607
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                                                                                                                                                           A, Title: Initial organization of the Drosophila dorsoventral axis depends A, Reference number: A47369; MUID:93279471; PMID:7684991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-469 <COL>
A;Cross-references: GB:Z92774; GB:AL123456;
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GB:S62100; NID:g385453; PIDN:AAB26989.1; tracted from NCBI backbone (NCBIN:132997,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156
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Pred. No.
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Pred. No. 16;
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59;
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ATCC824
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PID:g385455
NCBIN:132999,
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Hamlin, N.; Ho
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  NCBIP: 133001)
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Holroyd, S.
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44111
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K. submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable A;Reference number: S44105
A;Accession: S44111
Search completed: December 30, 2003, 11:03:18 Job time : 12.078 secs
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A;Molecule type: DNA
A;Residues: 1-120 <HAW>
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                                                                                                                                                                                                                                                                                                                                                                    Query Match 69.8%; Score 464; DB 2; Length 120; Best Local Similarity 71.4%; Pred. No. 1e-35; Matches 90; Conservative 12; Mismatches 18; Indels
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                                                                                           115 LVTVSS 120
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                                                                                                                                      121 MVTVSS 126
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A;Residues: 1-137 <CUI>
A;Ross-references: EMBL:Z14177; NID:g31020; PIDN:CAA78546.1; PID:g31021 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
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C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change
C;Accession: S19666
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.;
J. Mol. Biol. 222, 581-597, 1991
anti-SS-A/Ro 60K peptide heavy chain E-56 - human (fragment)
C;Species: Homo sapiens (man)
C;Bate: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C;Aaccession: PC4281
R;Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A;Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from A;Reference number: PC4279; MUID:97236289; PMID:9125110
A;Accession: PC4281
A;Accessi
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PC4281
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A; Residues: 1-121 < MAR>
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Best Local S
Matches 90
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Best Loc
Matches
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;Species: Homo sapiens (man)
;Date: 22-Jan-193 #sequence_revision 22-Jan-1993 #text_change
;Accession: S19666
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Pred. No. 1.4e-36;
5; Mismatches 13
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Pred. No. 2.6e-36;
5; Mismatches 17
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R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23624
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-143 < OLE>
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                                                                                                               ig heavy chain - human
(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;Date: 02-Dec.1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
(;Date: 02-Dec.1993 #sequence_revision 26.
(;Accession: S31120
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurm.
Bur. J. Immunol. 22, 247-251, 1992
Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third compl.
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31120
A;Accession: S31120
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A;Note: the nucleotide sequence was submitt
C;Superfamily: immunoglobulin V region; imm
C;Keywords: heterotetramer; immunoglobulin
                                                                 A;Status: preliminary; nucleic acid
A;Molecule type: mRNA
A;Residues: l-114 <RAA>
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                                                      EMBL: X62972
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                 was submitted to the EMBL Data Library, region; immunoglobulin homology
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Pred. No. 7.3e
13; Mismatches
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Pred. No. 3.3e-36;
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Ig heavy chain (subclass IgM) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: S31105
C;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31105
A;Accession: S31105
                                                                                                                             R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: F36005
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C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                           Ig heavy chain V region (M49) - human (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998 (C;Accession: F36005
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                    A;Cross-references: GB:M34026
C;Genetics:
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A; Residues: 1-118 < RAA>
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                                                                 A; Molecule type: mRNA
A; Residues: 1-119 <SCH>
                                                                                                           A; Status: preliminary
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75.4%;
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75.4%; Pred. No. 6.5e-37;
tive 11; Mismatches 12
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Pred. No. 5.7e-39;
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                Ig heavy chain V region - human (fragment)
C;Species: Homo gaptens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul
C;Accession: S31701
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity A;Reference number: S31585
A;Accession: S31701
A;Status: preliminary
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S31701
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10

immunoglobulin diversity operate

from the

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A;Cross-references: EMBL:X62966
A;Note: the nucleotide sequence was submitted to the EMBL Data C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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C;ACCession: S31116

C;ACCession: S31116

C;ACCession: S31116

Ext. J. Immunol. 22, 247-251, 1992

Ext. J. Immunol. 22, 247-251, 1992

A;Reference number: S31104; MUID:92111633; PMID:1730252

A;Accession: S31116
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C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31116
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A;Map position: 14932.33-14932.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-118 <RAA>
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                                                                ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATD-----
                                                                              ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
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Pred. No. 9.9e-37;
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A;Molecule type: mRNA
A;Residues: 1-145 <FEL>
A;Residues: 1-145 <FEL>
A;Cross-references: EMBL:X53613; NID:g23865; PIDN:CAA37675.1; PID:g762936
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Felgenhauer, M.; Kohl, J.; Rueker, F. Nucleic Acids Res. 18, 4927, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region - human (fragment) (FSpecies: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 (C;Accession: S11239
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F;15-98/Domain: immunoglobulin homology <II</pre>
A; Description: Mechanisms that generate human immunoglobulin diversity of A; Reference number: $31585
A; Accession: $31595
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-128 cCUI>
A; Cross-references: EMBL:Z14171; NID:g31007; PIDN:CAA78540.1; PID:g31008
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                               Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31595
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
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98; Conservative
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C;Accession: S31104
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma Bur. J. Immunol. 22, 247-251, 1992
Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31104
A;Accession: S31104
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                                                                                                                                                                                                           Ig heavy chain V region (clone alpha-THY-32) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36273
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, Carlossion: S36273
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, Carlossion: S36273
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A; Residues: 1-121 < RAA>
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
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                                                                                                                                        A,Title: Human anti-self antibodies with high specificity A;Reference number: S36256; MUID:93178448; PMID:7679990 A;Accession: S36273
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A;Cross-references: EMBL:Z18834; NID:g33116; PIDN:CAA79286.1; PID:g939896 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                A;Status: preliminary; nucleic acid sequence not A;Molecule type: mRNA A;Residues: 1-120 <GRI>
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ll; Mismatches 11
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ALIGNMENTS

RESULT 1 \$30532 Ig heavy chain V region - human C;Species: Homo sapiens (man) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996 C;Accession: \$30532 P.Mariette, X. - PMRI, Data Library, October 1992 A;Cross-references: EMBL:218318 C;Superfamily: immunoglobulin V region; immuno C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology <IMM> 밁 A; Molecule type: mRNA A; Residues: 1-123 < MAR> 문 A; Status: preliminary Best Matches Query Match Local 116 119 101; 61 61 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCA--LPYINSSNYRRGVAAFDIWGQ 118 Similarity GTMVTVSS 126 GTMVTVSS 123 ADSVKGRFAISRDNAKNSLYLQMNSLRAEDTALYYCAKDTPY--SSGWSN---AFDIWGQ EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGTLGY Conservative 78.9%; 78.0%; 11; Score 518.5; DB Pred. No. 1e-40; 1; Mismatches immunoglobulin homology BB 9; 2; Indels Length 123; 7; Gaps 60 60

Ig heavy chain - human
("Species: Homo Sapiens (man)
("Species: Homo Sapiens (man)
("Date: 02-Dec:1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
("Accession: S31118
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complen A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31118

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A;Cross-references: EMBL:X62969
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology

A;Status: preliminary; nucleic acid sequence A;Molecule type: mRNA A;Residues: 1-121 <RAA>

not shown; translation

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NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS: 73

CORRESPONDENCE ADDRESS: 73

CORRESPONDENCE ADDRESS: 73

CORRESPONDENCE ADDRESS: 73

CORPORESS: American Cyanamid Company

STREET: 858 American Cyanamid Company

STREET: 107470-8426

COMPUTER: 15 A. 72

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RESULT 14
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Best Local Similarity 64.0:
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Sequence 45, Application PC/TUS9501219
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SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304-1018
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                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                 110 YRGDYXFDYWGQGTLV 125
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                                                                                                                                                                   60 FAQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGFAPYY----- 113
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                                                                                                                                                YAQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCAR-----APGYGSGGGC 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DO COUTO, FERNANDO J.R. CERIANI, ROBERTO L.
                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                             65.1%; Score 428.5; DB 64.0%; Pred. No. 1e-39; ative 10; Mismatches
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Sequence 19, Patent No. 5

 Application US/08253877C 5773001

GENERAL INFORMATION:

Hamann,

Philip R

APPLICANT:

Tsou, Hwei-Ru Weiss, Martin J.

INVENTION:

Conjugates of Methyltrithio Antitumor

APPLICANT:

APPLICANT:
APPLICANT:
APPLICANT:

Hinman, Lois Hollander, Irwin Holcomb, Ryan Hallett, William

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TYPE: amino acid
sTRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: prote
PCT-US95-01219-45
RESULT 15
US-08-253-877C-19
                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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APPLICANT: Bendig,
APPLICANT: Leger,
APPLICANT: Saldanh
APPLICANT: Jones,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/18(
FILING DATE: 25-JAN-1994
ATTORNEY AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 1
FILING DATE: 25-JAN-:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy |
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94105
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                                                                         110 YRGDYXFDYWGQGTLV 125
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                                                                                                                                                 61 YAQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCAR----
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                                                                                                                                                                                                                                                                                                                                          Length 129;
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TELEPHONE:

: 650-855-0555 650-845-4166

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RESULT 11
US-08-264-093-3
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                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
TELEPAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Applic Patent No. 5639863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acid
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 incl
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,0:
FILING DATE:
FILING DATE:
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LIBRARY: SYNON
CLONE: 3551457
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TITLE OF INVENTION:
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                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
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                   STRANDEDNESS:
                                   TYPE: amino acid
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                                                      121 amino acids
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linear
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               not applicable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO CELL CYCLE-INDEPENDENT GLIOMA SURFACE ANTIGEN
26
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                                                                                                                                                                                                                                                                                                                                                                                            3.5 inch, 1.4 Mb storage
                                                                                                                                                                     NOVOP/106A/7551
                                                                                                                                                                                                                                             5639863 applicable
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                                                                                                                                                                                                          TELEPAX: 415-54 NO: 45:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45, Approx No. 5840299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 65.3%; Score 429.5; DB 1
Best Local Similarity 66.4%; Pred. No. 7.2e-40;
Matches 81; Conservative 17; Mismatches 19
                                                    Query Match
Best Local Similarity 64.0
Conservative
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECHOME: 415-543-9600
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: One Market L
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 LV 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AQXFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT 120
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                     1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMCWMNP-NSGNAG 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    California
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Leger, Olivier J.
Saldanha, Jose
Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                   64.0%;
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                                                                     10;
                                                                   Score 428.5; DB
Pred. No. 1e-39;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version
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                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                       14;
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                                                                       Indels
                                                                                                  Length 129;
                                                                       25;
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                                                                   Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 1.128
; OTHER INFORMATION: /label= HUMAN_I
US-08-202-047-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 1413
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 22,
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Best Local :
                    APPLICATION NUMBER: US/08
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com)
                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CHESNUT,
APPLICANT: POLLEY, N
APPLICANT: PAULSON,
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             NITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 128 amino
TYPE: amino acid
STRANDEDNESS: sin
                                                                                                        APPLICATION NUMBER: US/08/964,690 FILING DATE: CLASSIFICATION:
   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CTTY: San Francisco
                                                                                                                                                                                                                                                                  ZIP: 94105
                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 YRGDYFDYWGQGTLV 124
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6033667
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                                                                                                                                                                                                                                                                                              California
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JONES, S. Tarran
SALDANHA, Jose W.
                                                                                                                                                                                                                                                                                 USA
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William M.
NUMBER: 30,223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.1%; Score 435; DB 1; Length 128; 64.4%; Pred. No. 1.9e-40; tive 11; Mismatches 13; Indels
                                                                   US/08/202,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14137-77
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13,
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                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                     ATTORNEY/AGENT INFORMATION: NAME: Cerrone, Michael C
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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LENGTH: 128 amino acid
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein
LOCATION: 1..128
OTHER INFORMATION: /label= HUMAN_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 YRGDYFDYWGQGTLV 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YAQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCAR-----
                                                                                                                                                                                                                                                                         94304
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                                                                                                                                                                                                                                                                                                         Palo Alto
: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNGDTN 60
                                                                                                                                                                                                                                                                                                                                           E: Incyte Pharmaceuticals,
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09049672A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang, Yue, Henry
                                                                                                                                                                                                                                                                                           USA
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   PF-0497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-477-989B-94
                                                                                                                                                                                                                                               APPLICANT: Kaplan, Ruth
APPLICANT: Kieber Emmons, Thomas
APPLICANT: Postema, Christina E.
APPLICANT: Postema, Christina E.
APPLICANT: White-Scharf, Mary
TITLE OF INVENTION: LO-CD2a Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: T-Cell Activation and
TITLE OF INVENTION: Proliferation
TITLE OF INVENTION: Proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-472-281A-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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APPLICANT: Bazin, He
APPLICANT: Latinne,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/11:
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/02:
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
           COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                               ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                           STREET: 6 L. STREET: Noseland CITY: Roseland PATE: New Jersey 11 S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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APPLICATION NUMBER:
FILING DATE: 29-MAR-
                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LV 122
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                                                                                                                                                                                             6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bazin, Herv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                    Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1995
                                                                                        inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.5%; Score 437.5; DB 69.7%; Pred. No. 9.7e-41 tive 13; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Dominique
US/08/477,989B
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RESULT 8
US-08-202-047-22
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Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: CHESNUT, Robert W.
APPLICANT: POLLEY, Margaret J.
APPLICANT: PAULSON, James C.
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, Jose W.
APPLICANT: BENDIG, Mary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-147
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APPLICATION NUMBER: 08/4
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/1
FILING DATE: 09-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                           COUNTRY:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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o. 5800815
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RESULT 5
US-08-477-877B-94
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FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latine, Dominique
APPLICANT: Latine, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ
NUMBER OF SEQUENCES: 96
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                    CITY: Roseland
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                           E: Carella, Byrne, Bain, Gilfillan, E: Cecchi, Stewart & Olstein 6 Becker Farm Road
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1251 Avenue of the Americas
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69.7%;
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Pred. No. 3.3e-41;
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US-08-477-877B-94
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 94, Application US/08472281A Patent No. 5817311
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                 COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WOXGDerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
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LENGTH: 123 amino acid
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                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                       APPLICANT: Latinne, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ
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PRIOR APPLICATION DATA:
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             APPLICATION NUMBER: US/08/472,281A FILING DATE: 07-JUN-1995
                                                                                                                                                                                                               STREET: 6 Becker Farm Road CITY: Roseland
                                                                                                                                                                                                                                               ADDRESSEE: Carella, Byrne, Bain, Gilfillan, ADDRESSEE: Cecchi, Stewart & Olstein
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APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
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                                                                                                                                                                           STATE: New Jersey COUNTRY: U.S.A.
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REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61
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CLASSIFICATION:
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05-MAR-1993
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US-09-025-769B-59
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                                                                                                                                                                                                                          Query Match
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APPLICANT: Knappi
APPLICANT: Pack,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
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APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
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CITY: New York
STATE: New Yor
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Local Similarity 71.5%;
nes 88; Conservative
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ZIP: 10021
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                                   AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAVYYCAR-----WGGDGFYAMDYWGQG 113
                                                     AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGFAPY-YDSWGQG 119
                                                                                                             QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60
TLV 122
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Pack, Peter
Ilag, Vic
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(212) 596-9090
---- Th NO: 59:
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                                                                                                                                                                                  Score 451; DB 4; Length 120; 
Pred. No. 3.1e-42; 
9; Mismatches 18; Indels
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                                                                                                                                     Sequence 22, Application US/09025769B Patent No. 6300064
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Matches (
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GENERAL INFORMATION:
Taguku
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ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION UNMBER: 29,066
REFERENCE/DOCKET NUMBER: 0650
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 617-542-8906
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                    GENERAL INFORMATION:
APPLICANT: Knappi
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APPLICANT:
APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TYPOLOGY: line
OLECTION
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FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
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TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Honjo, APPLICANT: Matsud
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APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueskthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
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STREET: 225 Franklin Street
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Pred. No. 5e-42;
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Result
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Maximum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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658
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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                      Minimum Match 0%
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Listing first 45 summaries
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                                            GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
        US-09-025-769B-36
US-09-025-769B-59
US-08-545-809A-96
US-09-025-769B-22
US-08-477-987B-94
US-08-477-989B-94
US-08-477-989B-94
US-08-264-690-3
US-08-961-521-45
US-08-961-521-19
US-08-961-521-521-19
US-08-961-521-19
US-08-961-521-19
US-08-961-521-19
US-08-961-521-19
US-08-961-521-19
US-08-961-521-10
US-08-961-99-149-3
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45, Appl
46, Appl
18, Appl
19, Appl
19, Appl
19, Appl
19, Appl
11, Appl
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411.5 62.5 121 3 US-08-964-690-23 406.5 61.8 119 1 US-08-478-039-65 406.5 61.8 119 1 US-08-476-349A-65 405.5 61.6 119 2 US-08-561-521-12 405.5 61.6 123 1 US-08-483-389-86 405.5 61.6 123 2 US-08-483-389-86 405.5 61.6 123 2 US-08-483-389-86 405.5 61.6 123 2 US-08-483-393-86 405.5 61.6 123 2 US-08-483-932-86 405.5 61.6 123 2 US-08-714-017-86 405.5 61.6 123 3 US-08-714-017-86 405.5 61.6 123 3 US-08-714-017-86 405.5 61.6 123 3 US-08-714-017-86 403.5 61.3 140 3 US-08-836-561-63	45	44	43	42	41	40	39	38	37	36	35	<u>ي</u>	ω ω	32	31	30	29
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P # W W W W N N N N P U N P P W	61.2	61.3	61.3	61.3	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.8	61.8	62.5
1 US-08-964-690-23 1 US-08-478-039-65 1 US-08-476-349A-65 1 US-08-476-349A-65 2 US-08-482-862-86 2 US-08-483-389-86 2 US-08-483-389-86 2 US-08-483-392-86 2 US-08-483-912-86 2 US-08-483-912-86 3 US-08-714-017-86 3 US-08-714-017-86 3 US-08-816-63	119	140	140	140	123	123	123	123	123	123	123	123	119	119	119	119	121
US-08-964-690-23 US-08-476-339A-65 US-08-476-339A-65 US-08-561-521-12 PCT-US95-01219-12 US-08-483-389-86 US-08-4873-130-86 US-08-4873-503-86 US-08-4873-503-86 US-08-473-503-86 US-08-473-680-86 US-08-473-680-86 US-08-473-680-86 US-08-473-680-86 US-08-483-31-86	_	4.	w	w	w	w	N	N	N	N	N	_	U	N	_	_	w
	US-08-491-845-10	US-09-434-122-63	US-08-569-147-82	US-08-836-561-63	US-08-475-680-86	US-08-714-017-86	US-08-720-420A-86	US-08-483-932-86	US-08-473-503-86	US-08-487-113D-86	US-08-483-389-86	US-08-482-882-86	PCT-US95-01219-12	US-08-561-521-12	US-08-476-349A-65	US-08-478-039-65	US-08-964-690-23
	10,	63	82,	63,	86,	96,	86,	86,	86	86,	86,	86,	12,	12,	65,	65	23,
10, 10, 10, 10, 10, 10, 10, 10, 10, 10,	App	App	App	App	App	App	App	App	App	App	App						

ALIGNMENTS

; TYPE: amino acid ; STRANDEDNESS: ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-09-025-769B-36 US-09-025-769B-36 Sequence 36, Application US/09025769B Patent No. 6300064 Query Match Best Local Similarity 71.9 Matches 88; Conservative APPLICATION NUMBER: US/09/025,769B FILING DATE: 18-FEB-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION: NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: GENERAL INFORMATION: APPLICANT: Knappik, Ach APPLICANT: Pack, Peter APPLICANT: Ilag, Vic COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version APPLICANT: Ge, Liming APPLICANT: Moroney, Simon APPLICANT: Plueskthun, Andreas TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373 CORRESPONDENCE ADDRESS: ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CURRENT APPLICATION DATA: STREET: 1251 Ave CITY: New York STATE: New York COUNTRY: TELEPHONE: LENGTH: 10021 : 120 amino acids amino acid (212)596-9090 USA Knappik, Achim (212) 596-9000 68.5%; 71.5%; 36: Score 451; DB 4; Pred. No. 3.1e-42; 9; Mismatches 18 #1.30 (EPO Length 120;

Indels

8,

Gaps

Publication No. US20 GENERAL INFORMATION:

US20030157109A1

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APPLICANT: CONTAINN.

APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao

APPLICANT: Feng, Xiao

APPLICANT: Yang, Xiao-Dong

APPLICANT: Chen, Francine

APPLICANT: Gazit, Gadi

APPLICANT: Bezabeh, Binyam

ITILE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES

ITILE OF INVENTION: THEREOF

FILE REFERENCE: ABGENIX.051A

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEO ID NOS: 377

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 241

LENGTH: 126

TYPE: PRT

ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
ITITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 204
LENCTH: 126
TYPE: PRT
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                                                                             Query Match
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Matches 91
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 241, Appropriate Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
                                                                                           Match 71.9%; Score 473; DB 12; Length 126; Local Similarity 72.8%; Pred. No. 5e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 72.8 es 91; Conservative
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AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR---DIVVVVTATDYYYGMDVWG 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10041860
                                                                             Conservative
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Pred. No. 5e-41;
                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 126;
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RESULT 15

US-10-041-860-38

Sequence 38, Application US/10041860

Publication No. US20030157109A1

GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Yang, Xiao-Chi

APPLICANT: Feng, Xiao

APPLICANT: Yang, Xiao-Dong

APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND

TITLE REFERNCE: ADSENIX.051A

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07
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APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 349, Application US/10041860 Publication No. US20030157109A1
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Best Local Similarity
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APPLICANT:
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
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TYPE: PRT
ORGANISM: homo sapiens
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SEQ ID NOS: 377
FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYDINWVRQATGQGLEWMGWMNPNNGNTGY 60
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Yang, Xiao-Dong
Chen, Francine
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APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FORSESEQ for Windows Version 4.0
SEQ ID NO 201
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-201
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US-10-041-860-201
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                                                                                 GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
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Best Local Similarity
Matches 93; Conserv
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       APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
REFERENCE: ABGENIX.051A
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Chen, Francine
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Pred. No. 3.9e-41;
8; Mismatches 18;
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; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 288
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-288
                                                                                                                                                                                                                                                                                                        APPLICANT: COTVALAN, JOSE R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PO
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
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Best Local Similarity 74.4%;
Matches 93; Conservative
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                                                                                                                                                                                    Matches
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Best Local
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                                                                                                                                                                                                                                                                                                 LENGTH: 126
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                          118 QGTLV 122
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                                                         61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR---DIVVVVTATDYYYGMDVWG
                                                                                     61 AOKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYY---DSWG
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                                                                                                                    h 71.9%;
Similarity 72.8%;
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122
                                                                                                                                                                                   ; Score 473; DB 1; Pred. No. 5e-41; 11; Mismatches
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Pred. No. 3.9e-41;
B; Mismatches 18
                                                                                                                                                                                                                    DB 12;
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RESULT 12 US-10-041-860-204

Sequence 204,

Application US/10041860

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US-10-041-860-202
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 37
LENGTH: 126
TYPE: DET
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 377

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 202

LENGTH: 126

TYPE: PRT

ORGANISM: homo sapiens
                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 202,
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APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Biryam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
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Local Similarity 72.8%;
                                                                                                                                                                                                                                                    Match 72.2%;
Local Similarity 72.8%;
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                                                                                                                                                                         1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF 60
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Chen, Francine
                                    OGTLV 122
                                                                           AQKFQGRVTMTRNTSLSTAYMELSSLRSEDTAVYYCAR---DIVVVVAATNYYNGMDVWG 117
                                                                                                 AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYY---DSWG 117
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                                                                                                                                                      QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYDINWVRQATGQGLEWMGWMNPNSGNTGY 60
QGTTV 122
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3%; Pred. No. 3.1e-41;
11; Mismatches 17
                                                                                                                                                                                                                                  Score 475; DB 12; Length 1
Pred. No. 3.1e-41;
11; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                      Length 126;
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APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
APPLICANT: Bezabeh, Binyam
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO P
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOUTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 126
TYPE: PAT
ORGANISM: homo sapiens
US-10-041-860-19
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 239
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-239
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US-10-041-860-19
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US-10-041-860-239
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Query Match 72.
Best Local Similarity 74.
Matches 93; Conservative
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APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
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Chen, Francine
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Chen, Francine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                  72.0%;
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                  Score 474; DB 12;
Pred. No. 3.9e-41;
   Mismatches
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                                  Length 126;
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118 QGTTV 122

118

QGTLV 122

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APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Yeng, Xiao-Dong
APPLICANT: Yeng, Xiao-Dong
APPLICANT: Yeng, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Francine
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.OSLA
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 199
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
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; TYPE: PRT; ORGANISM: homo sapiens US-10-041-860-236
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                                                          FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 236
LENGTH: 126
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APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                     APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
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APPLICANT:

Feng, Xiao Yang, Xiao-Dong Chen, Francine Gazit, Gadi Weber, Richard

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CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOPTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 294
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-294
RESULT 5
US-10-041-860-37
US-10-041-860-37, Application US/10041860
; Sequence 37, Application US/10041860
; Publication No. US/20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Yang, Xiao-Dong
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APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.6%; Score 478; DB 12; Local Similarity 74.4%; Pred. No. 1.5e-41; Les 93; Conservative 10; Mismatches 16
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/DT05 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10 PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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658
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
478 478 478 478 475 475 475 477 477 477 477 477 477 473	Score
77 77 77 77 77 77 77 77 77 77 77 77 77	Query Match
126 126 126 126 126 126 126 126 126 126	Length
	BB
US-10-041-860-21 US-10-041-860-199 US-10-041-860-236 US-10-041-860-294 US-10-041-860-37 US-10-041-860-39 US-10-041-860-202 US-10-041-860-201 US-10-041-860-201 US-10-041-860-204 US-10-041-860-204 US-10-041-860-204 US-10-041-860-204 US-10-041-860-204 US-10-041-860-349 US-10-041-860-349	ID
Sequence 21, Appl Sequence 294, App Sequence 294, App Sequence 297, Appl Sequence 291, Appl Sequence 201, Appl Sequence 201, Appl Sequence 204, Appl Sequence 308, Appl Sequence 308, Appl	Description

45 44					_	39	38							31 462	30 462	29 462	28 464										18 472		716
447.5	449	449	449	449	449	449	449	449	449	449	453.5	460	2.5	5	5	.5	4.5	.5	464.5	464.5	465	465	466	468	468	469	.5	5	
68.0	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.9	69.9	70.3	70.3	70.3	70.3	70.6	70.6	70.6	70.6	70.7	70.7	70.8	71.1	71.1	71.3	71.8	71.8	
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		Sequence 1	Sequence .3			Sequence 3						æ									Sequence 5			O	\mathbf{L}	Sequence 4	Sequence 3		
930, App	1389, Ap	l, Appli	.361, App		344, App	342, App	•		290, App			238, App	372, App		200, App	48, App	360, App	242, App			•	927, App	61, Appl	0		47, Appl		_	J. J. C

ALIGNMENTS

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APPLICANT: CORVALAN, JOSE R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PO
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT PILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
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US-10-041-860-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
                                                                                                                                           Query Match 72.6%; Score 478; DB 12; Best Local Similarity 74.4%; Pred. No. 1.5e-41; Matches 93; Conservative 10; Mismatches 16;
1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
                                                                         QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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CC important in physiological phenomena such as cell rolling, metastasis and confident in physiological phenomena such as cell rolling, metastasis and confident in physiological phenomena such as cell rolling, metastasis and confident in physiological phenomena such as cell rolling, metastasis and control of the physiological phenomena in the complex comprising at least one control of the physiological physiological physiological physiological comprising at least one control of the physiological physi
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                 Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favour of other
                                                                                                                                                                                       Hagai Y, I
Plaksin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adeno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Fv molecule hypervariable region related peptide #45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2002
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                                                                                                                                                                                                                                                                                                                                29-DEC-2000; 2000US-0751181.
                                                                                                                                                                                                                                                                                                                                                                                        31-DEC-2001; 2001WO-US49440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200259264-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lymphoma; myeloma;
                                                                                                                                   WPI; 2002-619166/66.
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                                                                                                                                                                                          Lazarovits J,
, Peretz T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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84.7%;
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Best Local S
Matches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, lukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region
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                                                                                                                                                                                                                                                                                                                                                                               Primer: PCR; amplify; human; immunoglobulin; variable; heavy chain;
cosmid; placenta; vector; pJB81; E.coli; mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunoglobulin variable heavy chain #8
                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
02-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR66302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         related peptide of the invention.
Protein sequences (AAR66295-51) are novel chain sequences encoded by novel isolated (AAQ78939-79002) were isolated and cloned
                                                           Claim 17; Page 41-42; 130pp; Japanese.
                                                                                      DNA fragment comprising human immunoglobulin Vh production of human immunoglobulin in mammalian
                                                                                                                                  N-PSDB; AAQ78946.
                                                                                                                                                 WPI; 1995-006791/01.
                                                                                                                                                                            Honjo T,
                                                                                                                                                                                                                                  10-MAY-1993;
                                                                                                                                                                                                                                                                 10-MAY-1993;
                                                                                                                                                                                                                                                                                            24-NOV-1994.
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                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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84.7%;
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Pred. No. 8.9e-36;
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The genes
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; heavy chain; antibody; factor VIII; hemostatic;
hemophilia A; scFv; A3-C1.
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    WPI; 2000-053102/04
                                                                                                                                                                                                                                              08-MAY-1998;
                                                                                                                                                                                                                                                                                                                            07-MAY-1999;
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                                                                                                                                                                (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
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                                                                                  Brink EN,
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Pred. No. 7.2e-36;
9; Mismatches 18
                                                                                  Turenhout EAM;
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ARESULT 13
ABG91861
ID ABG91
XX ABG91
AC ABG91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastesis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hybridizable polynucleotides) comprising a contiguous nucleotide sequent coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them
                                                                                      Novel isolated epitope present on cancer cells and important physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardicinflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human factor VIII antibody A3-C1 specific scFv protein DP-15 which is used
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                                                                diseases, and cancer
                                                                                                                                                                                                              WPI; 2002-674776/72.
                                                                                                                                                                                                                                                                     Lazarovits J, Hagai Y, Szanthon E, Richter T,
                                                                                                                                                                                                                                                                                                                                                                                                                      29-DEC-2000; 2000US-258948P.
29-DEC-2000; 2000US-0751181.
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                                                                                                                                                                                                                                                                                                                                                            (BIOT-) BIO-TECHNOLOGY GEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9A; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.2%;
                                                                                                                                                                                                                                                                         Plaksin D, Vogel T, Amit B, Kooperman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       novel polynucleotide (I) (and complements and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 449; DB 21;
Pred. No. 8.9e-36;
7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₿
                                                                                                                                                                                                                                                                            Nimrod A,
Peretz T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                               or cardiovascular
                                                                                                                                                                                                                                                                            Mar-Haim
Levanon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
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Disclosure;

Page 246; 310pp; English

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RESULT 10
ABB57555
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and neutralises a matrix metalloprocease (MMP)-inhibiting activity of CTMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and a variable light chain (VLC)DR3 region. An antibody preparation of the cartivity of a TIMP-1. It is especially useful for decreasing an MMP-inhibiting activity of a disorder in which TIMP-1 is elevated, e.g. liver activity of a disorder in which TIMP-1 is elevated, e.g. liver CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon CC cancer. The antibody is also useful for detecting a TIMP-1 in a test preparation, or in diagnosing a disorder in which a TIMP-1 level is CC elevated. The sequences shown in ABRO1502-ABRO1545 represent the heavy CC chain regions of a human anti-TIMP-1 antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates antibody, which binds and neutralises a mat
                                                                                                                                                                                                                                                                          neuroprotective; antiinflammatory; antidiabetic; antipsoriatic; immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis; thyromimetic; hepatotropic; immune response suppressor; narcolepsy; rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulitis; crave's disease; insulin-dependent diabetes; Hashimoto's disease; systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis; transplant rejection; graft versus host disease; pemphigus vulgaris; glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunomodulatory human MHC class II antigen-binding protein; HLA; human leukocyte antigen; immune system; immunosuppression; antibody; major histocompatibility complex; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA-DR-specific protein MS-GPC3 VH sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB57555 standard; Peptide; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAR-2002
                                 12-MAY-2000; 2000EP-0110063
06-OCT-2000; 2000US-238762P
                                                                                                                                                                   WO200187338-A1
                                                                                                                                                                                                                         Homo sapiens.
                                                                                        14-MAY-2001; 2001WO-US15626.
(GPCB-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF 60
GPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAP----YYDSW 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEMMGWINPNSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOGTLY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
BIOTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۶
۶
                                                                                                                                                                                                                                                              disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.7%; Score 452; DB 24; 70.6%; Pred. No. 1.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to a novel purified preparation of a human to a tissue inhibitor of metalloprotease-1
                                                                                                                                                                                                                                                              Sjogren's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metalloprotease-1 (TIMP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                  cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 11
AAW27551
ID AAW27
XX
AC AAW27
XX
AC AAW27
XX
DT 23-JF
XX
DT 23-JF
XX
Humar
XX
Humar
XX
KW Humar
XX
KW Heavy
XX
KW Homo

23-JAN-1998

(first entry

AAW27551

standard; Protein;

Human; antibody; preparation; library; VH1B; variable region; heavy chain; consensus.

Human Ab heavy chain variable region VH1B consensus

ð ₽ Ś 문 S

121

LV 122

ĽV 112

61 13

AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT

120 60 60

QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNDNSGNAGF

ب _ Query Match Best Local S Matches 86

Similarity

68.5%;

96;

Conservative

10;

Score 451; DB 23; Pred. No. 6.9e-36; 0; Mismatches 16;

Length 116; Indels

10;

Gaps

Sequence

116 AA;

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The present invention describes a composition (I), comprising a composition expressed composition with binding specificity for an antigen expressed on the composition with binding specificity for an antigen expressed on the composition with binding specificity for an antigen expressed on the composition with binding specificity for an antigen expressed on the composition of immune response is I microm or less. (I) has compression of an immune response, and the IC50 for the suppression of immune response. (I) has compile the interest of the suppression of an immune response, and the IC50 for antidiabetic, antiarthritic, neuroprotective, antifilammatory.

CC antithroid, nephrotropic, thyromimetic and hepatotropic activities, and can be used as a suppressor of immune response. (I) is useful for compressing activation or proliferation of a cell of the immune system, suppressing the cell, the interaction of a cell of the immune system, compressing a patient and for compressing a recreasing an antigen, human leukocyte antigen (HLA)-DR compressing a patient and for compressing a pharmaceutical preparation of a call to the killing. (I) (optionally linked to cytotoxic or immunogenic agent) is useful for preparing a pharmaceutical preparation for the treatment of rheumatoid arthritis, juvenile arthritis, multiple sclerosis, Grave's disease, compressing a pharmaceutical preparation for the treatment of rheumatoid host disease, hashimoto's disease, myssthenia gravis, pemphigus vulgaris, compression, primary biliary compressed to the present invention.
Composition for suppressing immune response, treating diseases immune system, has polypeptide comprising antibody-based antigen-binding domain of human composition, which binds antigenties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed on a cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-075289/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Fig 15; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MORP-) MORPHOSYS
                                                        exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tesar M, Thomassen-Wolf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĄG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binds antigen
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RRESULT 8
AAB674619
ID AAB6
XX AAB6
XX AAB6
XX AAB6
XX Huma
XX Huma
XX Huma
XX Homc
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 85
                                                                       Novel isolated human immunoglobulin or functional immunoglobulin fragment specific for human leukocyte antigen Cw6, useful for treatment of humans and for human leukocyte antigen phenotyping -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing, miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB67619 standard; Protein; 245 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB67619;
       Claim
                                                                                                                                                                                                                                       WPI; 2001-218451/22.
                                                                                                                                                                                                                                                                                                               Kretzschmar T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-2000; 2000WO-EP08388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200114558-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 2456-2457; 3148pp; English
                                                                                                                                                                                                                                                                                                                                                                                               (MORP-) MORPHOSYS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 TLV 122
       3; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQKFQGRVTMTRDTSISTAYMELGRLRSEDTAVYYCARMEYDILTGYYG--GYFDYWGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLI-WFGPAPYYDSWGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVOLVESGPEVKKPGTSVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPNSGGTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99EP-0116691
       23pp; English
                                                                                                                                                                                                                                                                                                               Tesar M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.9%;
                                                                                                                                                                                                                                                                                                           Marget
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Pred. No. 9.1e-36;
6; Mismatches 19
                                                                                                                                                                                                                                                                                                               Z,
                                                                                                                                                                                                                                                                                                                   Kroenke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB67617-23 represent single chain antibody (scFv) fragments which are specific for human leukocyte antigen (HAA)-Cw6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoglobulin fragments specific for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping.
                                                                                                                                                                                                                                                                                                                                                                                                Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer; idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
                                              New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human anti-TIMP-1 antibody heavy chain #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                  hypertrophy or lung cancer
                                                                                                                N-PSDB; ABZ74785
                                                                                                                                                             Pan C,
                                                                                                                                                                                                                                            24-APR-2001; 2001US-285683P
                                                                                                                                                                                                                                                                          24-APR-2002; 2002WO-US12801
                                                                                                                                                                                                                                                                                                          31-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                              (MORP-)
                                                                                                                               2003-129114/12.
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                                                                                                                                                             Knorr AM, Schauer M,
                                                                                                                                                                                            MORPHOSYS A
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                                                                                                                                                             Hirth-dietrich C,
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Claim 20;

Page 155-156; 228pp; English

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel antibodies that immunospecifically bind B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                             Human immunodeficiency virus-1; HIV-1; human monoclonal antibody; envelope glycoprotein; gp120; diagnosis.
                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                       03-APR-2001
            WPI; 2001-112438/12.
                                                                                                                                                                                      WO200100678-A1
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AAF29048
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72.2%;
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Pred. No. 7.1e-37
9; Mismatches 1
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variable regions of human monoclonal antibodies which are immunors with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein These can be used in diagnosis and therapy of HIV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human BLyS binding
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                                                                                                    WPI; 2002-114799/15.
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                                                                                                                                                  Barash SC,
                                                                                                                                                                                                                                                                     ; 2000US-212210P.
; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
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                                                                                                                                                                                                   ANTIBODY TECHNOLOGY.
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73.2%;
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Pred. No. 7e-37;
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                                                                                                                                                       Hilbert
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RESULT 4
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ID ABP4
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AC ABP4
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DT 19-J
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KW E
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                       16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240B16P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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                                Claim
                                                                                   Antibodies against B Lymphocyte Stimulating the diagnosis and treatment of cancers and i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JAN-2002.
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                                                                                                                                                                                                                                                                                          (CAMB-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLyS binding scFv SEQ ID
                          1; Page 1508-1509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
                                                                                                                                                                                                                                                                                       HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARXRRWELL--GMMWDFDYWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWVGWMNPNSANTGY
                                                                                                                                                                                                                                 Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 AA;
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                                                                                                                                                                                                                                 SC,
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                                                                                                                                                                                                                                 Choi
                       3148pp;
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                                                                                                                                                                                                                              GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 AA
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Pred. No. 2e-37;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      927.
                          English
                                                                                                                                                                                                                              Vaughan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunodeficiency syndrome
                                                                                      polypeptides, useful for 
immune disorders -
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                                                                                                                                                                                                                                 Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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RESULT 5
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XX ABP4
XX BLY6
AC BLY6
KW Lumc
KW immm
XX imm
XX Syst
KW comm
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                               16-JUN-2000; 2000US-212210P.
17-CCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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                                                                                                                 (HUMA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   common variable immunodeficiency; acquired immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2001; 2001WO-US19110
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                                            X.
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                                                                                                                     CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                      HUMAN GENOME SCI INC
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                                            Barash
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72.2%;
                                            Choi GH,
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Pred. No. 7.1e-37;
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                                            Vaughan
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                                            Hilbert
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Best Local S
Matches 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human FVIII antibody A3-C1 scFv
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This invention describes a novel polymucleotide (I) (and complements and hybridizable polymucleotides) comprising a contiguous nucleotide sequency coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the
                                                                                                                                                                                                                  New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1999
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hemophilia A; scFv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-1998;
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                                                                                                                                                             Example 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SANQ-)
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                                                                                                                                                             Fig 9A; 61pp; English
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A3-C1.
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Pred. No. 8.6e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor VIII; hemostatic;
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          AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB5224 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antilifective and antibacterial activities, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB53510 standard; Protein; 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                 Colon cancer associated gene sequences, antigens, useful for the treatment, prevdisorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                               08-MAR-2000; 2000WO-US05883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer antigen protein sequence SEQ ID NO:1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   reproductive disorder; gastrointestinal disc
infectious disease; cardiovascular disorder.
                                                                                                     Claim 11; Page 1631; 2104pp; English.
                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                   L2-MAR-1999;
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DB; AAC98267.
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96.7%;
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                                                                                                                                                 prevention,
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                                                                                                                                                   as colon c
diagnosis
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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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468
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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Match
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AAY50966
AAY50959
AAB43910
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ABP44937
AAB62747
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Human FVIII antibo
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Human BLyS binding
Human HIV-1 monocl
Human HIVS binding
Human HIVS binding
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
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251	250	248	123	250	249	238	251	221	251	476	251	470	251	248	248	241	228	248	146	249	251	241	251	199	247	120	120	251	251	117	98	98	98	120	116
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ABP45867	ABP45711	9	AAW79228	ABP45549	ဖ	ABP45896	96	ABR01537	ABP45551	AAW88464	ABP45727	AAU74296	ABP45858	98	Ф	w	ABR01526	ABP45461	AAW22841	ABP45624	ABP45859	ABP46020	ABP45575	AAY34302	ABP45718	ABJ18719	67	491	ABP45378	630	ABG78170	96	0	2755	ABB57555
bindin		BLyS	Heavy chain variab		Human BLyS binding	Human BLyS binding			Human BLyS binding		Human BLyS binding				Human BLyS binding	S	Human anti-TIMP-1	Human BLyS binding				BLyS	Human BLyS binding	IgM antibody CEM 1	Υ.	_	11	š	Human BLyS binding	Human immunoglobul	Human Fv molecule	Human antibody fra	FVIII ant	Human Ab heavy cha	HLA-DR-specific pr

23-MAR-2000 AAY50966; AAY50966 standard; Protein; (first entry) 122 ₽

ALIGNMENTS

Human FVIII antibody heavy chain variable region B38 protein fragment.

Human; heavy chain; antibody; factor ${\tt VIII}$; hemostatic; variable region; hemophilia ${\tt A}$.

RRSULT 1
ANY5096
ID ANY5
XX ANY5
XX ANY5
XX ANY5
XX Huma
XX Huma
XX Homo
XX Ho 08-MAY-1998; 18-NOV-1999. Homo sapiens 07-MAY-1999; WO9958680-A2 (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING 98EP-0201543. 99WO-NL00285

Voorberg JJ, Van Den Brink EN, Turenhout EAM

WPI; 2000-053102/04. N-PSDB; AAZ43863.

New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for

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Q99LC
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Best Local S
Matches 70
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Q9D8L4;

Q9D8L4;

Q9D8L4;

Q9D8L4;

Q1-JUN-2001 (TrEMBLrel. 17, Created)

Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)

Q1-JUN-2003 (TrEMBLrel. 23, Last annotation update)

Q1-JUN-2003 (TrEMBLrel. 23, Last annotation update)

Q2-JUN-2003 (TrEMBLrel. 23, Last annotation update)

Q3-JUN-2003 (TrEMBLrel. 23, Last annotation update)

Q4-JUN-2003 (TrEMBLrel. 23, Last annotation update)

Q5-JUN-2003 (TrEMBLrel. 17, Last sequence update)

Q6-JUN-2003 (TrEMBLrel. 17, Last sequence update)

Q7-JUN-2001 (TrEMBLrel. 17, Created)

Q8-JUN-2001 (TrEMBLrel. 17, Last sequence update)

Q8-JUN-2001 (TrEMBLrel. 17, Last sequence update)

Q8-JUN-2001 (TrEMBLrel. 17, Last sequence update)

Q8-JUN-2003 (TrEMBLrel. 17, Last sequence update)

Q8-J
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_MIC; 1.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 463 AA; 51007 MW; I
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Q99LC4;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUB-Pancreas;
MEDLINE-21085660; PubMed-11217851;
MEDLINE-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Aizawa K., Izawa M., Nishi K., Bono H., Kasukawa T., Saito Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC003435; AAH03435.1; HSSP; P01842; 7FAB.
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Submitted (FEB
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
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55.1%; Pred. No. 2.6e-30;
tive 18; Mismatches 23
                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Matches 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL, AK007918; BAB25349.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 4.
SMART; SM00406; iGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 473 AA; 51699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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133
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                                                                                                                                                              80 NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGYD-YDWFA-----YWGQGT
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72; Conserv
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                                                                                 LV 122
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ilarity 59.0%;
Conservative 1
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; Pred. No. 3.1e-30;
14; Mismatches 29;
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RESULT 12
Q8VCX
ID Q8VCX
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Best Local S
Matches 72
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095978;
01-MAY-1999
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SEQUENCE
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of patient with mixed cellularity Hodgkin's disease is associated somatic mutations within the untranslated regions of rearrange class switch recombinated Ig genes.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Peripheral blood;
Jox A., Zander T., Kueppers R., Irsch
Bohlen H., Diehl V., Wolf J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ005570; CAA06599.1; -. HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VH1 protein
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01-MAR-2003
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SMART; SM00406; IGv;
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   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG_LIKE; 1
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72; Conserv
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157
157 AA;
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 23, Last annotation updat
precursor (Fragment).
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157
17304 MW; 86986EDDA84D88B5 CRC64;
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                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 68
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Best Local 9
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS508290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0920E8 PREMAINS.....
0920E8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation variable
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in Mammalian Cells";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF307936; AAL09420.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR0030596; Ig_v.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
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61
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NQKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVYYCA----VIYYGNSPAWFAYWGQG
                                        AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAP-YYDSWGQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WGQGTLV 140
                                                                                                                                                                                                                                                                                                                                                                                                                        120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                       120
13204 MW; DC4834AB1DE56F3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.9%; Score 361.5; DB 1 55.9%; Pred. No. 1.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53208 MW;
                                                                                                                                                                                                                                                                          54.8%; Score 360.5; DB 1
55.3%; Pred. No. 3.6e-31;
tive 25; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jennings I.G., Horaitis O.,
Hotope of Pterin-Mimicking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC85B1194DAFEF2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length
                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 120;
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ing Antibodies E
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; Murinae; Mus
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RESULT RE
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Best Local S
Matches 76
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Q9UL89;
01-MAY-2000
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
"I'iu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                Q9GYZZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
SEQUENCE FROM N.A.
Song X.T., Feng Z.Q., Gu
"Amplification, cloning
variable region gene of
                                                                                                                                  Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
Monoclonal anti-idiotypic ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01810; 2FBJ.
InterPro; IPR007110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment)
                                                                                                             NCBI_TaxID=6182;
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AF035025; AAD56261.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGTLV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGFAQKF
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                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                Guan X.H.;
  and sequence analysis of the heavy monoclonal anti-idiotypic antibody

    Last sequence update)
    Last annotation update)
    antibody NP30 heavy chain

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                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 381; DB 4;
Pred. No. 2.1e-33;
4; Mismatches 22
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C8F9131DE13EA898 CRC64;
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                                                                                                                                    Trematoda; 1
Schistosoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                WGPYWYFDLWGRGTLV
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RESULT
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Best Local S
Matches 73
                                                                                                                                                                   Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                             Strauberg R.;
Strauberg R.;
Submitted (JUL-2001) to the EMBL/GenBar
EMBL; BC099851; AAH09851.1; -.
Interpro; IPR000005; HTHAraC.
Interpro; IPR007110; Ig-like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003296; Ig_v.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS00041; HTH ARAC_FAMILY_1; 1.
PROSITE; PS00041; HTH ARAC_FAMILY_1; 1.
PROSITE; PS00090; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 614 AA; 67921 MW; 55EF536E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_Mic.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; P850835; IG_LIKE; 1.
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Q96GA6;
01-DEC-2001 (
01-DEC-2001 (
01-MAR-2003 (
Hypothetical )
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
EMBL; AF285622; AAG01452.1; -
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
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                                                                                                                                                                                         Local
                                                                                                                                                                                                            Match
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80
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                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -WGQGTLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OVOLLOSAADVKKPGASVKVSCTASGYIPTSYDINWVRQATGQGLEWMGWNNPNSGNAGF
                     AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT
                                                                                QMQLVQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMGWITPFNGNTNY
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ilarity 57.0%;
Conservative 1
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                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13567 MW;
                                                                                                                                                                                         56.8%;
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19,
23,
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Last sequence update)
Last annotation update)
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Pred.
                                                                                                                                                                                         Score 373.5; DB Pred. No. 1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vi
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BA893873FD5FA6AB CRC64;
                                                                                                                                                                                                                                                        55EF536E77AA9BBB CRC64;
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  LSSLRSEDTAMYYCARGYSS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae;
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                                                                                                                                                                       26;
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      DDAFDIWGQGT
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Best Local S
Matches 83
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O9BRVO;
O1-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                096QS0; PRELIMINARY; PRT; 159 AA.
096QS0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLE 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Homo sapiens putative microfibrillar protein with Ig-like domain MRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY039025; AAK82649.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003065; Ig-WHC.
InterPro; IPR003596; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SPROSITE; PS50835; IG LIKE; 1.
SEQUENCE 159 AA; 17497 MW;
  Strausberg R.;
Submitted (APR-2001) to the
EMBL; BC005951; AAH05951.1;
HSSP; P01789; IMCP.
                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                               Hypothetical protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tilson M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                           TISSUE=Prostate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVWGQGTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSWGQGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQKFQGRLTMTRDTSTSTVYMDLSSLRSDDTAVYFCAR---EMEITFGGAVSKGFYYYGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAP-----YY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY
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                                                                                                                                                                                    Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
                                                                                                                                                                                    Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                            17,
17,
23,
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                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 409;
Pred. No.
                                                                                                                                                                                 Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                            Vertebrata; Euteleostomi;
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                                                                                                                                                                                      Hominidae;
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                                                databases
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                                                                                                                                                                                      Homo
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RESULT 7
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Best Local
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 500 AA; 54154 MW;
                                                                                                                                                                          InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IG; I.
PR0SITE; PS50835; IG; ILKE; 1.
SEQUENCE 147 AA; 16274 MW; (
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Q925S3;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                the same strain.";
Int. J. Radiat. Biol. Relat. Stud. Phys. Chem.
EMBL; AF240166; AAK43731.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mechanism of exogenous nucleic acids and the repair of intestinal epithelium after World J. Gastroenterol. 6:709-717(2000).
                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of mouse genes
of the irradiated mice !
                                                                                                                                                                                                                                                                                                                                                                                                                          "Cui D., Zeng G., Yan X., Li X.,
"Cloning of mouse genes related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cui D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=11819679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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01-MAR-2003
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QVKLHQSGPEVVKPGASVKLSCKASGYIFTSYDIDWVRQTPEQGLEWIGWIFPGEGSTEY
                                           QVQLLQSAADVKKPGASVKVSCTASGY1FTSYD1NWVRQATGQGLEWMGWMNPNSGNAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSWGQGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKKFQGRVTLTTDTSTSTVYMELRSLRSDDTAVYYCARRYCSYSSCQNDYYYY-----YM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVHLVQSGAEVMSPGASVRVSCKTSGYAFHTYSIIWVRQAPGQGLEWMGWISPSSDNTRF
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                                                                                          Conservative
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                                                                                       14;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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Pred. No. 4.8e-34;
L3; Mismatches 27
                                                                                     Score 381.5; DB 11;
Pred. No. 2.5e-33;
4; Mismatches 26;
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                                                                                                                                                                               800594A12B97191F CRC64;
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                                                                                                                                 DB 11; Length 147;
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RESULT 2
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Best Local Similarity
Matches 80; Conserv
                                                          QUIL92;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
01-MAR-2003 (TrEMBLrel. 23) Last annotation updat
v.cain-reactive immunoglobulin heavy chain variat
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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01-MAY-2000
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Myosin-reactive autoantibodies in rheumatic
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125 AA;
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ilarity 65.6%;
Conservative 19
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Pred. No. 1.3e-37;
5; Mismatches 26;
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Catarrhini; Hominidae;
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QEQLEQSGAEVTKPGASVKVSCKASGYTFIAYDINWVRQAPGQGLEWMGWMVPQTGNTEF

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RESULT
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Best Local S
Matches 82
                                     Query Match
Best Local 9
                                                                     Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong "Identification and characterization of SNC66, a down-regulated in colorectal cancer."

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ dailenterpro; IPR0077110; Ig-like.

Interpro; IPR00306; Ig-WHC.
Interpro; IPR00306; Ig-WHC.
Interpro; IPR00356; Ig-V.
Pfam; PP00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS05035; IG-LIKE; 4.
PROSITE; PS05035; IG-LIKE; 4.
PROSITE; PS05039; IG-WHC; 1.
SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5
                            Matches
                                                                                                                                                                                                                                                                                                               Q8WY24
Q8WY24;
01-MAR-2002
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Tin B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF035022; AAI
HSSP; P01772; 2FB4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in
                                                                                                                                                                                                                                                                                 SNC66 protein.
                                                                                                                                                                                                                                                                                           01-MAR-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fetus."
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                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMVPNSGNAGF
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IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124
124 AA;
                                                                                                                                                                                                                                                                                          (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13580 MW;
                                      62.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.2%; Score 416; DB 4;
66.1%; Pred. No. 3.9e-37;
cive 16; Mismatches 20
                                                                                                                                                                                                                                                                                          20,
20,
23,
                              13;
                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87:184-192 (1998)
                            Score 410.5; DB
Pred. No. 8e-36;
3; Mismatches
                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1BAAACBD96ACD2A2 CRC64;
                                                                        F24D08DFA5A663E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalis N.N.,
                                                                                                                                                                                           Fang Y., Do
                                                                                                                                                                                                                                                                                                                                         497
                                                 DB 4;
                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
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                              28;
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Ig-like
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                                                 Length
                              Indels
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                              ۲,
                              Gaps
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Run
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                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                               US-09-674-752-40
658
1 QVQLLQSAADVKKPGJ
                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
                                                                                                                                                                  SPTREMBL 23:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
    December 30, 2003, 10:46:19; Search time 29.7319 Seconds (without alignments) 1058.876 Million cell updates/
                                                                                                                                                                                                                                                                                                                                    830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
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sp_plant:*
sp_vrodent:*
sp_virus:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	80	7	0	υ	4	u	2	1	Result No.
356.5	358.5	359	360.5	361.5	367.5	373.5	374.5	381	381.5	394	409	410.5	416	420.5	428.5	Score
54.2	54.5	54.6	54.8	54.9	55.9	56.8	56.9	57.9	58.0	59.9	62.2	62.4	63.2	63.9	65.1	Query Match I
481	473	463	120	489	157	614	119	116	147	500	159	497	124	125	119	Query Match Length DB
11	11	11	11	H	4	4	G	4	11	4.	4	4	4	4	4	₩
Q91WT1	Q9D8L4	Q99LC4	Q920E8	Q8VCX4	095978	Q96GA6	Q9GYZ2	Q9UL89	Q925S3	Q9BRV0	Q96QS0	Q8WY24	Q9UL92	Serned	Q9UL94	ID
Q91wt1 mus musculu	Q9d8l4 mus musculu	Q991c4 mus musculu	Q920e8 mus musculu	Q8vcx4 mus musculu	O95978 homo sapien	Q96ga6 homo sapien	Q9gyz2 schistosoma	Q9ul89 homo sapien	Q925s3 mus musculu	Q9brv0 homo sapien	Q96qs0 homo sapien	Q8wy24 homo sapien	Q9u192 homo sapien	Q9u195 homo sapien	Q9ul94 homo sapien	Description

43 44 338.5 45 337	41 339 42 339	_	38 339.5 39 339	_				33 341					28 343.5			25 345.5							18 351.5	17 356
51.5 51.4 51.2	51.5	51.5	51.6 51.5	51.7	51.7	51.8	51.8	51.8	52.0	52.1	52.1					52.5				53				54.1
142 118	145	145	168 137								143				145	117	143	146	117	150	613	241	146	145
11 Q924Q1 11 Q921C4	11 Q924R4 11 Q99L25	11 Q924R3	11 Q8VDC9 11 Q924R6	11 Q924P5			11 Q924P9	11 092400	11 Q91WR1	_	11 Q924R0	_	_	11 Q924R1	11 Q924Q6	11 Q9QXE9	11 092405	11 Q924Q8	11 Q9QXF0	4 Q9Y298	11 Q8VCX7	11 Q921A6	11 Q924R8	11 Q924Q7
Q960k0 nomo Q924q1 mus Q9z1c4 mus	Q924r4 mus Q99125 mus		Q8vdc9 mus Q924r6 mus	Q924p5 mus	Q924r2 mus	Q921k1 mus	Q924p9 mus	Q924q0 mus	Q91wr1 mus	Q924q9 mus	Q924r0 mus	Q91v67 mus	Q8k0z4 mus	Q924r1 mus	Q924q6 mus	Q9qxe9 mus	Q924q5 mus	Q924q8 mus	29qxf0 mus	Q9y298 homo	Q8vcx7 mus	Q921a6 mus	Q924r8 mus	Q924q7 mus
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ALIGNMENTS

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RESULT 1
Q9UL94
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Best Local Similarity
Matches 80; Conserv
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InterPro; IPR003006; Ig_MGC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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NON_TER
SEQUENCE
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Q9UL94;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Tin B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wu X., Liu B., Van Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF035020; AAD56256.1; -. HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
119 AA;
                                                                                                                                                                                                                                                                                             119
                                                                                                               Conservative
                                                                                                                                                                                                                      119
13205 MW; 13E64F5345F4A16E CRC64;
                                                                                                                                            65.1%;
                                                                                                           16;
                                                                                                           Score 428.5; DB 4; Length 119;
Pred. No. 1.6e-38;
L6; Mismatches 19; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kalis N.N., Berney S.M.,
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; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region
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RESULT 15
HV11_MOUSE
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Best Local (
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                                                                                    PIR; A02038; G2MS43.

HSSP; P01810; 2FBJ.

InterPro; IPR007110; Ig-like.

InterPro; IPR003506; Ig_MHC.

InterPro; IPR003596; Ig_v.
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SEQUENCE
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region S43 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HV11 MOUSE
P01755;
                                                                                                                                                                                                                                                                                                           "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).

-i- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A93708; GVMS11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res.
                                                                                                                                                             EMBL; J00539; AAA38172.1; -.
                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  Baltimore
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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                                                                  SMART; SM00406;
                                                     PROSITE;
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                                       mmunoglobulin
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.Pro;

.rPro; IPRUv_.

.m; PF00047; ig; 1.

.ART; SM00406; IGv; 1.

...TTE; PS50835; IG LIKE; 1.

...lin V region; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDNLKGKATLTADTSSSTAYIQLSSLTSEDSAIYHCARG----IYYNSSPYFDSWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAQLQQSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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121 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 336.5; DB 1; Pred. No. 2.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137
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  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                            Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRNA ISOLATED
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                                                                                                                                                                                                                                                          collaboration -
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                                                                            Similarity
               AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT
                                 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY
                                                   QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCAR - - -
                                                                                                     20
20
50
55
69
86
118
123
41
41
137
AA;
                                                                    Conservative
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49
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68
117
117
122
137
                                                                                                      15200
                                                                           50.6%;
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3
3
                                                                  ; Score 33; DB 1;
; Pred. No. 7.8e-29;
17; Mismatches 30
                                                                                                                                              IG HEAVY CHAIN V REGION S43.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                      D SEGMENT.
JH2 SEGMENT.
BY SIMILARITY.
                                                                                                      ADD5881BF44B8EC9
                                                                     30;
                                                                                     Length 137;
                                                                                                      CRC64;
                                                                     Indels
 ----YRLGRYFDYWGQGT
                                                                     8
                                                                    Gaps
131
                  120
                                   79
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Search Job tim rch completed: December 30, time: 7.54102 secs 2003, 10:55:53

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RESULT 12
HV52_MOUSE
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Matches 62
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                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region VH558 Al/A4 precursor.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M13787; AAA38499.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unrearranged VH gene segments.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                        PIR; A02029; HVMSA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yancopoulos G.D., Alt F.W.; "Developmentally controlled and tissue-specific expression
                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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80
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                                                            1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDIN#VRQATGQGLEHMGHMNPNSGNAGF
                                                                                               62;
                                                                                                          Similarity
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                  AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCAR
NEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR 117
                                              QVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPGQGLEWIGWIYPGDGSTKY
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117
                                                                                               Conservative
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                                                                                                          51.8%;
                                                                                                                                              12971 MW;
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                                                                                                                                                                                             IG HEAVY CHAIN V REGION VH558 A1/A4. FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                         Score 341; DB 1
Pred. No. 9e-30;
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BY SIMILARIT
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                                                                                               Mismatches
                                                                                                                                                                       SIMILARITY
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                                                                                                                     DB 1;
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RESULT 14
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Best Local S
Matches 65
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P01745;
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NON TER
SEQUENCE
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lymphocytes is encoded by a large set of
EMBO J. 3:517-523(1984)
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region AC38 15.3.
Mus musculus (Mouse)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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SMART; SM00406; IGv; 1.
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"A V region
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequents-SEP-2003 (Rel. 42, Last annoting heavy chain V region MPC 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                               "Cloning and sequence of the cDNA corresponding region of immunoglobulin heavy chain MPC11."; Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                Zakut R., Cohen J.,
           REVISIONS.
                                                                          MEDLINE=81053741; PubMed=6253904;
                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                  61 NEKFKSKATLTVDKSSSATYMQLSTPTSEDSAVYYCARWD-----YEGDRYFDVWGTGT
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65; Conserv
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 Cohen J.,
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01, Last sequence up
42, Last annotation
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inant (idiotope) e
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  Givol D.
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D SEGMENT.
J SEGMENT.
BY SIMILAR
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Pred. No. 1
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ID HV48
AC P0398
AC 23-OC
DT 23-OC
DT 15-JU
DE IM ME
OS MUS m
OC EUKAR
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Pfam; PF00047; ig; 1.

SMART; SM00406; ICv; 1.

PROSITE; PS50835; IG LIKE; 1.

PROSITE; PS50835; IG LIKE; 1.

InterPro; IPROUS.; 1.

PROSITE; PS50835; IG LIKE; 1.

PROSITE; PS50835; IG LI
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Best Local Similarity
Matches 68; Conserv
    SIGNAL
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                       "Illegitimate recombination generates a class delta in an IgD-secreting plasmacytoma."; Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(198 PIR; A02033; HVMST7. HSSP; P01810; 2FBJ. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Tesam. DEFONGAT. 10.1
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Biochemistry 21:5415-5424(1982)
-!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS 1
PROTEIN HAS ALSO BEEN DETERMINED.
-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal
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P03980;
23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig heavy chain V region TEPC 1017 prec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=84248078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J.E.,
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P01789; 1MCP.
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Pred. No. 2.3e
17; Mismatches
    IG HEAVY CHAIN V REGION FRAMEWORK-1.
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tes 28;
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Best Local S
Matches 69
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
21-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V region (Anti-arsonate antibo)
Mus musculus (Mouse)

Ebkaryota; Metazoa; Chordata; Craniata; Verte
Ebkaryota; Butheria; Rodentia; Sciurognathi; M
                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                    Capra J.D., Nisonoff A.;
"Structural studies on induced antibodies with defined idiotypic specificities. VII. The complete amino acid sequence of the heavy chain variable region of anti-p-azophenylarsenate antibodies from mice bearing a cross-reactive idiotype.";
J. Immunol. 123:279-284(1979).
                                                                                                                                                                                              -!- SIMILARITY: Contains 1 immunoglobulin-like
PIR; A02022; GIMSAA.
HSSP; P01772; 2FB4.
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                                                                                                                                                                                                                                              -!- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHA:
                                                                                                                                                                                                                                                                                                                                           STRAIN=A/J;
MEDLINE=79195438; PubMed=109536;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                   REGION SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYD---SWG
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1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
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                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                          12555 MW;
                          52.3%; Score 344; DB 1;
55.7%; Pred. No. 4.2e-30;
tive 23; Mismatches 23
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55.2%; Pred. No. 4.6e-30;
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                                                                                                 IG-LIKE
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FRAMEWORK-4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-2.
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                                                                         99DD8F0B6A69F4BE CRC64;
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e antibody).
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Best Local :
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01-JAN-1988
01-JAN-1988
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NON TER
SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ol-JAN-1988 (Rel. 06, Created)
Ol-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region AC38 205.12.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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s musculus (Mouse)
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                                                          NQKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCAR---
                                                                                        AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT
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nilarity 57.5%;
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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Pred. No. 2.7e-31;
0; Mismatches 25
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D SEGMENT.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                         Score 352; DB 1; Length 118; Pred. No. 6e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                 94F7BEE4C762A018 CRC64;
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                                                                                                                  120
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RESULT 8
                                                                                                                                         RESULT 9
HV12 MOUSE STANDARD; PRT; 117 AA.
ID HV12 MOUSE STANDARD; PRT; 117 AA.
AC P01756;
BT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 42, Last annotation update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse)
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Best Local S
Matches 68
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seque 15-8EP-2003 (Rel. 42, Last annot Ig heavy chain V region J558.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Ci Mammalia; Eutheria; Rodentia; Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
NON TER
SEQUENCE
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DOMAIN
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"Amino acid sequence of homogeneous antibodies to dextran and
"rearrangements in heavy chain V-region gene segments.";

Nature 28:35-40(1980).

-!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT
BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY
WHICH OCCUR IN THE D AND J SEGMENTS.

-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR; A26242; MINSJ5.
                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; MuBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003596; Ig_v. pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=80078170; PubMed=6765983;
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SEQUENCE, AND CARBOHYDRATE-LINKAGE MEDLINE=83075344; PubMed=6816276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NOKFKGKATLITVDKSSSTAYMQLNSLTSEDSAVYYCARD----RYW-----YFDVWGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVÓLQÓSGPELVKÞGÁSVRMSCKÁSGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWNNPNSGNAGF
                                                                                                                                                                                                                                                                                                                                                                                                                         TV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT 120
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117
117
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55.7%;
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Pred. No. 1.8e-30;
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BY SIMILARITY.
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Sciurognathi; Muridae;
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                            SITE
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                                                                                                     Murinae; Mus
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RESULT 5
HV02 MMOUSE
ID HV02 MM
AC P01746
AC P01746
DT 21-JUL
DT 21-JUL
DT 21-JUL
DT 21-JUL
DT 21-JUL
OC Mammal
OX MUSELT
RN [1]
RR SEQUEN
RC STRAIN
RX MEDLIN
RX MEDLIN
RX Capra-
RT "Somat
RT "Somat
RT "Somat
RT "Somat
RT "Somat
RT Edwar
RT "Somat
RT Gentin
CC ----SI
CC ----SI
CC ----SI
CC ----SI
CC -----
CC -----
DR EMBL;
DR PIR; A
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Best Local S
Matches 69
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P01746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=83131846; PubMed=6186498; Siekevitz M., Gefter M.L., Brodeur P., Marshak-Rothstein A.;
                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region 93G7 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
NON TER
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V regīon; Hybridoma.
DOMAIN 1 111 IG-LĮI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
        EMBL; J00493; AAA38128.1; PIR; A94264; HVMSG7.
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=82152818; PubMed=6801765; Sims J., Rabbitts T.H., Estess P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The
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                                                                                                                                                                                                                                                                                                        Science 216:309-311(1982).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                          Capra J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                           Lmmunoglobulin heavy
                                                                                                                                                                                                                                                                                                                                                                                           "Somatic mutation in genes for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED SEGMENT, JH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNDNSGNAGFA
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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120 AA;
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Rodentia;
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Pred. No. 3e-3
22; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                        variable portion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                              Slaughter C.,
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Best Local
                                                              EMBL; J00529; AAA38170.1; -.
PIR; A90809; MHMS18.
PDB; 1A6U; 27-MAY-98.
PDB; 1A6W; 15-JUL-98.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-C57BL/6;
MEDLINE=81234548; PubMed=6788376;
MEDLINE-81234548; Paskind M., Reth
                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                              "Heavy chain variable region antibodies: somatic mutation Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region B1-8/186-2 precurso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
          Immunoglobulin
SIGNAL 1
                                 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                              Baltimore D.;
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                    V region; Signal; 3D-structure
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Ig_MHC.
Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    annotation update)
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Pred. No. 5.4
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  IG
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                                                                                                                                                                                                                                                         MRNA WAS CLONED FROM A HYBRIDOMA (4-HYDROXY-3-NITROPHENYL) ACETYL
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                                                                                                                                                                                                                                                                                                                        Imanishi-Kari T., Rajewsky
                                                                                                                                                                 Noved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                                                                  There are no restrictions
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RESULT 3
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HV1B_HUMAN
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PIR; AA2024; HVHUHG.
HSSP; P01772; ZFB4
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0003825; P:immune response; NAS.
InterPro; IPR003006; Ig_NHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Best Local (
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P01744;
21-JUL-1986
16-OCT-2001
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SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Signal
SIGNAL 1 19
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
ra heavy chain V-I region HG3 precursor.
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P01743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.T...
MEDILINE=83144028; PubMed=6298778;
Rechavi G., Ram D., Glazer L., Zakut R., Givol
"Fin-lutionary aspects of immunoglobulin heavy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
NON_TER
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c. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                              HUMAN
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                                                                                                                                                                                                                                                                                                                                                    QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
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                                                                                                                                                                                                                                                                                                                 QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWVRQAPGQGLEWMGIINPSGGSTSY
                                                                                                                                                                                                          AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR 117
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117
117 AA;
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(Rel. 01, Created) (Rel. 40, Last seq
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                                                                              STANDARD;
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74.5%;
  sequence update)
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Pred. No. 4.9e-35;
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| NOUSE | STANDARD; | PO1747; | PO17

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

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R HSSP; P01789; IMCP.

R GO; GO:0005576; C:extracellular; NAS.

R GO; GO:0003523; F:antigen binding activity; NAS.

R GO; GO:0003955; P:immune response; NAS.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003006; Ig-MHC.

R InterPro; IPR003596; Ig-WC.

R InterPro; IPR003596; Ig-V.

R Pfam; PF00047; Ig; 1.

R SMART; SM00406; IGv; 1.

R PROSITE; PS50835; IG LIKE; 1.

R Inmunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
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Mammalia; Eutheria; Pri
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-I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYEL
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Bell L.O., Gould H.J.;
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Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S20783
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: S20764
A;Accession: S20784
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A;Note: the difference for residues 41-60 results from misplacement of 10 bases in the C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
Search completed: December 30, 2003, 11:03:18 Job time : 11.6946 secs
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Best Local S
Matches 82
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 63.4%; Score 417.5; DB 2; Length 121; Best Local Similarity 67.2%; Pred. No. 6.2e-33; Matches 82; Conservative 11; Mismatches 24; Indels 5
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                                                                                                              116 LV 117
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                                                                                                                                                                                                                  61 AQKLQGRATMTRDTSTSTVYMDLSGLRSEDTALYYCARGSDT----SPASTIDYWGQGT 115
                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVTVSCKASGYTFTSYFMHWVRQAPGQGLEWMGMINPHGGSTTF
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C;Superraming
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F;15-98/Domain: j
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C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_chan:
C;Accession: S46393 #sequence_revision 27-Jan-1995 #text_chan:
C;Accession: S46393 #sequence_revision 27-Jan-1995 #text_chan:
C;Accession: S46393 #sequence_revision 27-Jan-1995 #text_chan:
A;Fitle: In vitro assembly of repertoires of antibody chains of A;Title: In vitro assembly of repertoires of antibody chains of A;Accession: S46390; MUID:94254092; PMID:8196048
A;Accession: S46393
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment C;Species: Homo sapiens (man)
C;Species: O3-Feb-1994 #sequence_revision O3-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36260
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Emble on, M.J.; McCafferty, EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from hage display libraries A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36260
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S36260
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A; Residues: 1-129 < FIG>
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Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
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                                                                  AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCAR-----CDTTL1
                                                                                                                                                         OVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMC MVPNSGNAGF 60
  --DSWGQGTLV
                                                                                                                                  QVQLQQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWM
                                             AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSFGYCSST--
                                                                                                                                                                                                                                                                                                           immunoglobulin homology < IMM>
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                                                                                                                                                                                                                         12;
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Pred. No. 4.7e-34;
2; Mismatches 19
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                                             ---SCPYYYY 114
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J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0956
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A;Title: Developmentally restricted immunoglobulin heavy chain variable region A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: A33548
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C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: A3548; PH0956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-30/Region: framework 1
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A; Residues: 1-129 <M
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C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C;Accession: S19665; S24442
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                                         submitted to the EMBL Data Library, A;Reference number: S24442 A;Accession: S24442
                                                                                                             R; Jones, P.T.
                                                                                                                                                                                                  A;Title: By-passing immunization. Human antibodies from A;Reference number: S19663; MUID:92085276; PMID:1748994 A;Accession: S19665
                                                                                                                                                                                                                                                                  R;Marks, J.D.; Hoogenboom, H.R.;
J. Mol. Biol. 222, 581-597, 1991
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      A;Molecule type: mRNA
A;Residues: 1-40,'GLSGWDGSALTMVTQSILDK',61-118,'T',120-124 <JON>
                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-124 < MAR>
                                                                                                                                  A;Cross-references: EMBL:X61647
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Similarity 67.2%; Pred. No. 2.70
84; Conservative 12; Mismatches
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<u>د</u>

Gaps

60

120 117

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C;Accession: S36265

R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Emble BMBO J. 12, 725-734, 1993

A;Title: Human anti-self antibodies with high specificity from A;Reference number: S36256; MUID:93178448; PMID:7679990

A;Accession: S36265
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                                                                                                                                                                                          A;Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; P:C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
336265
19 heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #text_change 23-Jul-1999
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A;Residues: 1-110 <HIL>
A;Residues: 1-10 <HIL>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: PH1670

R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 31-336, 1993

A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to A;Reference number: PH1642; MUID:93301610; PMID:8315388

A;Accession: PH1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region (clone 2A12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
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                                                                                                                                            Similarity
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AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT
                                                    QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY
                                                                          QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVPQATGQGLEWMGWMNPNSGNAGF
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                                                                                                                            Conservative
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73.7%;
                                                                                                                                       67.0%; Score 441; DB 2; 70.5%; Pred. No. 3.4e-35;
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Pred. No. 2.6e-35;
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R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. BMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36271
                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:218832; NID:g33115; PIDN:CAA79284.1; C;Superfamily: immunoglobulin V region; immunoglobulin homolog C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36271
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A;Title: Developmentally restricted immunoglobulin heavy A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: D33548
A;Status: preliminary; nucleic acid sequence not shown; raystratus: preliminary; nucleic acid sequence nucleic acid sequence not shown; raystratus: preliminary; nucleic acid sequence not shown; raystratus: preliminary; nucleic acid sequence not shown; raystratus: preliminary; nucleic acid sequence nucleic acid
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A; Residues: 1-123 < KIP>
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C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
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                                                                              1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF 60
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QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                                                                            Score 431.5; DB 2
Pred. No. 2.9e-34;
l3; Mismatches 24
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Pred. No. 9.6e-35;
4; Mismatches 19
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AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT 120

AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCA-ADTGRIDDFWSGYNFDYWGQGT

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Ig heavy chain V region (DP-15) - human (fragment)
C.Species: Homo sapiens (man)
C.Japecies: Homo sapiens (man)
C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C.Accession: S26918
R.;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A.;Title: The repertoire of human germline V(H) sequences reveals about fifty growth sequence number: S26885; MUID:93021117; PMID:1404388
A.;Reference number: S26885; MUID:93021117; PMID:1404388
A.;Cession: S26918
A.;Status: preliminary
A.;Molecule type: DNA
A.;Residues: 1-98 <TOM>
A.;Residues: 1-98 <TOM>
A.;Residues: 1-98 <TOM>
A.;Cross-references: EMBL:Z12317; NID:932857; PIDN:CAA78187.1; PID:932858
C.;Superfamily: immunoglobulin V region; immunoglobulin homology
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R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate
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A; Accession: S31596
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C;Species: Homo Bapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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A; Residues: 1-132 < CUI>
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Best Local S
Matches 87
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; Pred. No. 3.4e-36;
12; Mismatches 9
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Matches
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anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human C;Species: Homo Bapiens (man) C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Ju1-1999 C;Accession: S49530
                                                                            C;Accession: S23623
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23623
A;Atatus: preliminary
A;Molecule: Upe: DNA
A;Residues: 1-171 <OLE>
A;Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S23623
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A;Residues: 1-135 kMaH;
A;Cross-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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A; Accession: S49530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D
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83; Conser
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69.7%; Pred. No. 1e-35;
tive 11; Mismatches
                  67.3%;
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Pred. No. 4.9e-36;
Score 443; DB 2;
Pred. No. 3.2e-35;
5; Mismatches 17
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       Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pr
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658
1 QVQLLQSAADVKKPG;
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length: 2000000000
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4: pir4:*
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       GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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399 60.6 98 2 \$26919 Ig heavy 398 50.6 126 2 If4151 Ig heavy 398 60.5 110 2 PH1669 Ig heavy 397 60.4 125 2 \$68170 Ig heavy 397 60.3 128 2 PH0952 Ig heavy 397 60.3 128 2 PH0952 Ig heavy 397 60.3 122 2 PH0952 Ig heavy 395 60.1 131 2 \$26920 Ig heavy 395 60.0 98 2 \$26920 Ig heavy 395 60.1 22 \$26920 Ig heavy 396 59.8 133 2 \$214683 Ig heavy 391 59.8 627 2 \$14683 Ig heavy 393 59.7 117 2 \$18553 Ig heavy 393 59.6 117 1 HVHU35 Ig heavy 393 59.6 117 1 HVHU35 Ig heavy 394 599 59.6 136 2 PH0960 Ig heavy 395 59.8 136 2 PH0960 Ig heavy 397 59.6 137 1 HVHU35 Ig heavy 398 59.6 137 1 HVHU35 Ig heavy 399 59.6 136 2 PH0960 Ig heavy	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31
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ALIGNMENTS

RESULT 1 S31600

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Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S34014; S30535
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Bur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidic sequence analysis of the variable domains of four humar A;Reference number: S34001; MUID:93209281; PMID:7681398
A;Accession: S34014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-136 <CUI>
A; Cross-references: EMBL: Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology <IMM>
A;Molecule type: mRNA
A;Residues: 1-127 <MAR>
A;Cross-references: EMBL:Z18321
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31600
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
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A; Accession: S31600
                                                                                               A; Status: preliminary
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91; Conserv
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74.6%;
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Pred. No. 1.4e-38;
9; Mismatches 12
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 502 or 558X

OPERATING SYSTEM: 1BM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION NUMBER: US/08/526,136
FILING DATE: MordPerfect (Version 5.0)
CURRENT APPLICATION NUMBER: US/08/526,136
FILING DATE: MordPerfect (Version 5.0)

PRIOR APPLICATION NUMBER: US/08/214,036
FILING DATE: MordPerfect (Version 5.0)
FILING DATE: MordPerfect
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19413
LENGTH: 217
TYPE: PRT
                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-343-011B-1
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US-09-252-991A-19413
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US-09-343-011B-1
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US-09-157-370-1
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; Sequence 1, Application US/09157370A
                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09343011B
patent No. 6300473
GENERAL INFORMATION:
APPLICANT: Stephane Richard
TITLE OF INVENTION: SLM-1 AIKE MAMMALIAN P
FILE REFERENCE: A32561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                        Query Match 33.2%;
Best Local Similarity 36.7%;
Matches 11; Conservative
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/343,011B
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: CA 2265271
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
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                                                                                274
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                                                                              DGYGGEYDDQTYEAYDNSYVTPTQSVPEYY 303
                                                                                                        DGGGGAYED----VWSGEY----
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                 SAM68-LIKE MAMMALIAN PROTEINS
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                                                                                                                                                        Score 44.5;
Pred. No. 93;
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Pred. No. 54;
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Pred. No. 23;
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LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-157-370-1
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APPLICANT: STEIPE, Boris
APPLICANT: STEINBACHER, Stefan
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STE
FILE REFERENCE: P8341-8072
CURRENT APPLICATION NUMBER: US/09/157,370A
CURRENT FILING DATE: 1998-09-21
EARLIER APPLICATION NUMBER: 08/765,179
EARLIER APPLICATION NUMBER: PCT/EP95/02626
EARLIER APPLICATION NUMBER: PCT/EP95/02626
EARLIER APPLICATION NUMBER: DE/P44 25 115.7
EARLIER APPLICATION NUMBER: DE/P44 25 115.7
EARLIER PILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 10
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US-08-526-136-13
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Best Local Similarity
Thes 8; Conserve
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US-09-328-352-5411
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Acinetobacter baumannii US-09-328-352-5411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQ ID NO 5411
; LENGTH: 229
; TYPE: PRT
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Best Local S
Matches 7
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APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                             Sequence 13, Applion Patent No. 6107089
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                                                                                                                                           GENERAL INFORMATION: APPLICANT: Towle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 8252
                                                                                      NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                          APPLICANT: Towle, Christine A. TITLE OF INVENTION: ANNEXIN XI
STATE: Massachusetts COUNTRY: U.S.A.
                                     CITY: Boston
                                                    STREET:
                                                                       ADDRESSEE:
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                                                      225 Franklin Street
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                                                                         Fish & Richardson
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57.1%;
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70.0%;
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Pred. No.
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GENERAL INFORMATION:

APPLICANT: Young et al.

TITLE OF INVENTION: 207 Human Secreted Proteins

FILE REFERENCE: PZ007P1

CURRENT APPLICATION NUMBER: US/09/205,258

CURRENT APPLICATION NUMBER: PCT/US98/11422

EARLIER APPLICATION NUMBER: FOT/US98/11422

EARLIER FILING DATE: 1998-06-04

EARLIER FILING DATE: 1998-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER APPLICATION NUMBER: 60/049,375
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INFORMATION FOR SEQ ID NO: 68
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acide
TYPE: amino acid
STRANDEDNESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,846
FILING DATE: 09-FEB-1998
CLASSIFICATION + 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9-027015
FILING DATE: 10-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-024045
APPLICATION NUMBER: JP 8-024045
FILING DATE: 06-EEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 745, Application US/09205258 Patent No. 6525174
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Best Local 9
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
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                                                                           APPLICATION NUMBER: 60/048,880 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,896
                                                          FILING DATE: 1997-06-06
                                                                                                                                       APPLICATION NUMBER: 60/048,881 FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                    APPLICATION NUMBER: 60/049,020
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82 DGGCSGGAYDIIGSGE 97
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10; Conserv
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60/048,876
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Pred. No.
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SOFTWARE: PatentIn Ver. (SEQ ID NO 745); SEQ ID NO 745; LENGTH: 105; TYPE: PRT; ORGANISM: Homo sapiens US-09-205-258-745
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NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                         EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
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EARLIER FILING DATE: 1997-12-18
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APPLICATION NUMBER: 60/048,895
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,884
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                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/048,877 FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/048,883
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                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/048,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/048,949
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                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/048,962
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; LENGTH: 285
; TYBE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-128-352-7483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Marc J. R.
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-09-252-991A-31155
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31155
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 69, Application US/09020846 Patent No. 6322965
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                          ZIP: 2007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                APPLICANT: HASEGAWA, Akira
TITLE OF INVENTION: CHIMERA ANTIGEN PEPTIDE
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                      STREET: 3000 K Street: Washington
                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                         STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 33.6%; Score 45; Local Similarity 42.9%; Pred. No. es 9; Conservative 2; Mismatc
            APPLICATION NUMBER: US/0 FILING DATE: 09-FEB-1998
                                                                                                                                                                                                                                             ADDRESSEE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGGAYEDVWSGEYPEYYAMDV 23
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                                                                                                                                                                                                                                                                                                                    CHIBA, Yunz.
CHIBA, Yunz.
ThGI, Shintaro
                                                                                                                                                                                                                            3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                        KASHIWAKUMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                           FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rubenfield et al.

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                           US/09/020,846
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 338;
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Sequence 68, Patent No. 6

6322965

Application US/09020846

GENERAL INFORMATION:
APPLICANT: YAMAGUCI
APPLICANT: KASHIWAI
APPLICANT: CHIBA,

APPLICANT: YAMAGUCHI, Kenjiro
APPLICANT: KASHIWAKUMA, Tomiko
APPLICANT: CHIBA, Yukie
APPLICANT: YAGI, Shintaro
APPLICANT: HASEGAWA, Akira
TITLE OF INVENTION: CHIMERA ANTIGEN PEPTIDE

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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30606
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US-09-252-991A-30606
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US-09-020-846-68
              RESULT 9
                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SEQ ID NO 30606
LENGTH: 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 33.6%;
Best Local Similarity 62.5%;
Matches 10; Conservative
                                                                                                                                            Matches
                                                                                                                                                            Best Local Similarity
                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30606, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Wegner, Harold C.
REGISTRIC NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 05.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 8 FILING DATE: 09-FEB-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9
FILING DATE: 10-FEB-1997
PRIOR APPLICATION DATA:
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                                                                      DGDGDAHDMPLWLCSVWTGESGFLYKLDL 365
                                                                                                        DGGGGAYE-----DVWSGEYPEYYAMDV 23
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                                                                                                                                            Conservative
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; Pred. No. 95;
5; Mismatches
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Pred. No.
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                                                                                                                                             8,
                                                                                                                                                                             Length 410;
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                                                                                                                                            Gaps
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RESULT 4
US-08-183-213-2
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Patent No.
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SEQUENCE CHARACTERISTICS:
LENGTH: 276 amin
                                                                                                                        Matches
                                                                                                                                                   Query Match
                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 111 CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                          MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 34.3%;
Local Similarity 42.1%;
hes 8; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: U. FILING DATE: 19920513 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                           TOPOLOGY: unl
                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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    Application US/07882329
    5308765

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                                                                                       GGGAYEDVWSGEYPEYYAMDV 23
                                                           GHGRSSQVWDGHDMDHYADDV 79
                                                                                                                                                                                                 1: Pseudomonas
MR-2068 (FERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBZAWA, RYOZO
NVENTION: ESTERASE GENES, ESTERASE, RECOMBINANT
NVENTION: PLASMIDS AND TRANSFORMANTS CONTAINING THE RECOMBINANT
NVENTION: PLASMID AND METHODS OF PRODUCING OPTICALLY ACTIVE
NVENTION: CARBOXYLIC ACIDS AND THEIR ENANTIOMERIC ESTERS USING SAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                   (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ozaki, Eiji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sakimae, Akihiro
                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                         single
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                                                                                                                                   33.6%;
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ER: 7005-046-999
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4 BP-3846)
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Pred. No. 2.
                                                                                                                        Mismatches
                                                                                                                                     Score 45; DB 1; Length 276; Pred. No. 60;
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US-09-328-352-7483
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Sequence 7483, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08183213
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/183,213
FILLING DATE: 14-JAN-1994
CLASSIFICATION DATA:
APPLICATION UNBER: US 07/882,329
FILLING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ozaki, Biji
APPLICANT: Sakimae, Akihiro
APPLICANT: Numazawa, Ryozo
APPLICANT: Numazawa, Ryozo
TITLE OF INVENTION: ESTERASE GENES, ESTERASE, RECOMBINANT
TITLE OF INVENTION: PLASMIDS AND TRANSFORMANTS CONTAINING THE RECOMBINANT
TITLE OF INVENTION: PLASMID AND METHODS OF PRODUCING OPTICALLY ACTIVE
TITLE OF INVENTION: CARBOXYLIC ACIDS AND THEIR ENANTIOMERIC ESTERS USING SAID
TITLE OF INVENTION: TRANSFORMANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 790-90
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 9; Conserv
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STRAIN: MR-2068 (FERM BP-3846)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
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1155 Avenue of the Americas
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Pred. No.
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Result
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       December 30, 2003, 10:47:45 ; Search time 2.3355 Seconds (without alignments) 416.677 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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134
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   US-09-562-737-12
US-09-252-991A-29606
US-07-882-329-2
US-08-183-213-2
US-09-328-352-7483
US-09-252-991A-31155
US-09-252-991A-30606
US-09-252-991A-19413
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US-09-328-352-5411
US-09-328-352-5411
US-09-328-352-5411
US-08-313-528-13
US-08-914-375C-79
US-08-914-375C-71
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Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 7483, Ap
Sequence 31155, Ap
Sequence 31155, Ap
Sequence 69, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 11, Appl
Sequence 1, Appli
Sequence 13, Appl
Sequence 2, Appl
Sequence 7, Appl
Sequence 71, Appl
Sequence 25819, Appl
Sequence 41, Appl
Sequence 130, App
Sequence 130, App
Sequence 130, App
Sequence 29, Appli
Sequence 29, Appli
Sequence 9, Appli
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RESULT 2 US-09-252-991A-29606 ; Sequence 29606, Application US/09252991A ; Sequence 29606, Application US/09252991A ; Patent NO. 6551795 ; GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS ; TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ; FILE REFERENCE: 107196.136 ; CURRENT APPLICATION NUMBER: US/09/252,991A ; CURRENT FILLING DATE: 1999-02-18 ; PRIOR APPLICATION NUMBER: US 60/074,788 ; PRIOR APPLICATION NUMBER: US 60/094,190 ; PRIOR FILLING DATE: 1998-07-27 ; NUMBER OF SEQ ID NOS: 33142 ; SEG ID NO 29606 ; LENGTH: 1287	8 EDVWSGEY	Query Match 34.3%; Score 46; DB 4; Length 659; Best Local Similarity 34.6%; Pred. No. 1.2e+02; Matches 9; Conservative 3; Mismatches 4; Indels 10; Gaps 1;	RESULT 1 US-09-562-737-12 US-09-562-737-12 Sequence 12, Application US/09562737 Patent No. 6428967 Patent No. 6428967 Patent No. 6428967 GENERAL INFORMATION: APPLICANT: Herz, Joachim APPLICANT: Gotthardt, Michael TITLE OF INVENTION: LDL Receptor Signaling Pathways FILE REFERENCE: UTSW0708 CURRENT APPLICATION NUMBER: US/09/562,737 CURRENT FILING DATE: 2000-05-01 NUMBER OF SEQ ID NOS: 132 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 12 LENGTH: 659 TYPE: PAT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic JOTHER INFORMATION: Sequence	ALIGNMENTS	28 43 32.1 197 2 US-09-047-370-9 Sequence 9, Appli 32.1 271 4 US-09-229-583A-6 Sequence 6, Appli 32.1 270 2 US-08-859-201-4 Sequence 4, Appli 32.1 270 2 US-08-859-201-4 Sequence 36, Appli 32.1 275 2 US-08-701-191A-36 Sequence 36, Appli 32.1 275 2 US-08-701-191A-36 Sequence 36, Appli 32.1 314 299 4 US-09-205-258-265 Sequence 265, Appli 33.2.1 314 299 4 US-09-205-258-265 Sequence 2316, Appli 32.1 461 4 US-09-114-001C-3316 Sequence 316, Appli 32.1 462 1 US-08-458-023B-2 Sequence 2, Appli 32.1 463 3 US-08-156A-2 Sequence 2, Appli 32.1 463 3 US-08-160-758-2 Sequence 2, Appli 32.1 463 3 US-09-107-532A-4797 Sequence 4797, Ap 43 32.1 659 4 US-09-107-532A-4797 Sequence 2, Appli 43 32.1 659 4 US-09-396-149-8 Sequence 11, Appli 42 43 32.1 660 3 US-08-819-177-1 Sequence 1, Appli 43 43 32.1 660 3 US-08-819-177-1 Sequence 1, Appli 44 43 32.1 660 3 US-08-819-177-1 Sequence 1, Appli 44 43 32.1 660 3 US-08-819-177-1 Sequence 2, Appli 54 42.5 31.7 817 4 US-09-252-991A-25598 Sequence 27, Appli 54 42.5 31.7 817 4 US-09-252-991A-25598 Sequence 27, Appli 64 42.5 31.7 817 4 US-09-252-991A-25598 Sequence 27, Appli 64 42.5 31.7 817 4 US-09-252-991A-25598 Sequence 27, Appli 64 42.5 31.7 817 4 US-09-252-991A-25598
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RESULT 15
US-09-840-459-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/062,254

CURRENT FILING DATE: 2002-02-01

PRIOR APPLICATION NUMBER: 09/630,346

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: 60/146511

PRIOR APPLICATION NUMBER: 60/156006

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 60/156899

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 60/157287

PRIOR APPLICATION NUMBER: 60/157287

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/169767

PRIOR APPLICATION NUMBER: 60/17054

PRIOR APPLICATION NUMBER: 60/171054

PRIOR APPLICATION NUMBER: 60/172958

PRIOR APPLICATION NUMBER: 60/171515

PRIOR APPLICATION NUMBER: 60/171515

PRIOR APPLICATION NUMBER: 60/171515

PRIOR FILING DATE: 1999-12-22

PRIOR APPLICATION NUMBER: 60/171515

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US-10-062-254-246
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Sequence 77, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION:
APPLICANT: LAROSA, Gregory J.
APPLICANT: Horvath, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 375
SOFTWARE: Microsoft Office 97
SEQ ID NO 246
LENGTH: 389
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                         Matches
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APPLICANT: Cahoon, Rebecca E
APPLICANT: Falco, Saverio Carl
APPLICANT: Fang, Yiven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhu, Qun
TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                   Local Similarity 50.0
                                                                                                                                                                                                                                       359 NSGGGFGRDCFVWSPQYPYAYA 380
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Zheng, Peizhong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee,
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Search completed: December 30, 2003, 11:45:23 Job time : 4.93258 secs

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APPLICANT: UGUED, S. LELLANI:
APPLICANT: O'RETEN, SIOBHAN H.
APPLICANT: O'KEETE, THERESA
ITITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
ITITLE OF INVENTION: METHODS OF USE THEREFOR
ITILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: DY/US01/03537
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SEQTIMARE: PastSEQ for Windows Version 3.0
SEQ ID NO 77
LENGTH: 128
                                                                                                                                                                         GRGANISM: Homo sapiens
GRGATURE:
FEATURE:
NAME/KEY: VARIANT
LOCATION: (11)...(128)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-77
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                                                                                       Matches
                                                                                                           Query Match 36.2%; Score 48.5; Best Local Similarity 66.7%; Pred. No. 32
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APPLICANT:
APPLICANT:
104 DFWSGXY-YYYGMDV 117
                                           9 DVWSGEYPEYYAMDV 23
                                                                                       10; Conservative
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                                                                                    Mismatches
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GAYYDILTGYYP--YGMDV 115

RESULT 10 US-09-880-748-1695

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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1695
LENGTH: 252
TYPE: PRT
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/210,210
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/276,248
                                                                                                                                                ; ORGANISM: Homo sapiens US-09-880-748-1698
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US-09-880-748-1698
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US-09-880-748-1695
                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1698
LENGTH: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1698, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ruben et al. TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLySFILE REFERENCE: PF523
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PRIOR FILING DATE: 2001-05-25
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                                                 11; Conservative
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Similarity 57.9%;
GAYEDVWSGEYPEYYAMDV 23
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                                                                     38.8%;
                                           Score 52; DB Pred. No. 21; 2; Mismatches
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Pred. No. 21;
                                                                     DB 11; Length 252; 21;
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                                           Gaps
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US-09-880-748-839
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CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-10-17

PRIOR PPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25
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US-09-880-748-839
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2172
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PRIOR APPLICATION NUMBER: 00/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR PELICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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                                                                                                                                                                                                         SEQ ID NO 839
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SEQ ID NO 2172
LENGTH: 21
                                                            Query Match
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Best Local
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NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                       LENGTH: 25
TYPE: PRT
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
37.3%; Score 50; DB Local Similarity 55.6%; Pred. No. 40; 198 10; Conservative 2; Mismarchen
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GAYYDILTGYYP--YGMDV 115
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Pred. No. 3
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                                                          DB 11; Length 256;
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            Indels
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RESULT 6 US-09-880-748-926

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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/21,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-05-25
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1394
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                                                                                                          Query Match 38.8%; Score 52; DB Best Local Similarity 50.0%; Pred. No. 21; Matches 9; Conservative 3; Mismatches
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Best Local Similarity 57.9%;
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TITLE OF INVENTION: Ant
FILE REFERENCE: PF523
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TYPE: PRT
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101 SYYDILTGYYVHYYGMDV 118
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Pred. No. 21;
                                                                                                                Mismatches
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1674
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1646
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SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 1646
LENGTH: 252
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                                                                           Query Match
Best Local
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                                                            Matches
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Best Local Similarity
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/293,499
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5 GAYEDVWSGEYPEYYAMDV 23
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                                                            Conservative
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Pred. No.
                                                                             Score 52;
Pred. No.
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                                                              Mismatches
                                                                               DB 11; Length 252; 21;
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US-09-880-748-2860
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/21,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
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                                                                           Query Match 38.8
Best Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                                                                                                                        SOFTWARE: PatentIn
SEQ ID NO 2860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 1777
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
FILE REFERENCE: PF523
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/293,499
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PRIOR FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                   TYPE: PRT
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                                  GAYEDVWSGEYPEYYAMDV 23
                                                                                                  38.8%; Score 52; DB 57.9%; Pred. No. 1.3;
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                                                                           Mismatches
                                                                                                                       DB 11;
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CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/2140,816

PRIOR PILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/270,399

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239
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US-09-880-748-918
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US-09-880-748-2743
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR PPLICATION NUMBER: 60/276,248
PRIOR PPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR PPLICATION NUMBER: 60/277,379
PRIOR PPLICATION NUMBER: 60/277,379
PRIOR PPLICATION NUMBER: 60/277,379
PRIOR PPLICATION NUMBER: 60/277,379
PRIOR PRILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
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                                                                                                                                                                                                                                                                      SOFTWARE: Pat
SEQ ID NO 918
                                                                                                              Query Match
Best Local :
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                                                                                         Matches
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APPLICANT: Ruben et al.
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Publication No. US20
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                  LENGTH:
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Local Similarity 50.0%;
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o. US20030059937A1
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Pred. No. 21;
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Pred. No. 1
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                     Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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77, A		. 658	Sequence 2172, Ap	Sequence 1698, Ap	Sequence 1695, Ap	sequence 16/4, Ap	1 1 0	1646	Sequence 1394. Ap	sequence 926, App	מיקעריירה איני אלולי	010	Seguence 2743. An	Sequence 2860, Ap			Sequence 3082. An		Description

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CURRENT APPLICATION NUMBER: US/09/880,748 CURRENT FILING DATE: 2001-06-15 PRIOR APPLICATION NUMBER: 60/212,210 PRIOR RILING DATE: 2000-06-15 PRIOR APPLICATION NUMBER: 60/240,816 PRIOR FILING DATE: 2000-10-17 PRIOR APPLICATION NUMBER: 60/276,248 PRIOR PILING DATE: 2001-03-16 PRIOR PILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/277,379 PRIOR PILING DATE: 2001-03-21 PRIOR PILING DATE: 2001-03-25 NUMBER OF SEQ ID NOS: 3239 SOFTWARE: PATENTIN OF SEQ ID NOS: 3239 SOFTWARE: PATENTIN VET: 2.0 SEQ ID NO 3082 LENGTH: 21 TYPE: PRT ORGANISM: Homo sapiens RESULT 1 US-09-880-748-3082 Sequence 3082, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION: APPLICANT: Ruben et al. TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS FILE REFERENCE: PF523 Matches Query Match Best Local : ch 41.4%; 1 Similarity 54.5%; 12; Conservative 2 GGGGAYEDVWSGEYPEYYAMDV 23 GDFGDY-DILTGYYPVYYGMDV 21 ; Score 55.5; DB; Pred. No. 0.56; 2; Mismatches DB 11; Length 21; Indels ۲. Gaps

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                                                                                                                                                                                                                     invention.
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GAYYDILTGYYP -- YGMDV 115
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immune disorders -
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                                                                                                                           Length 252;
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RESULT 10
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ID ABP44
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Best Local :
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                                                                                                                                                                                                                                                   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (cVID) and acquired immunodeficiency syndrome (AIDS)), ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
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16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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                                                                                                                                                                                Sequence
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17-OCT-2000;
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CAMBRIDGE ANTIBODY TECHNOLOGY
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RESULT 11
ABP45383
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; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
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RESULT 12

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GAYYDILTGYYP--YGMDV 17

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RESULT 8
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16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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                                                                                                                                  Sequence
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                                                                                                                                      249 AA;
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17-OCT-2000; 2000US-240816P.
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21-MAR-2001; 2001US-277379P.
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                                                                                                                                                                                            This invention describes novel antibodies that immunospecifically bind to CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell continuous and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC cytostatic and antiAIDS activity and can be used in vaccines to CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC biological samples and may be used in this way to diagnose disease CC administered to treat disease associated with aberrant ELyS expression ad activity such as cancer, immune, and autoimmune disorders and CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, C immunodeficiency (e.g. common variable immunodeficiency (CVID) and CC define antibodies and fragments of the antibodies described in the method CC of the antibodies and fragments of the antibodies described in the method
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21-MAR-2001;
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                                                                                                                                                                                of the invention.
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                                    Similarity
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CAMBRIDGE ANTIBODY TI
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2001US-276248P.
2001US-277379P.
2001US-293499P.
      Conservative
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                                 38.8%;
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                                 Score 52; I
Pred. No. 1
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               Mismatches
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                                                            멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y polypeptides, useful for immune disorders -
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            4
                                                            Length 17;
               Indels
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            ب
               Gaps
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CC AAH19170-AAH19250 represent cDNAs corresponding to 27 human secreted CC protein genes, and AAG62156-AAG62235 represent the proteins they encode. CC AAG62236-AAG62233 represent human secreted protein fragments. The genes CC and their corresponding secreted proteins are useful for preventing. CC treating or ameliorating medical conditions, e.g., by protein or gene CC amount of the new genes. Specific uses are described for each of the CC amount of the new genes. Specific uses are described for each of the CC 22 genes, based on the tissues in which they are most highly expressed, CC and include developing products for the diagnosis or treatment of CC proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, CC AIDS, autoimmune diseases (e.g., Alzheimer's disease, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC parkinsons's diseases (e.g., porilasis), sepsis, disbetes, atherosclerosis, CC gastrointestinal disorders, pregnancy-related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound CC sunburn, to maintain organs before transplantation, for supporting cell CC cognate ligands or binding partners, and in chemetaxis, and can be used CC antibodies specific for a protein of the invention can be used in claimanoassave to immunoassave e.g., radioimmunoassave mentioned above, and CC in diagnostic immunoassave e.g., radioimmunoassave mentioned above, and CC in diagnostic immunoassave e.g., radioimmunoassave mentioned above, and CC in diagnostic immunoassave e.g., radioimmunoassave representations of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and conditions and conditions and conditions and can be used to make the conditions and can be used and conditions.
Query Match 44.4%;
Best Local Similarity 50.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder, AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; AIDs disease; estima; sethma; skinnon's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; tumour; endocrine disorder; infection; wound healing; vulnerary; cell: culture; chemotaxis; food additive; expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 62; 594pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel 27 isolated human secreted proteins and polynucleotides encoding them useful for treating, diagnosing, preventing Alzheimer's disease, Parkinson's disease, AIDS, rheumatoid arthritis, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-335835/35
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30-JUN-2000; 2000US-0215131.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene
                                                                                                                                                                                                                                                 in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2000; 2000WO-US29362.
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Score 59.5; DB Pred. No. 0.92; 2; Mismatches
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                                                 This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVLD) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 3111-3112; 3148pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAR-2001; 2001US-276248P
21-MAR-2001; 2001US-277379P
25-MAY-2001; 2001US-293499P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human BLyS binding
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                                                                                                                                                                                                                                                                                                                                                                                                       Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
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17-OCT-2000; 2000US-240816P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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                                       invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAMBRIDGE ANTIBODY TECHNOLOGY
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Query Match Best Local Similarity Matches 12; Conserv

Conservative

2;

Score 55.5; DB Pred. No. 0.43; 2; Mismatches

23;

Length

21;

7:

Gaps

41.4%;

Sequence

21

B

Example 4; Fig

Ĉ;

61pp;

Sequence

23 AA;

Length

23;

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presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human anti-factor VIII antibody VH IT-2 protein CDR3 fragment which is used in the method of the invention.

hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the

This invention describes a novel polynucleotide (I) (and complements and

Length

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RESULT 2
AAY50950
ID AAY5
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Best Local S
Matches 23
                        This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilla A patients. This sequence represents the human anti-factor VIII antibody clone IT-2 protein which is used in the method of the invention.
                                                                                                                                                                                                       New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human anti-factor VIII antibody VH clone IT-2 encoded protein.
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                                                                                                                                                                                                                                                                                                                                                                              07-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; heavy
hemophilia A
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                                                                                                                                                                             Example 4; Fig 4A; 61pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-1999
                                                                                                                                                                                                                                                                                                                       (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chain; antibody; factor VIII; hemostatic;
; VH gene.
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Pred. No. 3.9e-12;
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Sequence

132 AA

AAG62284
ID AAG6
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AC AAG6
XX
DT 18-0

AAG62284 standard;

Protein;

129

18-JUL-2001 AAG62284;

(first

entry)

RESULT 4

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RESULT 3
AAY5053
AID AAY50
XX AAY50
XX AAY50
XX AAY50
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Best Local :
                                                                                                                                                                                                                                                                                                           hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human anti-factor VIII antibody VH IT-2 protein which is used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polymucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Voorberg JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-1998;
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hemophilia A
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                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                   of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel polynucleotide (I) (and complements and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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                                                                                                              .0%; Score 134; DB 21;
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0; Mismatches 0;
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Listing first 45 summaries
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12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

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length: 2000000000
is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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493.415 Million cell updates/sec
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249	20	17	253	21	129	132	132	23	% Query Match Length DB
23	23	23	23	23	22	21	21	21	
ABP44907	ABP46732	ABP46849	ABP45766	ABP47071	AAG62284	AAY50953	AAY50950	AAY50957	ID
Human BLyS binding	BLys	BLys	Human BLyS binding	BLys	gene	Human anti-factor	Human anti-factor	Human anti-factor	Description

New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -

WPI; 2000-053102/04.

45	44	43	42	41	40	39	38	37	36	35	34	IJ IJ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	IJ	12	11	10	
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ABB97254	AAE06620	σ	AAU09026	AAB42978	ABG25421	108	AAG50642	AAG13980	AAU72500	AAG50643	AAG13981	AAG50644	AAG13982	ABP45614	ABP31473	AAB41476	ABP46976	ABP44927	ABP46750	ABB07347	AAM42096	ABG09454	AAE07014	ABP34925	ABP44828	ABJ36933	μ	616	ø	56	ABP45684	ABP45663	ABP45635		ABP44915	
Novel human protei	Human protein havi	Human PRO4994 poly	ള		Novel human diagno	n	chali	hali	Arabidopsis partia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	_	Human ORF446 prote		Human BLyS binding	Human BLyS binding	BLyS	lori	Human polypeptide	Novel human diagno	Human heavy chain		Human BLyS binding	വ	heavy	Human BLyS binding	=					bine	_	

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hemophilia A; VH protein.
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                                                                                                                                                                                                                                                                                 Voorberg JJ, Van Den Brink EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-1999;
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Best Local S
Matches 90
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

REMBL; BC020240; AAH20240.1; -.

R InterPro; IPR007010; Ig-like.

R InterPro; IPR003006; Ig_WHC.

R InterPro; IPR003596; Ig_V.

R Pfam; PF00047; ig; 5.

R Pfam; PF00040; IGV; 1.

R SMART; SM00406; IGV; 1.

R PROSITE; PS00930; IG_MHC; 3.

W Hypothetical protein.

Q SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;
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QBWUK1;
01-MAR-2002 (TrEMBLrel. 2:
01-MAR-2002 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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Ol-MAY-2000 (TrEMBLrel. 23, Last annotation update)
Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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                                                                                                    Wu X., Liu B., Van der Merwe P.L., Young D.C.;
                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                            "Myosin-reactive autoantibodies in rheumatic
                                                                                              Young D.
                                                                                                                                                                                                                          CBI_TaxID=9606;
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Immunol. Immunopathol. 87:184-192(1998) AF035023; AAD56259.1; -.
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O (TrEMBLrel.
3 (TrEMBLrel.
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Primates;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 479; DB 4; Length 613; Pred. No. 2.5e-40;
                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESULT 4
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Matches 93
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Matches 92; Conserv
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InterPro; IPR007110; 1
InterPro; IPR003006; 1
InterPro; IPR003596; 1
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
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Q9UL71;
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035043; AAD56279.1; -.
HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fetus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coung D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIMVIVS 125
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                                                                                        EVQLVESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGGSTYY
                                                                                                                QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
                                            ADSVKGRPTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
  ADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGKV-TTIYDR
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121 AA;
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                                                                                                                                                                                                                                                            121
13154 MW; 2F045CCFA5D50736 CRC64;
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Ig_MHC.
Ig_v.
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73.2%;
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Pred. No. 3.5e-39;
                                                                                                                                                                                       Score 457.5; DB 4
Pred. No. 5.1e-39;
3; Mismatches 16
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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
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     100
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                        456
446.5
443.5
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length: 2000000000
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
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Match
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Gapop 10.0 , Gapext 0.5
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    QVQLVQSGGGLVQPGKSLRL....
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                      sp_organelle:*
sp_phage:*
sp_plant:*
sp_rotant:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_mammal:*
sp_mhc:*
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     573
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Q8WUX1
Q9UL91
Q9UL71
Q9HCC1
Q8TC77
                                Q96BB9
Q9UL93
Q8N5K4
Q9UL90
Q9Y509
Q9YL84
Q8NCL6
             Q9UL72
Q96K68
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O8wu38 homo sapien
O8wuk1 homo sapien
O9u191 homo sapien
O9u171 homo sapien
O9tcc1 homo sapien
O9tcc77 homo sapien
O9tb9 homo sapien
O9u193 homo sapien
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O9u184 homo sapien
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O9u186 homo sapien
O9u187 homo sapien
O9u188 homo sapien
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45.5	45.6	45.7	46.4	46.7	47.1	47.1	48.0	48.9	48.9	49.2	49.6	49.6	50.1	50.7	51.1			53.9							57.4	57.8	59.7	61.6
146	150	241	119	142	500	159	121	484	125	614	482	124	124	124	112	437	480	521	298	484	486	95	469	479	131	119	487	104
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Q924R8	Q9Y298	Q921A6	Q9UL94	Q924Q1	Q9BRV0	Q96QS0	Q99NG4	Q99LA6	Q9UL95	Q96GA6	Q91X92	Q9NOW6	Q9NOW4	Q9UL92	Q9UGP3	Q9R1A4	Q91XE1	Q8N4Y9 .	O3AAO	Q8VEA0	Q91Z07	Q9ULB6	Q8R3V9	Q91WP5	Q9UL88	Q920E7	Q99KA4	Q9UL87
Q924r8 mus musculu	Q9y298 homo sapien	ana B	Q9ul94 homo sapien	Q924q1 mus musculu	homo	homo	Q99ng4 mus musculu	muø	homo		Bru	Q9n0w6 oryctolagus	Q9n0w4 oryctolagus	Q9u192 homo sapien	homo	Q9rla4 mus musculu	Bnm	homo	Q9qyf0 mus musculu	Q8vea0 mus musculu	Q91z07 mus musculu	Q9ulb6 homo sapien	anus	B nw	Q9ul88 homo sapien	Q920e7 mus musculu	8nm	Q9ul87 homo sapien

ALIGNMENTS

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RESULT 1
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

REMBL; BC021276; AAH21276.1; -.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR007016; Ig_WHC.

R InterPro; IPR00306; Ig_W.

R Pfam; PF00047; 19; 4.

R SMART; SM00406; IGv; 1.

R SMART; SM00406; IGv; 1.

R PROSITE; PS05035; IG_LIKE; 2.

                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 96; Conserv
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8WU38, PRELIMINARY;
Q8WU38; PRELIMINARY;
Q1-MAR-2002 (TrEMBLrel. 20,
Q1-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Tonsil;
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        80
                                                                                    61
                                                                                                                                                                         20
                                                                                                                                                                QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
:|||:||||||||::|: :|: :|:
EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAWHWVRQAPGKGLEWVSGISWNSGSIGY
ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKH--GSGSYIGYYYGMDVWGQGT 137
                                                     ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT
                                                                                                                                                                                                                                                                                                                                          75.5%; Score 502; DB 4; Length 573; llarity 76.2%; Pred. No. 1e-42; Conservative 12; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
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ID HV3L-HWAN
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DT 21-7U
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                                                                                         Query Match
Best Local S
Matches 74
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Best Local S
Matches 77
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Immunoglobulin V region.
DOWALN
NON_TER 115 115
SEGUENCE 115 AA.
                                                                                                                                                                                                             DOMAIN
MOD RES
DISULFID
CARBOHYD
NON TER
                                                                                                                                                                                                                                                                                 PIR; A02056; A1HUBR.
HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo Bapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putnam F.W., Liu Y.-S.V., Low T.L.K.;
"Primary structure of a human 19A1 immunoglobulin. I
IgA1 protease, digestion, Fab and Fc fragments, and
amino acid sequence of the alpha 1 heavy chain.";
J. Biol. Chem. 254:2865-2874(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V-III region BUR.
                                                                                                                                                                                       SEQUENCE
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MEDLINE=79151016; PubMed=107164;
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SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
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1 Similarity 61.1%;
77; Congervation
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                                                                                                                    Similarity
QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
|||||:|||:||: ::: |: :: |: :|
QVQLVESGGGVVQAGTSLRLSCTASAFNLSDYAMHWVRQAPGKGLZWVALISYGGSBTYY
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                                                                                                                                                                                       119 AA;
                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                     12981 MW;
                                                                                                               59.1%;
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                                                                                       21; Mismatches
                                                                                                                 Score 386.5; DB 1
Pred. No. 4.1e-33;
                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .).
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                                                                                                                                       DB 1;
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                                                                                                                                  Length 119;
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Search completed: December Job time: 6.75548 secs

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RESULT 15
HV01-P
HV01-P
ID HV01-P
AC P017-B
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D0 15-SE
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OC Eukar
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Best Local S
Matches 78
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HSSP; P01772; ZEB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
DOMAIN
1 112 IG
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SEQUENCE
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"primary structure of the variable regions of two canine immunoglobulin heavy chains.";
Biochemistry 16:3160-3168(1977).
-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P01784;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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109
                                                   121 MVTVSS 126
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                                                                                                                                                                                                                           μ
                                                                                                                                                                                                                                                                                                                                   h 57.4%; Score 382; DB 1; Similarity 61.9%; Pred. No. 1.1e-32; 78; Conservative 17; Mismatches 19
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  114
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SETTING DESCRIPTION OF THE PROPERTY OF THE PRO
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Best Local
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21-JUL-1986
15-SBP-2003
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HV3 F HUMAN
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MEDLINE=81101090; PubMed=6450418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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EMBL; M35415; AAA58735.1; -.
PIR; A02047; H3HU26.
PDB; 1HOU; 23-DEC-99.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V-III region BUT.
19 heavy chain (Human)
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GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activ
GO:0006955; P:immune response; NAS
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bbulin V region; Signal; 3D-structure.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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117 AA;
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ain V-III region VH26 precursor.
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Immunoglobulin V region.
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SMART; SM00406; IGv;
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                                                               -!- SIMILARITY: Contains 1 immunoglobulin-like PIR; A02048; H3HUTL. HSSP; P01772; 2FB4. GO: GO:0005576; C:extracellular; NAS. GO: GO:0003823; F:antigen binding activity; NAS. GO: GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                 regions of a mu and a gamma2 chain.
J. Biol. Chem. 252:7192-7199 (1977).
I- MISCELLANEOUS: THE SEQUENCES OF
OF IGM AND IGG2 ISOLATED FROM A
GAMMODATHY ARE IDENTICAL. THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                         Wang A.-C., Wang I.Y., Fudenberg H.H.; "Immunoglobulin structure and genetics. Identity regions of a mu and a gamma2 chain.";
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15 heavy chain V-III region TIL.
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RESULT 10
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MEDLINE=77100368; PubMed=401950;
Secher D.S.;
Milstein C., Secher D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation - the European Bioinformatics Institute of here are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
SEQUENCE, AND DISULFIDE BONDS.
MEDILINE-83289131; PubMed=6884994;
MEDILINE-83289131; PubMed=6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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21-JUL-1986 (Rel.
15-SEP-2003 (Rel.
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                                                                                                                                  Ig heavy chain V-III region Homo sapiens (Human).
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[TE; PS50835; IG_LIKE; 1.
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IPR003596; Ig_v.
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DN -> ND (IN REF. :)
W -> H (IN REF. 2)
Y -> W (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 409; DB 1;
Pred. No. 2.3e-35;
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D SEGMENT.
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                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2276A98DBDBF7016 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                            update)
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MEDLINE=81072295, PubMed=7441755;

Marquart M., Deisenhofer J., Huber R., Palm W.;

"Crystallographic refinement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment and 1.0-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TURN
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; 3D-structure;

DOMAIN 1 112 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding activ GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-1ike. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_V.
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PDB; 2IG2; 12-JUL-89.
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 112
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                                -- DIWGQGTMVTVSS
                                                                                          ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAF------
                                                                                                                                      OVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
 GPDYWGQGTPVTVSS
                                                                   ADSVKGRPTISRDNSKNTLFLQMDSLRPEDTGVYFCA-----RDGGHGFCSSASCF 111
                                                                                                                                                                                                                                                                             Conservative
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 126
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                                                                                                                                                                                                                            Score 398;
Pred. No. 2.
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                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                              Length 126;
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RESULT 11
HV3C_HUMAN
ID HV3C_HUMAN
AC P01764;

STANDARD;

PRT;

117

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RESULT 8
HV3A HUMAN
ID HV3A HUMAN
AC P01762;
DT 21-JUL-1986
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HV3B_HU
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Matches 82
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P01763;
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"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";

Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

-I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLAYED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.
-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1. SMART; SM00406; ICv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN 1 112 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last seques)
15-SEP-2003 (Rel. 42, Last annotes)
Ig heavy chain V-III region WEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P01772; 2FB4.
HSSP; P01772; 2FB4.
SG; GO:0005576; C:extracellular; NAS.
GO; GO:0003B23; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR0030596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                QVQLVDSGGGLVBPGGSLRLSCSASGFTFSANDMNWVRQAPGKGLEWLSFIGGSGSTIYY
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114 AA;
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Last annotation update)
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PYRROLIDONE CARBOXYLIC ACID
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15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V-III region TRO.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                             HV16_MOUSE STANDARD; PRT; 136 AA.

P01783;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V region MOPC 21 precursor (Fragment).
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MEDLINE=76023781; PubMed=809331;
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"Heavy chain variable region antibodies: somatic mutation Cell 24:625-637(1981).
                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth
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                                                                                                                                          Baltimore
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13472 MW; 2E21A11DA04D80F9 CRC64;
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Pred. No. 9.8e-36;
                                                                                                                                                                             Reth
                                                                          evident in a gamma
                                                                                                              contribution to the NPb family
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                                                                                                                                                                                 Rajewaky
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                                                                          region.";
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Best Local S
Matches 83
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
                                                                                                        MEDLINE=79124695; PubMed=420800; Chiu Y.-Y.H., Lopez de Castro J.A., Pc "Amino acid sequence of the VH region cryoimmunoglobulin IgG Hil."; Biochemistry 18:553-560(1979).
                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Last sequence update)
15-8EP-2003 (Rel. 42, Last annotation updat ig heavy chain V-III region HIL.
                                                                                                                                                                                                                                                                                          HV3J_HUMAN
P01771;
                                                                                                                                                                                                                                                                                                                   HUMAN
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                                                         -1- SIMILARITY: Contains
PIR; A02054; G1HUHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MACROGLOBULIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                              -!- MISCELLANEOUS:
                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hilschmann N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISION TO 28-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
"The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), II: the amino acid sequence of the H-chain (m.
(mpe), subgroup H III. Architecture of the complete IgM-molecule.";
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                              Homo sapiens (Human
                                                                                                                                                                                                                                                                               21-JUL-1986
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        P; P01772; 2FB4.
GO:0005576; C:extracellular; NAS.
GO:000382; F:antigen binding activity; NAS
GO:0006955; P:immune response; NAS.
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GO:0005576; C:extracellular; NAS:
GO:0003523; F:antigen binding act
GO:0006955; P:immune response; NJ
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                                                                                                                                                                                                                                                                                                                                                                                        MVTVSS 126
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IPR007110;
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 Z. Physiol.

                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                              THIS CHAIN WAS ISOLATED
                                                                                                                                                                                                       Primates;
                                                                                                                                                                                                                Chordata;
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                                                                      immunoglobulin-like
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12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 424;
Pred. No. !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG-LIKE
                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2C67CA9AAAAA1282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    data
N WAS
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                                                                                                                               Poljak R.J.;
on of human m
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                                                                                                                                                                                                                                                                                                      121
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                                                                      domain
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                                                                                              MYELOMA
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                                      Query Match
Best Local S
Matches 77
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Best Local S
Matches 81
                                                                                                                   GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic ac.
                                                                               DOMAIN
MOD_RES
NON_TER
SEQUENCE
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InterPro; IPR003596; Ig_v.
Pfam; PP00407; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic DOMAIN
1 112
IG-LIKE.
                                                                                                                                                                                                                                                                               MEDLINE=74175307; PubMed=4208843; Florent G., Lehman D., Putnam F.W.; "The switch point in mu heavy chains of human IgM Biochemistry 13:2482-2498(1974).
                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up.
15-SEP-2003 (Rel. 42, Last annotation Ig heavy chain V-III region GA.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                     PIR; A02052; M3HUGA.
                                                                                                                                                                                                                                                MACROGLOBULIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                    MISCELLANEOUS: THIS
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                                                  Similarity
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VLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TMVTVSS 126
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121 AA;
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122 AA;
                                        Conservative
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                                                                                                                                                                                                                            2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                               122
13166 MW;
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13566 MW;
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                                                  63.0%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%;
                                                                                                                                                                                                                                                                    CHAIN WAS ISOLATED FROM A WALDENSTROM'S
                                        24;
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                                                  Score 419;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 422.5;
Pred. No. 8e
                                                                                                   PYRROLIDONE CARBOXYLIC ACID
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                                                                                                             IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                 74E5B6959E84100A
                                        Mismatches
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                                                            Length 122,
                                                                                 CRC64;
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Best Local Similarity
Matches 82; Conserv
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SMART; SM00406; IGv; 1.
POSITE; PS50835; IG LIKE; 1
Phulin V region.
112
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HV3U F
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Steiner L.A., Garcia Pardo A., Margolies M.N.;
"Amino acid sequence of the heavy-chain variable region of the
crystallizable human myeloma protein Dob.";
Biochemistry 18:4068-4080(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 18:4054-4067(1979).
--- MISCELLANEOUS: THIS GAMMA-1 MYBLOMA PROTEIN HAS A DELETION IN
HINGE REGION. THERE ARB NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The crystallizable human myeloma
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986
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                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region NIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=80020920; PubMed=114208;
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                        Homo sapiens (Human)
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-JUL-1986 (Rel. 01, Last sequence up-
-SEP-2003 (Rel. 42, Last annotation heavy chain V-III region DOB.
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GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity;
GO:0000585; P:immune response; NAS.
erPro; IPR007110; Ig-like.
erPro; IPR003006; Ig_MHC.
erPro; IPR003596; Ig_V.
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120 AA;
Metazoa;
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13440 MW;
Chordata; Craniata;
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65.1%;
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Pred. No. 2.5e
18; Mismatches
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Best Local S
Matches 84
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN

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TOTALINA CARPACYVITC I
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Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Rule of antibody structure. The primary structure of a monoclonal 1gG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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NCBI_TaxID=9606;
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                                                                                                                                                                         P01781;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region GAL.
                                                                                                                                                                                                                                                                                                                                   HUMAN
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MEDLINE=77070269; PubMed=826475;
                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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GO; GO:0006955; P:immune response; NAS.
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GO; GO:0005576; C:e
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                                                                                                                                                       Homo sapiens (Human)
  WEDLINE=75059123;
                                                                    NCBI_TaxID=9606;
                          SEQUENCE
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llarity 66.7%;
Conservative 1
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  PubMed=4803843
                                                                                                  Chordata;
Primates;
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Pred. No. 3.8e
.4; Mismatches
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PYRROLIDONE CARBOXYLIC ACID
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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-	MUTTUSS 126	SVKGRFTIS SVKGRFTIS	QVQLVQSGGGLVQPGKSLRLSCAAS : : : VELVESGGGVVZPGRSLRLSCAAS	Similarity 2; Conserva	122 AA;	< 5	IPR003596; 047; ig; 1 0406; IGv;	955; P:in	2; 2FB4.	PATIENT WITH MACROGLOBULINEMIA. SIMILARITY: Contains 1 immunogi		Bequence of		alia; Eutheria; _TaxID=9606;	s (Human) Metazoa;	986 (Rel. 01, 986 (Rel. 42, 003 (Rel. 42,	STANDARD		53.2 53.0 52.7				
		SRDNAI 	VQPGKS: : : /VZPGRS	66. 65.	122 13668	P P1	197	P:immune 110; Ig-1	ctrace	ROGIA	ole Ji Si. U THIS !	of t	PubMed=6774332	Primates;	Chore		E.		118 115 123	142	113 117	117	119 113
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		ADSYKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSYKRGVAAFDING - -	GFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIG 	9 444; DB 1; Length . No. 4.8e-39; ismatches 17; Inde	252F1C2 CRC	carboxylic acio		, NAS.	S	ē.	10	le region of a human		rhini; Hominidae;	ata; Vertebrata;	e update) ion update)	122 AA.	ALIGNMENTS					
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RESULT 15
US-09-791-537-69145
US-09-791-537-69145
; Sequence 69145, Application US/09791537
; GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 69145
LENGTH: 122
TYPE: PAT
ORGANISM: Homo Bapiens
US-09-791-537-69145
Search completed: December 30, 2003, 11:38:31 Job time: 192.162 secs
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Sequence 18, Application US/10371942

GENERAL INFORMATION:
APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
APPLICANT: Reiter, Yoram

TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
FILE REFERENCE: 10280-034001

CURRENT APPLICATION NUMBER: US/10/371,942

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: US 60/358,994

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GENERAL INFORMATION:

APPLICANT: Dyax Corporation, et al

TITLE OF INVENTION: MGC-PEPTIDE COMPLEX BINDING LIGANDS

FILE REFERENCE: 10280-034W01

CURRENT APPLICATION NUMBER: PCT/US03/05128

CURRENT FILING DATE: 2003-02-21

PRIOR APPLICATION NUMBER: US 60/358,994

PRIOR APPLICATION NUMBER: US 60/358,994

PRIOR FILING DATE: 2002-02-20

NUMBER OF SEQ ID NOS: 121

SOFTWARE: PSEUSEQ for Windows Version 4.0

SEQ ID NO 18

LENCTH: 120
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 102506
LENGTH: 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-791-537-102506
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CURRENT FILING DATE: 2001-02-22
SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 18
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| Similarity 80.0%;
| 96; Conservative
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nilarity 82.4%;
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Pred. No. le-42;
7; Mismatches
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Pred. No. 1e-42;
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Sequence 19813, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 26.1/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 19813
LENGTH: 132
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; TYPE: PRT
; ORGANISM: Homo s
US-10-371-942-18
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US-09-791-537-19813
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                                                                                                               CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOPTWARE: Patentin version 3.0
SEQ ID NO 31924
                                                                                                                                                                                                                                                                                                             Sequence 31924, Application US/09791537 GENERAL INFORMATION:
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Best Local Similarity
                Query Match
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEME
TITLE OF INVENTION: METHODS OF USB THEREOF
FILE REFERENCE: 261/210
FILE REFERENCE: 261/210
                                                                                   LENGTH: 11
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                  ORGANISM: Homo sapiens
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80.7%;
80.8%;
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Pred. No. 1e-42;
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Pred. No. 1.3e-42;
Score 502; DB 22;
Pred. No. 1.3e-42;
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
ITITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
ITITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 106428
RESULT 8
US-09-791-537-102505
; Sequence 102505, Application US/09791537
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-791-537-68722
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US-09-791-537-106428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 68722
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT PEPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Josep
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                                                                                                                                                                                                                                                                                               97;
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Pred. No. 4e-43;
8; Mismatches 13;
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Pred. No. 3.8e-43;
7; Mismatches 13
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RESULT 10 US-09-791-537-102506

, Sequence 102506, Application ; GENERAL INFORMATION:

US/09791537

APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek

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LENGTH: 125
; TYPB: PRT
; ORGANISM: Homo sapiens
US-09-791-537-31283
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US-09-791-537-31283
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US-09-791-537-102505
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LENGTH: 119
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Best Local Similarity 81.5%;
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Best Local :
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APPLICANT: Danzer, Joseph
TITLE OP INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
TITLE OP INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FAPILLOATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT PEPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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NUMBER OF SEQ ID NOS: 153055
SOPTWARE: PatentIn version 3.0
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                                    117 TVSS 120
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                                                                               ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKDYNYYDSSGYYSLDYWGQGTLV 120
                                                                                                                                                               EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
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83.2%;
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Pred. No. 5.4e-43;
7; Mismatches 12;
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Pred. No. 4.6e-43;
7; Mismatches 12
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US-09-791-537-87993
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APPLICANT: Bebe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 87993
LENGTH: 121
TYPE: PAT
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GENERAL INFORMATION:
APPLICANT: Voorberg, Johannes
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TITLE OF INVENTION: Inhibitor
FILE REFERENCE: Sequence Nos 1-59 for 294-86 PCT/US
CURRENT APPLICATION NUMBER: US/09/674,752
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: PCT/NL99/00285
PRIOR PILING DATE: 1999-05-07
PRIOR PILING DATE: 1999-05-07
PRIOR PILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 50
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
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Best Local
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l Similarity 81.7%;
98; Conservative
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                                                                              Score 518; DB 22;
Pred. No. 3.2e-44;
6; Mismatches 16;
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
ITILE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROFITE OF INVENTION: METHODS OF USE THEREOF
ITILE OF INVENTION: METHODS OF USE THEREOF
ITILE OF INVENTION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT ELING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 31853
LENGTH: 121
TYPE: PRT
                                                                                                                                                                                                                                 FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
CURRENT FOR SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 69157
LENGTH: 117
TYPE: PRT
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US-09-791-537-31853
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Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31853, Appl GENERAL INFORMATION:
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                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                   Matches
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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                 61 ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLIESNIAEALMGOGTLVTVSS 120
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82.5%;
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Pred. No. 2.6e-43;
                                                                                                                                 Score 508.5; DB 2
pred. No. 2.8e-43;
7; Mismatches 11
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RESULT

Perfect score: Sequence:

Title:

US-09-674-752-46 622

1 EVQLVESGGGLVQPGRSLRL.....IESNIAEALWGQGTLVTVSS 120

OM protein - protein search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

92:

December 30, 2003, 10:54:45; Search time 191.162 Seconds (without alignments)

571.193 Million cell updates/sec

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

5728757

5728757 segs, 909918778 residues

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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                               Score
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Match Length DB ID
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/cgn2_6/ptodata/1/paa/
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'cgn2_6/ptodata/1/paa/US081_COMB.pep:*
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'cgn2_6/ptodata/1/paa/US098_COMB.pep:*
'cgn2_6/ptodata/1/paa/US102_COMB.pep:*
    120 20 US-09-674-752-36
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Sequence 36, Appl
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-09-403-10/-14	-09-403-107-144	-09-791-537-96305	-09-791-537-12	-09-791-537-171	-09-791-537-1166	-09-791-537-31907	-09-791-537-71	-09-791-537-1161	-60-418-031-43	-10-269-711-	-09-791-537-10	-US03-09625-100	-09-972-656-76	-US02-33556-	-09-791-537-1024	91-537-	92-088-11	36107-114	91-537-6	09-000-802-	-60-418-0	-10-269-711-7	-09-791-537-6	-10-371-942-6	-10-371-942	-US03-05128-6	-US03-05128-54	-09-791-537-6326	-09-791-537-	-09-791-537-6334	-09-791-537-6914	-09-791-537-3192	-09-791-537-1981	-10-371-94	T-US03-05128-1	S-09-791-537-1025	S-09-791-537-31283	-09-791-537-1025	-09-791-537-6872	9-791-537-1064	-09-791-537-69157	-09-791-537-3185	03-131-331-0133
sequelice 144, App	equence 144	equence 96305.	equence 128053,	e 171	nce 11	equence 31907	equence 717	equence 116	equence 43,	equence 43,	e 1064	quence 100,	Sequence 76,	quence 76, 1	e 102461	e 106426	equence 1	quence 114, Ap	equence 69606,	equence 1	equence 7,	equence 7, Appl	equence 69270,	e 62,	equence 54, App	quence 62,	quence 54, Appl	equence 63269	equence 80297,	equence 63340	equence 69145,	equence 31924	e 19813,	e 18, Ap	18, App	equence 1025	equence 31283	ce 102	e 68722	e 1064	equence 69157,	equence 31853,	eductice over

ALIGNMENTS

RESULT 1 US-09-674-752-36

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GENERAL INFORMATION:

APPLICANT: Voorberg, Johannes

ITILE OF INVENTION: Method For Diagnosis and Treatment of Haemophilia A Patients With

ITILE OF INVENTION: Inhibitor

FILE REFERENCE: Sequence Nos 1-59 for 294-86 PCT/US

CURRENT FILING DATE: 12000-12-29

PRIOR APPLICATION NUMBER: US/09/674,752

CURRENT FILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-05-07

PRIOR FILING DATE: 1998-05-08

NUMBER OF SEQ ID NOS: 59

SOPTWARE: Patentin version 3.1

SEQ ID NO 36

LENGTH: 120

TYPE: PAT

CORGANISM: Homo Bapiens

US-09-674-752-36

Query Match

100.0%; Score 622; DB 20; Length 120;

Best Local Similarity 100.0%; Pred. No. 8.6e-55;
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US-10-041-860-211
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-211
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Waber, Richard
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FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 127
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 211
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 211, Application US/10041860 Publication No. US20030157109A1
                                                                                                                                                                                                                                                Matches
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TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
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ORGANISM: homo sapiens
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Local Similarity 74.8%;
121
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74.8%;
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Pred. No. 2.8e-40;
8; Mismatches 17
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APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ADGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FREESEQ FOR Windows Version 4.0
SEQ ID NO 331
LENGTH: 127
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-331
                                                                                               ; ORGANISM: Homo sapiens US-09-880-748-1912
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                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILLING DATE: 2000-06-15
PRIOR PELLORITION NUMBER: 60/240,816
PRIOR PELLORITION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILLING DATE: 2001-03-16
PRIOR PILLING DATE: 2001-03-21
PRIOR PILLING DATE: 2001-03-21
PRIOR PILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILLING DATE: 2001-05-25
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Publication No. US20030059937A1
GENERAL INFORMATION:
                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1912
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Query Match 79.3%;
Best Local Similarity 79.2%;
Matches 95; Conservative
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Best Local S
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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                                                                                                                                            LENGTH: 240
TYPE: PRT
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74.8%; Pred. No. 2.8e-40;
Live 8; Mismatches 17
  Score 493.5; DB:
Pred. No. 5.6e-40,
9; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 127;
                                               Length 240;
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SEQ ID NO 512

LENGTH: 249

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-512
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PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-25
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SCFTWARE: PatentIn version 3.0
SEQ ID NO 80
Query Match 79.6%;
Best Local Similarity 77.0%;
Matches 97; Conservative
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Best Local Similarity 78.3%;
Matches 94; Conservative
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APPLICANT: Ruben et al
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TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID
TITLE OF INVENTION: TARASPORTER
PILE REFERENCE: 2183-4080US
CURRENT APPLICATION NUMBER: US/09/315,175
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: US/09/315,926
PRIOR PILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: EP 99201593.3
PRIOR APPLICATION NUMBER: EP 99201693.3
PRIOR APPLICATION NUMBER: EP 98201693.3
PRIOR APPLICATION NUMBER: EP 98201693.3
PRIOR PILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: EP 98201693.3
PRIOR PILING DATE: 1998-05-20
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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LOCATION: (1)..(248)
OTHER INFORMATION: /note="hCAT1 amino acid sequence"
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OTHER INFORMATION: Description of Artificial Sequence: phage
FEATURE:
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TYPB: PRT
ORGANISM: Artificial Sequence
FEATURE:
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o. US20030059937A1
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Score 495; DB 11; Length 249; Pred. No. 4.2e-40; 7; Mismatches 16; Indels
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Pred. No. 4.2e-40;
9; Mismatches 17;
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     6.
     Gaps
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GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
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US-09-880-748-1109
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US-10-041-860-33
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; ORGANISM: Homo sapiens
US-09-880-748-1109
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2011-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2011-03-21
PRIOR PILING DATE: 2011-03-21
PRIOR PILING DATE: 2011-03-21
PRIOR PILING DATE: 2011-03-21
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1109
LENGTH: 249
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Best Local Similarity
Matches 96; Conserv
                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                             Sequence 33, Application US/10041860 Publication No. US20030157109A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
APPLICANT: Peng, Xiao-
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OP INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
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US-10-325-694-150
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           CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-12-05
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR APPLICATION NUMBER: 09/379,784
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR APPLICATION NUMBER: 08/79,784
PRIOR APPLICATION NUMBER: 08/692,084
PRIOR APPLICATION NUMBER: 08/692,084
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Best Local S
Matches 97
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TITLE OF INVENTION: RECEPTORS AND USES THEREOF
FILE REFERENCE: 38164000
CURRENT APPLICATION NUMBER: US/10/325,694
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/99/403,107
PRIOR FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 152
SOFTMARE: PATENTIN Ver. 2.1
SEQ ID NO 150
LENGTH: 138
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/10010729 Publication No. US20030185827A1 GENERAL INFORMATION:
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-10-325-694-150
                                                                                                                                                                                                                                        APPLICANT: Rodriguez, Moses
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Pease, Larry R.
APPLICANT: Pease, Larry R.
TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
TITLE OF INVENTION: System
TITLE OF INVENTION: System
FILE REFERENCE: 1199-1-005CIP2
FILE REFERENCE: 1199-1-005CIP2
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FILING DATE: 1996-08-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97;
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o. US20030148463A1
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76.4%;
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Pred. No. 1.6e-40;
8; Mismatches 15
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; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-729-7
                                                                                                                                                                                                                                                                                                                                                                                    COURENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/273,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1394
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Publication No. US20030059937A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 97; Conserv
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Best Local Similarity
Matches 97; Conserv
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TITLE OF INVENTION: Antibodies that Immunospecifically
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                        LENGTH: 252
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                      112 QGTLVTVSS 120
121 KGTLVTVSS 129
                                                                                                  61 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEA------LWG 111
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                                                                           61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKEESYYDILTGYYVHYYGMDVWG
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                                                                                                                                                                              EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
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nilarity 80.8%;
Conservative
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75.2%; Pred. No. 3.8e-40;
ative 9; Mismatches 14
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Pred. No. 1.
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US-10-235-175-80
, Sequence 80, Application US/10235175
; Publication No. US28030166287A1
; GENERAL INFORMATION:

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US-10-269-805-21
; Sequence 21, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION;
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
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US-10-325-694-144
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; ORGANISM: Homo sapiens
US-10-269-805-21
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PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PATENTIN VERBION 3.1
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 144
LENGTH: 138
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Best Local Similarity
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CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/09/403,107
PRIOR FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 152
                                                                                                                                                                                                                                                               Query Match 80.1%;
Best Local Similarity 79.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN TITLE OF INVENTION: RECEPTORS AND USES THEREOF FILE REFERENCE: 38164000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
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121
                                        118 VSS 120
                                                                                                                                                                                                                                                98; Conservative
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                                                                                                             61 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAK---DLIESNIAEALWGQGTLVT 117
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                                                                                                                                                              QVQLQESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
VSS 123
                                                                               ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGPVDFDYGDYAIDYWGQGTLVT 120
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77.2%;
                                                                                                                                                                                                                                            Score 498.5; DB 15; Length 123; Pred. No. 8.9e-41; 6; Mismatches 16; Indels 3;
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Pred. No. 8.1e-41;
7; Mismatches 15;
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COURENT APPLICATION NUMBER: US/09/880,748
COURRENT APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-25
PRIOR PILING DATE: 2001-03-25
PRIOR PILING DATE: 2001-05-25
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                                                                                                                TYPB: PRT; ORGANISM: Homo sapiens US-09-791-153A-63
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US-09-880-748-1731
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; Publication No. US20030059937A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-791-153A-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local
Query Match 80.0%;
Best Local Similarity 80.8%;
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Deshpande, Rajendra
APPLICANT: Hitz, Anna
APPLICANT: Boyle, William
APPLICANT: Sullivan, John
TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
FILE REFERENCE: A-633A
                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/791,153A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/511,139
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 154
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l Similarity 75.2%;
97; Conservative
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  Score 497.5; DB pred. No. 1e-40; 5; Mismatches
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Pred. No. 1.9e-40;
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                                                              DB 11;
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        Indels
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                                                              Length 113;
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        7;
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                       499.5
498.5
497.5
496.5
495.5
                    494
493.5
493.5
493.5
                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       derived by analysis of the total
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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622
                                                                                                                                                                                                                                                                                                                                                          Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       December 30, 2003, 11:01:15 ; Search time 25.7352 Seconds (without alignments) 927.994 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      724715 seqs, 199017464 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 BVQLVESGGGLVQPGRSLRL.....IESNIAEALWGQGTLVTVSS 120
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                US-09-972-656-76
US-10-325-694-144
US-10-269-805-21
US-09-80-748-1731
US-09-80-748-1731
US-10-3125-694-150
US-10-3125-694-150
US-10-3125-694-1394
US-09-880-748-1394
US-09-880-748-1394
US-09-880-748-1109
US-09-880-748-1109
US-09-880-748-1109
US-10-041-860-331
US-10-041-860-331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          score distribution.
                                                                                                                                                                                                                                                                                                                                                          Description
                                                                               Sequence 76, Appl
Sequence 114, Appl
Sequence 21, Appl
Sequence 1731, Ap
Sequence 150, Appl
Sequence 150, Appl
Sequence 150, Appl
Sequence 1904, Ap
Sequence 80, Appl
Sequence 512, Appl
Sequence 512, Appl
Sequence 1109, Ap
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45	44	43	42	41	40	39	38	37	36	35	34	<u>ω</u>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
485	485.5	LD.	486	486	486	486	486	487	487	487	488	488	488	488		488.5	489	489	490	490	490	490	490	490	490.5		9		493
78.0	78.1	78.1	•		78.1	•	78.1	78.3	•		78.5	-	•	•		78.5	•	•	•	•	•	78.8	•		•		79.0		79.3
122	241	123	254	254	251	251	122	249	249	249	254	252	247	118	451	238	252	249	249	249	249	247	241	241	119	122	123	109	248
10	11	15	11	11	11	11	15	11	11	11	11	11	11	12	15	11	11	11	11	11	11	11	11	11	12	15	15	12	11
US-09-144-886-68	•	US-10-243-265-2		US-09-880-748-981	US-09-880-748-982	US-09-880-748-952	US-10-269-805-53	US-09-880-748-1956	\vdash	US-09-880-748-911	US-09-880-748-977	US-09-880-748-1519	US-09-880-748-924	US-10-120-377-78	-382-	US-09-880-748-1931	US-09-880-748-1627	US-09-880-748-1117	US-09-880-748-1115	-09	US-09-880-748-397	US-09-880-748-1330	US-09-880-748-1901		US-10-120-377-76		US-10-269-805-1	US-10-309-764-1	US-09-880-748-1890
Sequence 68, Appl	e 205	e 2,	e 14:	Sequence 981, App	e 98	e 95	e 53	e 1956	e 1119	e 911,	e 977,	e 1519	•	78,	17,		1627	1117	1115	e 1102,	e 397,	e 1330,	e 190:	e 188'	e 76	е 39,	e 1, ,	e 1, App	Sequence 1890, Ap

ALIGNMENTS

RESULT 1 US-09-972-656-76

Sequence 76, Application US/09972656 Publication No. US20030099647A1

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US-09-972-656-76
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Deshpande, Rajendra
APPLICANT: Teai, Mei-Mei
TITLE OF INVENTION: Pully Human Antibody Fab Fragments with Human Interferon-Gamma
TITLE OF INVENTION: Neutralizing Activity
FILE REFERENCE: A-799
FILE REFERENCE: A-799
                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 227
TYPE: PRT
                                                                                                                                                                                                                                                                               Match 80.5%; Score 501; DB 11; Length 227; Local Similarity 77.4%; Pred. No. 1e-40;
121
                                      117 TVSS 120
                                                                                                                        61 ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLI----ESNIAEALWGQGTLV 116
                                                                                  61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASDLVLTMTSRRAAFDIWGQGTMV 120
                                                                                                                                                                      1 QVQLVETGGGVVQPGRSLRLSCAASGPTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
                                                                                                                                                                                          1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDXYY 60
                                                                                                                                                                                                                                                             96; Conservative
TV8S 124
                                                                                                                                                                                                                                                             9; Mismatches 15; Indels 4;
                                                                                                                                                                                                                                                             Gaps
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RESULT 2

01-DEC-1999.

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                                                                                                                                                                 Query Match
Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New gene therapy vectors, useful for treating balloon angioplasty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-025491/03.
N-PSDB; AAZ38921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Es H, Verlinden S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-1998;
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                                                                                                                                                                                                                                                                                         present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Fig 16; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INTR-) INTROGENE BV
                                                                              319 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGITVTKSRFDYMGQGTLVTVSS 378
                       61 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS 120
                                                                                                                                                             ch 79.6%; Score 495; DB 21; Length 490; I Similarity 78.3%; Pred. No. 6e-39; 94; Conservative 9; Mismatches 17; Indels
                                                                                                                                                                                                                                                    490 AA;
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Search completed: December 30, 2003, 10:54:35 Job time : 38.6861 secs

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AAY56287
ID AAY56
XX AAY56
XX AAY56
XX O8-FE
DT O8-FE
XX HCAT1
XX Human
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated with aberrant ELyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CYID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JUN-2000;
17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel antibodies that immunospecifically bind to Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TWF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1014-1015; 3148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-114799/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200202641-A1
                                                                                       AAY56287;
                                                                                                                    AAY56287 standard; Protein; 254 AA
                             HCAT1 clone 25 antibody variable heavy chain protein sequence.
                                                           08-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM,
                                                                                                                                                                                            121
                                                                                                                                                                                                                       115 LVTVSS 120
 cationic
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                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                           invention.
                                                                                                                                                                                                                                                                                                                                                                       97;
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CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                            MVIVSS 126
                                                                                                                                                                                                                                                   ADSVKGRFTISRDNSKNTLYLQMNSLRABDTAVYYCAKDGYYDILTGYSYYGMDVWGQGT
                                                                                                                                                                                                                                                                              ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKD-----LIESNIAEALWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2000US-212210P.
; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                          (first entry)
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 amino
                                                                                                                                                                                                                                                                                                                                                                                   79.6%;
acid
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 transporter; hCAT1;
                                                                                                                                                                                                                                                                                                                                                                                   Score 495; DB 23;
Pred. No. 2.8e-39;
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hilbert D
                                                                                                                                                                                                                                                                                                                                                                       16;
targeted delivery;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 249;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLyS
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                                                                                                                                                                                                                                                                                114
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Synthetic.

Homo sapiens

targeted delivery;

Virus-like particle; ligand; gene delivery; envelope protein; hCAT1; human cationic amino acid transporter 1; retrovirus; adenovirus;

gene therapy; balloon angioplasty

hCAT1 binding human antibody molecule protein sequence

22-FEB-2000

(first

entry)

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RESULT 15
AAY56637
ID AAY56637
AC AAY56
XX 22-FB
XX 22-FB
XX V1rus
KW human
KW targe
XX Homo
OS Synth
XX X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a virus-like particle or gene delivery vehicle comprising a ligand capable of binding to a human amino acid transporter. The method is useful for the target delivery of substances to cells e.g. gene therapy. A human cationic amino acid transporter (hcarl) targeted adenovirus is useful for local applications of adenoviral vector e.g. in patients with restences following balloon angioplasty where smooth muscle cells need to be transduced with an adenoviral vector carrying the CeNOS cDNA. More efficient transduction of tissues can be carried out therefore resulting in lower multiplicity's of infections that can be used and therefore less vector associated toxicity to the tissues surrounding the target cells. AAZ38737 to AAZ38770, and AAY56264 to AAY56287 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene delivery; virus-like particle; retroviral envelope molecule;
infection; gene therapy; restenosis; balloon angioplasty;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New virus-like particle or gene delivery vehicle, useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Fig 16; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   smooth muscle cell; transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INTR-) INTROGENE BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   AAY56637 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ADSVXGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALMGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGITVTKSRFDYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVQLVESCGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽,
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                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.6%;
78.3%;
                                                                                                                                                                                                                                                                                                                                                     490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 495; DB 21;
Pred. No. 2.8e-39;
9; Mismatches 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 254;
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CC signaling with oligodendrocytes. An humanised antibody to (I) can be selected from antibody sHIGM22 (LVM 22), ebvHigM MSI19D10, ebv HigM CC CB2bGB, AKM44, CB21812, CB2187 or MSI19R5. (I) is useful for stimulating CC CNS axons, or treating demyelinating proliferation of glial cells in CC CNS axons, or treating demyelinating proliferation of glial cells in CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS in a mammal in need CC of such therapy. (I) is capable of binding to structures and cells within CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS (CC CNS.) or of treating a human being having multiple sclerosis, or a post-curval disease of CNS. (I) is also useful for stimulating the proliferation of glial cells from mixed cell culture. (CC condition in a subject. Methods where (I) is administered to a patient condition in a subject. Methods where (I) is administered to a patient condition in a subject. Methods where (I) is administered to a patient condition of disease, and other conditions in the CNS where nerves are damaged as by trauma. The present sequence represents the shigM22 heavy chain variable region clone A amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 97
                                                                                                                                                                                            BLys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis -
                                                                                                                                                                                                                                                                                                                                                          19-AUG-2002
                    15-JUN-2001; 2001WO-US19110
                                                           10-JAN-2002
                                                                                                  WO200202641-A1
                                                                                                                                       Homo sapiens.
                                                                                                                                                                              common variable
                                                                                                                                                                                                                                                                                                                   Human BLyS
                                                                                                                                                                                                                                                                                                                                                                                                 ABP45383
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP45383 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADSVKGRFTISRDNSKNTLYLQMNSLTADDTAVYYCAKGVTGSPTLD-YWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                 binding scFv SEQ ID 1394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; 219pp; English.
                                                                                                                                                                            immunodeficiency; acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 495.5; DB 23; Pred. No. 1.1e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Best Local S
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant BLyS expression and activity such as cancer, immune, and activity may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and activity such as cancer.
                                           BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficie systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                      19-AUG-2002
                                                                                                                                                                                                                                                                                                 ABP44501;
                                                                                                                                                                                                                                                                                                                                              ABP44501 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 2066-2067; 3148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CAMB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ibodies against B Lymphocyte Stimulating polypeptides, useful diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 OCTLVTVSS 120
                                                                                                                                                                                                        BLyS binding scrv SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN GENOME SCI INC
CAMBRIDGE ANTIBODY T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEA-----LWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVOLVOSGGGVVOPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 AA;
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; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-273499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                      entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.7%;
75.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TECHNOLOGY
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                                                                                                                                                                                                           ID 512
                                                                                                                                                                                                                                                                                                                                                 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 495.5;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
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                                                                                          immunodeficiency;
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Homo sapiens

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RESULT 10
AAY44995
JD AAY44995
AC AAY44
XX AAY44
AX AAY44
AX BDCA
DT 23-M3
XX HD70,
KW EPCAN
KW IL-2,
KW Antil,
KW leuka
XX Cytoo
KW antil,
PD 10-FI
XX ATA
XX ATA
XX ATA
XX HD70,
XX HD70,
XX HD70,
XX HD70,
XX HD70,
XX HD70,
XX HOMO
XX HOM
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Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             different (poly)peptides lack an intrinsic affinity for one another and are linked via the constant domains. The heterominibodies have cytostatic, immunostimulatory, antileukaemia and antiproliferative activities. These compounds can be used for diagnosing, preventing and treating malignant cell growth related to malignancies of haematopoietic cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the left chain of a heterominibody comprising HD70 single-chain FV (scFV) fragment N-terminally linked to human CH1 domain which bears at its Cterminus the human inflammatory cytokine granulocyte/macrophage colony stimulating factor (GM-CSF), plus a hexahistidine sequence for ease of purification. HD70 scFV specifically recognises the human epithelial cell adhesion molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HD70; single-chain Pv fragment; scPv; antibody; 17-1A antigen; human; EpCAM; epithelial cell adhesion molecule; inflammatory cytokine; IL-2; interleukin-2; Ck-domain; kerner chain constant domain; heterominibody; multifunctional compound; immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis; prevention; antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanomas and sarcomas.
                                                                                                                                                      WPI; 2000-195265/17
N-PSDB; AAZ50588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HD70scFv-Ck-interleukin 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY44995 standard; Protein;
                                                                New multifunctional compounds useful for preventing and/or treating malignant cell growth and for detection and diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200006605-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                            Kufer P,
                                                                                                                                                                                                                                                                                                          (MICR-)
                                                                                                                                                                                                                                                                                                                                                                 28-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia; solid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202
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97; Conserv
                                                                                                                                                                                                                                                                                                       MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
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                                                                                                                                                                                                                                         Dreier T,
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Pred. No. 4.7e-39;
8; Mismatches 15;
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RESULT 11
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Matches 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the right chain of a heterominibody comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to the comprising the constant domain of immunoglobulin-kappa light chain) which bears at its C-terminus the human inflammatory cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the human epithelial cell adhesion molecule (EpCAM) also called 17-1A antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HigM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide antiparkinsonian; neuroprotective; nootropic; vulnerary.
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                                                                                                                                                                                                                                                                                                                                         30-MAY-2000; 2000WO-US14902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200185797-A1
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                                                                     WPI; 2002-066596/09
                                                                                                                                       Rodriguez M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                         (MAYO-) MAYO FOUND MEDICAL EDUCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 EVQLLESGGGVVQPGRSLRLSCAASGFTPSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
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Pred. No. 4.7e-39;
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This is the amino acid sequence of the human D4.5 heavy chain variable region, used in the method of the invention. for providing receptors that can be used for targeting antigens in humans without being immunogenic themselves. Such receptors can be used for treating
                                                                                                                                    Claim
                                                                                                                                                                                                            Production of anti-human antigen receptors combination of functionally rearranged VH and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-FEB-1999
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                                                                                                                                                                                        expressed from
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                                                                                                                                                                                                                                                                                                                                                                               Raum T;
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Pred. No. 9.3e-40;
B; Mismatches 15
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Best Local :
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The patent discloses heterominibodies which are multifunctional compounds produceable in a mammalian host cell as a secretable and fully functional heterodimer of two polypeptide chains, where one of the polypeptide chains comprises, a CHI-domain (constant domain of an immunoglobulin heavy chain) and the other chain comprises CI-domain (constant domain of an immunoglobulin light chain). The polypeptide chains further comprise, fused to the constant domains at least two (poly) peptides having different receptor or ligand functions, where further at least two of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EpCAM; epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF; granulocyte/macrophage colony stimulating factor; heterominibody; CHI-domain; multifunctional compound; heavy chain constant domain; immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis; antiproliferative; prevention; treatment; malignant; haematopoietic cell; lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases such as tumours or auto-immune diseases, graft rejection after transplantation, infectious diseases by targeting cellular receptors as well as allergic, inflammatory, endocrine and degenerative diseases by targeting key molecules involved in the
                                                                                                                                                                                                                                                                                                                                New multifunctional compounds useful for preventing and/or treating malignant cell growth and for detection and diagnosis \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-195265/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dreier T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW15522 standard; Protein; 115 AA.
                                                                Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosi immune and inflammatory disease
                                                                                                                                                                  Bacon L, Gr
Tempest PR,
                                                                                                                                                                                                                             19-JAN-1996;
06-OCT-1995;
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                                          Claim 4; Fig
                                                                                                                                                                                                      (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
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                                                                                                                                                                                 Green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathogen infection; therapy.
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                                                                                                                                                                     een JA, J
Thompson
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                                         2a(i); 184pp; English
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95GB-0020486.
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Vaughan TJ,
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In TJ, Williams
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ms AJ;
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This polypeptide sequence comprises the VH domain of human antibody 2A-H11 (also known as 6H1), which is specific for transforming growth factor (TGF) beta-2. It is encoded by

8CFV

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RESULT 7
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binding domains of human antibodies (see AAW15522-40) to TGF beta-1 and/or beta-2 can be used to counter the adverse effects of TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-
c angioplasty restenosis, scleroderma, vascular disorders, cataract, glaucoma, or esp. neural scarring and glomerulonephritis, also (not claimed) osteoporosis), or (ii) immune and inflammatory diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases or macrophage pathogen infection). Nucleic acids encoding human antibody VH and VL can be used for prodn. of recombinant antigenbinding domains. These are highly specific, have low dissociation.
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Best Local S
Matches 97
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The invention relates to a method of identifying binding site domains (BSD) that retain the capacity of binding to a predetermined epitope when positioned C-terminal of at least one further domain in a recombinant bior multivalent polypeptide. The method comprises (a) testing a panel of BSD displayed on the surface of a biological display system as part of a fusion protein for binding to a predetermined epitope, where the fusion
                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                     Phage display system for identification retaining capacity to bind an epitope
                                                                                                                                                                                                                                                                                                                                      WPI; 1999-338004/28.
N-PSDB; AAX77236.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Borschert K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KUFE/) KUPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease;
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isease; scFv-antibody;
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Pred. No. 8.3e-40;
6; Mismatches 12
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16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 2468-2469; 3148pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         invention.
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97; Conser
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CAMBRIDGE ANTIBODY TI
                                                                                                                                                       EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
                                         ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIE------SNIAEALWG 111
                                                                                                                          QVQLVESGGGVVQPGRSLRLSCAASGFTPSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
ADSVKGRFT I SRDNSKNTLYLQMNSLRAEDTAVYYCARDRLEYYDILTGYYYYYGMDVWG
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                                                                                                                                                                                                                                                                                                                                                                           252 AA;
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2001US-27624BP.
2001US-277379P.
2001US-293499P.
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                                                                                                                                                                                                                                                                        80.1%;
75.2%;
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                                                                                                                                                                                                                                              Score 498.5; DB 2
Pred. No. 1.3e-39;
9; Mismatches 14
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ð. 참 청

Best Local Similarity

80.0%;

Score 497.5; DB 23; Pred. No. 6.9e-40;

Query Match

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RESULT 5
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                                                         The invention provides a neuromodulatory agent (I) capable of promoting CC neurite outgrowth, regeneration, remyelination and neuroprotection in CC central nervous system (CNS). (I) is capable of inducing remyelination, CC promoting cellular proliferation of glial cells, and promoting Callar proliferation of glial cells, and promoting Callar collidary proliferation of glial cells, and promoting Callar collidary (CB2DGS, AKJR4, CB21E12, CB2IS2), ebvHigM MSIJD10, ebv HigM CC CB2DGS, AKJR4, CB21E12, CB2IS7 or MSIJDE5 (I) is useful for stimulating collidaring disease of CNS. (I) is preferably useful for treating a demyelinating disease of CNS. (I) is preferably useful for treating a demyelinating disease of CNS. (I) is preferably useful for treating a numan being having multiple sclerosis, or a collidaring the proliferation of solutions multiple sclerosis, or a post-collidaring the proliferation of glial cells from mixed cell culture. (I) is also useful for stimulating remyelination of CNS axons. The condition in a subject. Methods where (I) is administered to a patient condition in a subject. Methods where (I) is administered to a patient condition in that causes demyelinating infection by a bacterium, virus or conditions in the CNS where nerves are damaged as by trauma. The present sequence represents conditions in the CNS where nerves are damaged as by trauma. The present sequence represents conditions in the CNS conditions conditions in t
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        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 23; Fig 17; 219pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MAYO-) MAYO
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Best Local Sim:
Matches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel polynucleotide (I) (a hybridizable polynucleotides) comprising a contiguous coding for a human antibody with factor VIII specific; hemostatic activity. (I) is useful a primer or probe i presence of inhibitory antibodies directed against fac polypeptides of the invention and the antibodies generate useful in compositions for neutralizing factor VII antibodies in hemophilia A patients. This sequence refactor VIII antibody A3-C1 specific scFv protein B35 win the method of the invention.
This invention describes a novel polynucleotide (I) (a hybridizable polynucleotides) comprising a contiguous coding for a human antibody with factor VIII specific hemostatic activity. (I) is useful a primer or probe presence of inhibitory antibodies directed against fac polypeptides of the invention and the antibodies generate useful in compositions for neutralizing factor VII antibodies in hemophilia A patients. This sequence rep
                                                                                                                                          New polynucleotide, polypeptide and antibody useful for presence of neutralizing antibodies against factor VIT treatment of hemophilia A patients with these antibod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY50968 standard; Protein;
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                                                                                                                                                                                               WPI; 2000-053102/04.
N-PSDB; AAZ43865.
                                                                                                                                                                                                                                                                                      08-MAY-1998;
                                                                                                                                                                                                                                                                                                                07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                               Human; heavy chain; antibody; factor VIII; hemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY50968;
                                                                                                                                                                                                                                    Voorberg JJ,
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100.0%; Pr
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Pred. No. 9.5e-52;
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                                          letecting the VIII. The
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Matches 120; Conserv
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                                                                                                                                                                                                                                                                                                                        This invention describes novel recombinant anti-human TNF-alpha human monoclonal antibody consisting of a heavy (H) chain and a light (L) chain. The recombinant anti-human TNF-alpha human monoclonal antibody can be produced stably in a high purity and in a large amount.
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 12-13; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant anti-human TNF-alpha human monoclonal antibody produced stably with a high purity, and in large amounts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody; H chain;
tumour necrosis factor; light
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Pred. No. 9.5e-52;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB seq length:
DB seq length:
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA]
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA]
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA]
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ALIGNMENTS

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Human FVIII antibody A3-C1 scFv heavy chain protein B35
                                    23-MAR-2000
                                                                                                        AAY50963 standard; Protein;
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Human; heavy chain; antibody; factor VIII; hemostatic; hemophilia A; scFv; A3-C1.

Homo sapiens

WO9958680-A2

99WO-NL00285

08-MAY-1998; 98EP-0201543

(SANQ-) STICHTING SANQUIN BLOEDVOORZIENING

Voorberg JJ, Van Den Brink EN, Turenhout BAM,

WPI; 2000-053102/04.

New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -

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C TISSUE=Mammary gland;

I ISOGAI T., Ota T., Nishikawa T., Hayashi K., Otsuki T.

A Isogai T., Ota T., Nishikawa T., Ishii S., Kawai-Hio Y.

A Suzuki Y., Nagai K., Sugano S., Ishii S., Kojima S., Nag

A Mammoto J., Wakamatsu A., Nakamura Y., Kojima S., Nag

A Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S.,

Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

"NEDO human CDNA sequencing project.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ database

EMBL; AKO74651; BAC11114.1;

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig-Like.

R InterPro; IPR003596; Ig_MHC.

R InterPro; IPR00306; Ig_MHC.

R InterPro; IPR00306; Ig_MHC.

R InterPro; IPR00306; Ig_MHC.
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SMART; SM00409; IG; 4.

SMART; SM00407; IGC1; 2.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS508290; IG MHC; 1.
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Q8NCL6;
Q1-QT-2002 (TrEMBLrel. 22, Created)
Q1-QT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ90170.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
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119 AA; 13025 MW; F6E904044381CA7C CRC64;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC021276; AAH21276.1; -.
InterPro; IPR0070110; Ig-1ike.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003596; Ig_v.
R Pfam; PF00047; 1g; 4.
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InterPro; IPR007110; Ig-like.
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InterPro; IPR003596; Ig_v.
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SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UL72

Q9UL72;
Q9UL72;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                        NON TER
                                                                                                                                                                                                                                                                                          Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
SEQUENCE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Tonsil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89;
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  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKHGSGSYIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al protein.
573 AA; 62967 MW;
                                                                   118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                      ξ,
                                                                      12872 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.1%;
71.8%;
  67.2%;
72.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 436; DB
; Pred. No. 2.4e-
6; Mismatches
  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Eut
Catarrhini; Hominidae; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FD072344033AC530 CRC64;
                                                                      B4D1A5944B2D5CCA CRC64;
  418;
No.
                                                                                                                                                                                                                                                                                                                                                                                                     Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .4e-37;
es 25; Indel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                                                                                                                                                                                                                                          Berney
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RESULT 13
Q91Z05
ID Q91Z0
AC Q91Z0
AC Q91Z0
DT 01-DE
DT 01-MA
DE Hypot
GN AUU6 14
OS MUS 11
OC BUKAI
OC MAMMAN
OC MAMMAN
OC MIS 11
CRN (11)
RN Q920B7
ID Q920B
AC Q920B
AC Q920B
DT 01-DB
DT 01-MA
DB Pteri
DB (Frag
OS Mus m
OC Bukar
OC Mamma
OX NCBL
RN [1]
RN [1]
RP SEQUE
RT "Defi
RT in Ma
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Best Local S
Matches 83
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                                                                                                                                                                                                                                                                         Q920B7
Q920B7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; 1g; 3.

SMART; SM00406; IGv; 1.

PROSITE; PS00199; CYTOCHROME C; 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS00290; IG MHC; 1.

Hypothetical protein.

SEQUENCE 473 AA; 51946 MM; CF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Atkin J.D., Iape A., Jenning
"Definition of the Idiotope
in Mammalian Cells.";
                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUL-2001) to the
EMBL; BC010327; AAH10327.1;
MGD; MGI:2144967; AU044919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata;
Bukaryota; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:2144967; AU044919.
InterPro; IPR000345; CytC hem
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADSVKGRPAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIABALWGQGTLVTVSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAMYYCARELWLRRI - - DYWGQGTTITVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVOLVESGGGLVKPGGSRKLSCAASGFTFSDYGMHWVRQAPEKGLEWVAYINSGSTTIYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAFYYCARDRFGEFLFD-YWGQGTLVTVSS
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69.2%;
                                      Jennings I
liotope of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heme_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 416; DB 11;
Pred. No. 2.4e-35;
9; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
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                                                                                                                                                                                                         Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CF625F008932AF12 CRC64;
                                   Pterin-Mimicking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                      Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 473;
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                                                                                                                                                                                                             Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi; 
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                               region
                                                                          R.G.
                                      Expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
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RANDER PRESENTATION OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   유 성
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InterPro; IPRO07110; Ig_like.

InterPro; IPRO0306; Ig_MHC.

InterPro; IPRO03596; Ig_v.

Fram; PF00047; ig; 4.

SMART; SM00406; IGV; 1.

PROSITE; PS00835; IG_LIKE; 4.

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01-JUN-2002 (TREMBLrel. 21, Las
01-MAR-2003 (TREMBLrel. 23, Las
Hypothetical protein.
Homo sapiens (Human).
Bukaryotes, Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
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Q9UL91;
01-MAY-2000
01-MAY-2000
01-MAR-2003
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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PROSITE;
NON_TER
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035023; AAD56259.1; -.
HSSP; P01772; 2FB4.
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                                                                                                     Pfam, PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                  "Myosin-reactive autoantibodies
fetus.";
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                                                                                                                                                                                                                                                                                                                                                                    Young D.C.
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                                                                       9850835; IG_LIKB;
  118
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  12843 MW;
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, Last sequence up
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Pred. No. 4.4e-38;
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Catarrhini; Hominidae;
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Catarrhini; Hominidae;
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RESULT 11
Q8WU38
ID Q8WU3
AC Q8WU3
DT 01-W
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Best Local S
Matches 87
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A Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Nishikawa T., Nagai K., Sugano S., Shiracori A., Sudo H.,

A Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

A Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

A Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

A Watanabe S., Kimura K., Nakamura Y., Najahari K., Masuho Y.,

A Ninomiya K., Iwayanagi T.;

A Ninomiya K., Iwayanagi T.;

A Ninomiya K., Iwayanagi T.;

I "NEDO human cDNA sequencing project.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

BE EMBL; AKOZ7379; BAB55072.1; -.

BR EMBL; AKOZ7379; BAB55072.1; -.

BR InterPro; IPR003006; Ig_MHC.

BR InterPro; IPR00396; Ig_MHC.
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Q8WU38;
Q8WU38;
01-MAR-2002
01-MAR-2002
01-MAR-2003
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Q96K68;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical protein FLJ14473.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; 19; 4.

SMART; SM00406; IGv; 1.

PROSITE; P850835; IG LIKE; 4.

PROSITE; P800290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein SEQUENCE 494 AA;
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87; Conserv
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  (TrEMBLrel. (TrEMBLrel.
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                                                                                               PRELIMINARY;
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74.8%;
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Pred. No. 1.9e-38;
8; Mismatches 20
  Created)
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Last annotation updat
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Q9UL71,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                            "Myosin-reactive autoantibodies in fetus.";
Clin. Immunol. Immunopathol. 87:184
EMBL; AF035043; AAD56279.1; -.
HSSP; P01772; 2FB4.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
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EMBL; AF035030; AAD56266.1; -.
HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Dfam. DF0A77: (2.1)
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Young D.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI
                                                                                                                                                                                                                                                            Wu X., Liu B., Van Young D.C.;
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
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IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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122 AA;
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73.4%;
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                                                                                                                                                                                                                                                                                         P.L.,
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Pred. No. 6
                                                                                                                                                                  87:184-192(1998)
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Catarrhini; Hominidae;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ da
EMBL; BC015760; AAM15760.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 5.
Pfam; PP000406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50835; IG_LIKE; 5.
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SMART; SM00406; IGv; 1
PROSITE; PS50835; IG_L
NON TER 121 121
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Q96BB9;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat.
Bukaryota; Metazoa; Primates; Catarrhini; Hominid.
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Similarity 71.2%;
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                                                                                                                                   ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKD-----LIESNIABALWGQGTL
                                                  SSALA
                                                                                                    ADSVKGRFTISRDNSRDTLYLOMNSLRAEDTAVYYCAKDPRGYSASGNYTREDYWGQGTL
     SSAIA
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121 AA; 13154 MW;
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  144
                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                              65039 MW;
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71.3%;
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                                                                                                                                                                                                                                                                                                    Score 444.5; DB 4;
Pred. No. 3.3e-38;
8; Mismatches 23;
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Pred. No. 4e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2F045CCFA5D50736 CRC64;
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Best Local Similarity
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Q9UL90;
01-MAY-2000
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Q9UL93;
01-MAY-2000
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NON_TER
SEQUENCE
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
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Young D.C.;
"Myomin-reactive autoantibodiem in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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01-MAR-2003
                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                 01.MAY-2000 (TrEMBLrel. 13, Created)
01.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01.MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clin. Immunol. Immunopathol. EMBL; AF035024; AAD56260.1; HSSP; P01772; 2FB4.
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  InterPro;
InterPro;
                                          Clin. Immunol. Immunopathol. 87:184-192(1998) EMBL; AP035021; AAD56257.1; -. HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fetus."
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                                                                                                         fetus.";
                                                                                                                                                  Wu X., Liu B., Van der Young D.C.;
                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
Van der Merwe P.L.,
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                                                                                                                                "Myosin-reactive autoantibodies
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IPR007110; Ig-like IPR003006; Ig_MHC.
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113 AA;
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(TYEMBLrel 13, Last sequence update)
(TYEMBLrel 23, Last annotation update)
Live immunoglobulin heavy chain variable
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80.8%;
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Pred. No. 1.2e-44;
4; Mismatches 12
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Catarrhini; Hominidae;
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Catarrhini; Hominidae;
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Best Local (
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Eukaryota; Metazoa; Cl
Mammalia; Eutheria; P:
NCBI_TaxID=9606;
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01-NOV-1999
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IGLIKE; 1.

NON TER 1 1 116

NON TER 116 116
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"A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers." Leukemia 9:1948-1953(1995).

EMBL; S80866; AAD14339.1; -.

HSSP; P01772; 2EB4.
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NON TER 1 1 1
SEQUENCE 147 AA; 15768 MW;
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SMART; SM00406; IGv; 1.
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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116 AA; 12434 MW;
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Pred. No. 2.3e-43;
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Pred. No. 9.4e-41;
3; Mismatches 14
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Q8n5k4 homo sapien
Q9ylb6 homo sapien
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Q9yka4 mus musculu
Q91wp5 mus musculu
Q91207 mus musculu
Q9u188 homo sapien
Q8r3v9 mus musculu
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Q9r164 oryctolagus
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Q9u192 homo sapien
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Q9u195 homo sapien
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6: sp_mammal:*
7: sp_mhc:*
9: sp_phage:*
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Copyright (c) 1993 - 2003 Compugen
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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RINterPro; IPR007110; Ig-1ike.
RINterPro; IPR003106; Ig_MHC.
RINterPro; IPR003596; Ig_V.
REAM; PF00047; 1g; 5.
R Pfam; PF00047; 1g; 5.
R SMART; SM00406; IGV; 1.
R PROSITE; PS05035; IG LIKE; 5.
R PROSITE; PS05035; IG MHC; 3.
W Hypothetical protein.
Q SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;
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OBWUK1; PREMBLrel. 20, Created)

O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)

O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
Homo sapiens (Human).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                         ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLIESNIAEALMGOGTLVTVSS 120
    ADSVKGRFTISRDNSKVTLYLQMNSLRAEDTAVYYCAKDWSEGVETFDIWGQGTMVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.5%; Score 513; DB 4
larity 81.7%; Pred. No. 2e-45;
Conservative 7; Mismatches
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Indels

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Gaps

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RESULT 15
HV3N
ID HV3N
ID HV3N
AC P0177
AC P0177
DT 21-JU
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DE IG he
OS HOMO
OC EUKax
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RN [1]
RN [1]
RN [1]
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Best Local S
Matches 81
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PO1775;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-Yeavy chain V-III region LAY.
SEQUENCE.

MEDLINE-75046755; PubMed=4139708;

MEDLINE-75046755; PubMed=4139708;

Capra J.D., Kehoe J.M.;

"Structure of antibodies with shared idiotypy: the complof the heavy chain variable regions of two immunoglobulianti-gamma globulins.",

Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).

-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region POM.
Homo sapiens (Human)
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin v region.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLOBULIN ACTIVITY.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02057; M3HUPM.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-gamma globulins.";
Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WIT)
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Capra J.D., Kehoe J.M.;
"Structure of antibodies with shared idiotypy: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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81; Conserv
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119 A
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/FTId=VAR_003966.
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NTI-GAMMA

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Best Local S
Matches 79
                                                                                                                                                                                                                                                                                                                    GLOBULIN ACTIVITY.

-!- SIMILARITY: Contains 1 immunoglobulin-like PIR; A02058; M3HULY.

HSSP; P01772; 2FB4.

G0; G0:0005576; C:extracellular; NAS.

G0; G0:0005823; F:anntigen binding activity; NA

G0; G0:0006955; P:immune response; NAS.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                       Pfam; PF00047; 19; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1

Immunoglobulin V region.

DOMAIN 1 112

NON TER 119 119

SEQÜENCE 119 AA; 12858 MM
rch completed: December time : 6.43379 secs
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                                                                                                             N
                                                                                                                              2 VQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYYA 61
                                                                                                                                                                   . Similarity 79; Conserv
                                                    DSVKGRFAISRDNAKVTLYLQMNSLTIEDTAVYYCAKDL--IESNIAEALWGQGTLVT 117
                                                                                                           VQLLESGGGLVQPGGSLRLSCAASGFTFSASAMSWVRQAPGKGLEWVAWKYENGNDKHYA 61
                                                                                                                                                                 62.9%; Score 391; DB 1; llarity 66.9%; Pred. No. 2.4e-34; Conservative 11; Mismatches 26
                                                                                                                                                                                                                           12858 MW; D6338098794DCF5E CRC64;
             30,
             2003,
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              10:55:53
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Best Local
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3F HUMAN

HV3F HUMAN

STANDARD;

P01767;

P01767;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequenc

15-SBP-2003 (Rel. 42, Last annotat

19 heavy chain V-III region BUT.
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Pfam; PF00047; 1g; 1.

Pfam; PF00047; 1g; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

PROSITE; PS50835; IG LIKE; 1.

IG-LIKE.

PYRROLIDONE CARBOXYLIC

PYRROLIDONE CARBOXYLIC
Immunoglobulin '
DOMAIN 1
NON TER 115
SEQÜENCE 115
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GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc.
                                                                                                                    HSSP, P01789; IMCP.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                             "Complete amino acid sequence of the alpha 2 heavy chaing immunoglobulin of the AZm (2) allotype.", proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).

-i- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, AZM(2) REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.

-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                       MEDLINE=78137069;
Torano A., Putnam
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
                                                                                                                                                                      PIR; A02050; A2HUBU.
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROWALDENSTROM'S MACROGLOBULINEMIA.
SIMILARITY: Contains 1 immunoglobulin-like domain
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MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOC
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; P01772; 2FB4.
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                                   PS50835; IG LIKE;
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 115
115 AA;
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F.W.;
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Pred. No. 1
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                         IG-LIKE.
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  208876A7DF52DCF4
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RESULT 13
RESULT 10
REPORTS
ID HV02 CANPA
ID HV02 CANPA
ID HV02 CANPA
ID HV02 CANPA
ID HOSE
IT 21-JUL
DT 21-JUL
RA Wasser
RT Infanta
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Matches 75
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Best Local (
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HSSP; P01772; 2FB4.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PP00047; Ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

Immunoglobulin V region.
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NON TER
SEQUENCE
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V region MOO.
Canis familiaris (Dog).
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MCCumber L.J.; Capra J.D.;
MrcCumber E.J.; Capra J.D.;
MrcCumber E.J.; Capra J.D.;
MrcCumber L.J.; Capra J.D.;
MrcCumber L.J.; Capra J.D.;
MrcCumber L.J.; Capra J.D.;
Mol. Immunol. 16:565-570(1979);
MrcCumber L.J.; Capra J.D.;
Mr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wasserman R.L., Capra J.D.; Primary structure of the variable immunoglobulin heavy chains."; Biochemistry 16:3160-3168(1977).
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MEDLINE=77242268; PubMed=407924;
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Mammalia, Butheria; Carnivora; Pissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 113-117
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79; Conservative
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Pred. No. 2.9
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Pred. No. 3.8e-35;
9; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE
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Canis.
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GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; F:antigen binding activity; NAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003506; Ig_WHC.

InterPro; IPR003506; Ig_V.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V region MOPC 21 precursor (Fragment).
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PROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure
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                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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           MEDLINE=81234548; PubMed=6788376; Bothwell A.L.M., Paskind M., Reth
                                           SEQUENCE FROM N.A.
                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                  P01783;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
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Sciurognathi;
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MEDIJINE-83273707; PubMed=6410398; Goni F., Frangione B.; Goni F., Frangione B.; "Amino acid sequence of the Fv region of a human monoclonal : (protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33.";

Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

Craniata; Vertebrata; Catarrhini; Hominidae;

Hominidae,

Euteleostomi;

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P01763;
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pDB; IIGC; 03-JUN-95.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V-III region WEA.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable recell 24:625-637(1981).
                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adetugbo K., Milstein C., Secher D
"Molecular analysis of spontaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=77100368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 17-136.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mmunoglobulin
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                                                                                                                                                                                                                                                                                                                       82;
                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                           EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50835; IG LIKE; bulin V region; S:
                                                                                                                                                                                                                              ADTVKGRFTISRDNPKNTLFLQMTSLRSBDTAMYYCARWGNYPYYAMDYWGQGTSVTVSS
                                                                                                                                                                                                                                               ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS
                                                                                                                                                                                                                                                                            DVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTLHY
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120
38
75
89
115
120
136
136
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                           STANDARD;
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tein C., Secher
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136
112
78
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115
120
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68.3%;
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DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).
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D SEGMENT.
JH4 SEGMENT.
                                                                                                                                                                                                                                                                                                                                 Score 405; DB 1;
Pred. No. 9.4e-36;
                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                   2276A98DBDBF7016 CRC64;
                                                                                                                                                                                                                                                                                                                        Mismatches
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RESULTU
ID THYSLLHU
ID THYSLHU
ID THYSLHU
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DT 155
DT 211
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DT 211
DT 155
DT 15
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GO; GO:0006955; P:immune
GO:0006955; P:immune
R InterPro; IPR003906; Ig_MHC.
JR InterPro; IPR003906; Ig_V.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF000406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
Tmmunoglobulin V region; Glycoprotein; Pyrrolidone carb xylic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
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Best Local S
Matches 80
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Best Local Similarity
Matches 83; Conserv
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SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HV3L_HUMAN
P01773;
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NON TER
SEQUENCE
                                                                                                                                                  Immunoglobulin 1
DOMAIN 1
MOD RES 1
DISULFID 22
CARBOHYD 28
NON TER 119
SEQUENCE 119
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V-III region BUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE (MYELOMA PROTEIN BUR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A02056; A1HUBR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0005576;
GO:0003823;
GO:0006955;
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                                                                 Similarity
80; Conser
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EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLE
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F:antigen binding activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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67.2%;
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Pred. No. 4.2e
10; Mismatches
                                                                 Score 416.5;
Pred. No. 4.9e
L2; Mismatches
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                                                                                                                                                      12A709A75344D024 CRC64;
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4.2e-37;
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4.9e-37;
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HV3C HUMAN
ID HV3C HUMAN
ID HV3C HUMAN
AC P01764;
DT 21-JUL-1986
DT 21-JUL-1986
DT 15-SEP-2003
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Best Local (
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SMART; SMO0406; IGv; 1.
SMOSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
TOMBIN 1 112
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21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
15 heavy chain V-III region DOB.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steiner L.A., Garcia Pardo A., Margolies M.N.; "Amino acid sequence of the heavy-chain variable crystallizable human myeloma protein Dob."; Biochemistry 18:4068-4080(1979).
                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A90431; G1HUDB.
HSSP; PO1772; 2FB4.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0003823; F:antigen binding act
G0; G0:0006955; P:immune response; NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 18:4054-4067(1979)
-!- MISCELLANEOUS: THIS GAMMA-1
HINGE REGION. THERE ARE NO
DISULPIDE BONDS.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=80020920; PubMed=114208;
Steiner L.A., Lopes A.D.;
"The crystallizable human myeloma protein Dob has a hinge-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRYSTALLIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                     EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
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                                                                                                                                 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALMGQGTLVTVSS
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120 AA; 13440
(Rel. 01, Created)
(Rel. 01, Last sec
(Rel. 42, Last and
                                                                                                                                                                                                                       Conservative
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                                                    STANDARD;
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                                                                                                                                                                                                                                   66.4%;
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ARE NO LIGHT-HEAVY OR INTER-
                                                                                                                                                                                                                                                                          ₹
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                                                                                                                                                                                                                                                                                                                                                                                                       binding activity; response; NAS.
                                                                                                                                                                                                                        8
                                                                                                                                                                                                                       Score 413; DB 1;
Pred. No. 1.2e-36;
8; Mismatches 30
                                                                                                                                                                                                                                                                                                    IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                          880DDE307C4B2627 CRC64;
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                                                                                                                                                                                                                                                 Length 120;
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sequence up

update)

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PIR; A02055; G1HUKL.

PIR; APRIS, 2F84; 12-JUL-89.

PDB; 2F84; 12-JUL-89.

PDB; 2IG2; 12-JUL-89.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0006955; P:immune response; NAS.

AR GO; GO:0006955; P:immune response; NAS.

AR GO; GO:0006955; P:immune response; NAS.

AR GO; GO:0006955; P:immune response; NAS.

AR GO; GO:0006955; P:immune response; NAS.

AR GO; GO:0005576; Ig_MGC.

DR InterPro; IPR003006; Ig_MGC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PP00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

TMMUNOGlobulin V region; 3D-struct

TMMUNOGlobulin V region; 3D-struct

TMMUNOGlobulin V region; 3D-struct

TMMUNOGlobulin V region; 3D-struct
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P01772;
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MEDLINS-83289131; PubMed=6884994;

Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;

"Three-dimensional structure determination of antibodies structure of crystallized monoclonal immunoglobulin IgG1 Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Home.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region KOL.
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Immunoglobulin V region; Pyrrolidone carboxylic
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SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-81072295; PubMed=7441755;
Marquart M., Deisenhofer J., Fluber R., Palm W.;
"Crystallographic refinement and atomic models of the in-
immunoglobulin molecule Kol and its antigen-binding frag-
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InterPro; IPR003006;
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-I- SIMILARITY: Contains 1 immunoglobulin-like domain
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122 AA;
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nilarity 63.1%;
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13166 MW; 74E5B6959E84100A CRC64;
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Ig_MHC.
                                                                         3D-structure; Pyrrolidone carbo ylic
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Pred. No. 1.3e-39;
4; Mismatches 19
                          PYRROLIDONE CARBOXYLIC ACID
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P01781;
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21-JUL-1986 (Rel. 01, Created)
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15-SEP-2003 (Rel. 42, Last annot;
The heavy chain V-III region GAL.
-!- SIMILARITY: Contains
PIR; A02064; M3HUGL.
HSSP; P01772; 2FB4.
                       MEDLINE-75059123; PubMed=4803843;
Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
"The primary structure of a monoclonal IgM-immunoglobulin
"The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), II: the amino acid sequence of the H-chain (mutype), subgroup H III. Architecture of the complete IgM-molecule.";
typel, subgroup H III. Architecture of the complete IgM-molecule.";
Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                        HUMAN
                                               Hilschmann N.;
                                                                                                                                      NCBI_TaxID=9606;
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                                                       REVISION TO 28-33.
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               immunoglobulin-like domain
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Pred. No. 9.
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                               ISOLATED FROM A WALDENSTROM'S
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RESULT 3
HV3J_HUMAN
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AC P01771;
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HSSP; P01772; 2PB4.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; F:antigen binding activity; NAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-11ke.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003096; Ig_WHC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 1

SMART; SM00406; IGv; 1.
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P01770;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence upda
15-SEP-2003 (Rel. 42, Last annotation upda)
19 heavy chain V-III region NIB.
21-JUL-1986 (Re.
21-JUL-1986 (Re.
15-SEP-2003 (Re.
15 heavy chain V
Homo sapiens (Hu
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PROSITE; PS50835
Immunoglobulin V
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"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                           Similarity
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bulin V region; Pyrrolidone carboxylic acid
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                                                                                                                                                                       ADSVNGRFTISRNDSKNTLYLMMNSLRPEDTAVYYCAR-IRDTAMFFAHMGQGTLVTVSS
                                                                                                                                                                                                                               QVQLVQSGGGVVQPGRSLRLSCAASGFTFSRYTIHWVRQAPGKGLEWVAVMSYBGBBKHY
            ; (Rel. 01, Created)
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      (Human)
                                                                                             STANDARD;
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71.7%;
                                 Last sequence update)
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                                                                                                                                                                                                                                                                                           17; Mismatches
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Pred. No. 6.2e-41;
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PYRROLIDONE CARBOXYLIC ACID
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RESULT
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Best Local
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HUMAN
                                                                              SEQUENCE.

MEDLINE=74175307; PubMed=4208843;
Florent G., Lehman D., Putnam F.W.;

"The switch point in mu heavy chains
Biochemistry 13:2482-2498(1974).

-!- MISCELLANEOUS: THIS CHAIN WAS ISC
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P01769;
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SMART; SM00406; ICv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic DOMAIN
1 112
IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chiu Y.-Y.H., Lopez (
"Amino acid sequence cryoimmunoglobulin Ig
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Biochemistry 18:553-560(1979)
MACROGLOBULIN

I SIMILARITY: Contains 1 immunoglobul
PIR; A02052; M3HUGA.
HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:000823; F:antigen binding activ
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Create
21-JUL-1986 (Rel. 01, Last s
15-SEP-2003 (Rel. 42, Last a
Ig heavy chain V-III region
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GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Chiu Y.-Y.H., Lopez de Castro J.A.,
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Mammalia; Eutheria;
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121 AA;
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(Rel. 01, Last sequence up
(Rel. 42, Last annotation
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13566 MW;
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Primates;
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70.2%;
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             binding activity;
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                                                           immunoglobulin-like
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Pred. No. 8.1e
14; Mismatches
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Gapop 10.0 , Gapext 0.
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119 SS 121 SS	61 ADS : 61 ABS		atch cal 8	InterPro; IPRO Pfam; PF00047; SMART; SM00406 PROSITE; PS508 ITMUNDGIObulin DOMAIN MOD_RES NON_TER 12	HSSP; P01772; 2FB4. GO; GO:0005576; C:extracellular; N GO; GO:0003823; F:antigen binding GO; GO:0003823; P:immune response; InterPro; IPR0070110; IG MIC InterPro; IPR0070110; IG MIC	Proc. Natl. Aca -:- MISCELLANEO -:- PATIENT WIT -:- SIMILARITY: PIR: A02051: M3	SEQUENCE. SEQUENCE. MEDLINE=810: Lehman D.W. Pamino acid	21-JUL-1986 (Rel. 01, 21-JUL-1986 (Rel. 01, 15-SEP-2003 (Rel. 42, 15 heavy chain V-III Homo sapiens (Human). Eukaryota; Metazoa; C Mammalia; Eutheria; P NCBI TaxID=9606;	AN G HUMAN	358.59 357.55 357.55 357.55 357.55 357.55 357.55
120 122	SUKGRFAIS	EVQLVESGGGLVQPGRSLRLS : :	Similarity 9; Conservat	PR003596; 147; ig; 1 406; IGV; 50835; IG lin V reg 1 1 1 122 AA;	2; 2FB4. 576; C:ex 823; F:ar 955; P:in PR007110;	MISCELLANEOUS: THIS MU CHAIN WAS PATIENT WITH MACROSLOBULINEMIA. SIMILARITY: Contains 1 immunoglol A0205; M3HUAM.	ICE. 1D.W., Putnam F.W. acid sequence of 1	B6 (Rel. 01, 386 (Rel. 01, 386 (Rel. 01, 386 (Rel. 42, 203 (Rel. 42, 204) (Rel. 4	STANDARD	57.5 57.6 57.6 57.5 57.2 57.2 57.2 57.2
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	TLYLOMN	LRLSCVD	, ``	E; 1. Pyrrolidone Pyrrolidone PyRROLIE B MW; A42D06	llular; Ni binding a response; ike.	CHAIN ULINEMI immuno	774332; le variable		AL PRT	HV30 HV31 HV11 HV11 HV12 HV23 HV23 HV22 HV22 HV22
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	BLVBSGGVVZFGRSLKLSCAASGFTFSNYAMHWVRQFFGKGLEWVAVISYBG SVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIABALMGQG 	CVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY	B 1; e-43; 17;	في ا	ty; NAS.	(198 TED like	Of a	odate) update) ; Vertebrata; ini; Hominidae	AA.	
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Ig heavy chain precursor V region (mu) - human (fragment C; Species: Homo sapiens (man)
C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text C; Accession: S70442
R; Culsinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, Mol. Immunol. 29, 1363-1373, 1992
A; Title: IgM kappa/lambda EBV human B cell clone: an ear A; Fitle: new respectively for the content of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residuse: 1-133 <TIM>
A;Residuse: 1-133 <TIM>
A;Residuse: 1-133 <TIM>
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:64471, NCBIP:64470)
C;Superfamily: immunoglobulin vegion; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement A;Reference number: A49028; MUID:92008140; PMID:1915549
A;Accession: A49028
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C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: A49028
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A;Residues: 1-140 <CUI>
C;Superfamily: immunoglobulin V region; immuno
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVLQAPGKGLEWVAVIWYDGSNKYY
                                                                                                                                                                                                                                                                                                                         EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
                                                                                                                                            ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR-RLTIAAAGNFDYWGQGTLA 119
                                                                                                                                                                                                          ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLIESNIAEA----LWGQGTLV 116
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78.3%;
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78.2%;
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Pred. No. 1.4e
6; Mismatches
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Pred. No. 8.8e-39;
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. 1.4e-38;
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submitted to the EMBL Data Library, October 1994

A;Description: Molecular characterization of natural human anti-Sm autoantibodic
A;Reference number: S48797

A;Reference number: S48797

A;Reseidues: 1-128 <MAH>
A;Residues: 1-128 <MAH>
A;Residues: 1-128 <MAH>
A;Cross-references: EMBL:Z46379; NID:g587147; PIDN:CAA86512.1; PID:g1340168

A;Cross-references: EMBL:Z46379; NID:g587147; PIDN:CAA86512.1; PID:g1340168

A;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A;Title: The repertoire of human germline V(H) sequences reveals about fifty growth: File: The repertoire of human germline V(H) sequences reveals about fifty growth: Nacession: S26885; MUID:93021117; PMID:1404388

A;Residues: 1-98 <TOM>
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12350; NID:g32922; PIDN:CAA78220.1; PID:g32923
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C;Accession: S48797; S26893
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
S48797
                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14177; NID:g31020; PIDN:CAA78546.1; PID:g31021
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region - human (fragment)
c;Species: Homo sapiens (man)
c;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31701
C;Accession: S31701
C;Accession: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
S31701
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Best Local Similarity
Matches 94; Conserv
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61 ADSVKGRPAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALMGQGTLVTVSS
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                                                                                                                   1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
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                                                                                   QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
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75.0%;
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78.3%;
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Pred. No. 2e-38;
8; Mismatches
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Pred. No. 1.5e-38;
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A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14932.33-14932.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: E36005
                                                                                                                                                                                                                                                       R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19666
                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region (VH3DJH4) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19666
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A;Molecule type: mRNA
A;Residues: 1-122 <SCH>
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A;Residues: 1-121 <MAR>
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                                                                                                                                          ;Cross-references EMBL:X61646; NID:g37688; PIDN:CAA43827.1; P;Superfamily: immunoglobulin V region; immunoglobulin homology;Reywords: heterotectramer; immunoglobulin homology;15-98/Domain: immunoglobulin homology <IMM>
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Best Local
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                                                                          97;
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                     EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
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78.7%;
                                                                                        79.3%;
80.2%;
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Pred. No. 2.1e-39;
8; Mismatches 16
                                                                   Score 493.5; DB 2
Pred. No. 2.3e-39;
6; Mismatches 1:
                                                                                                       DB 2;
                                                                       17;
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                                                                       Indels
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k; Kaaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Recession: S31117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region - human (fragment)
c;Species: Homo sapiens (man)
c;Species: Homo sapiens (man)
c;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31679
C;Accession: S31679
C;Accession: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity opera
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A; Accession: S31679
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-134 < CUI>
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                                                                                                                                                     Score 489.5; DB 2
Pred. No. 6.1e-39;
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20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMMWVRQAPGKGLEWVAVISYDGSNKYY 79

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Ig neavy Chark (man)
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31112
C;Accession: S31112
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timmers, F.M
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Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin A;Reference number: A36005; MUID:90349571; PMID:2117273
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C;Species: Homo sarion
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C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-119 <SCH>
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A;Accession: F36005
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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A;Title: Restricted utilization of germ-line V(H)3 genes
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31112
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A;Gene: GDB:IGH@; IGHDY1
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Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
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Pred. No. 3.5e-40;
7; Mismatches 14
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                               Score 500; DB 2;
Pred. No. 5.6e-40;
7; Mismatches 17
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: GB:M34031
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
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C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990
C:Accession: G36005
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-114 <FIG>
A;Cross-references: EMBL:Z31686; NID:g509782; PIDN:CAA83491.1; PID:g1335143
A;Cross-references: EMBL:Z31686; NID:g509782; PIDN:CAA83491.1; PID:g1335143
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Title: In vitro assembly of repertoires of antibody chains A;Reference number: $46390; MUID:94254092; PMID:8196048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46390
                                                                                                                                                                                                                                                                                                                                                                    R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: G36005
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A;Amap position: 14932.33-14932.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology <IMM>
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Pred. No. 1.8e-39;
7; Mismatches 13
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Pred. No. 6.5e-40;
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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622
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	Ig heavy	Ig heavy	Ig heavy	Ig heavy	_	_	_		_	Ig neavy	Ig heavy	1g neavy	Ig heavy	Ig neavy	19 variar

ALIGNMENTS

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Ig heavy chain - human
(Species: Homo sapiens (man)
(Species: Accession: S31116
(Accession: S31116
A. Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar R.Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar R.Raeference number: S31104; MUID:92111633; PMID:1730252
A.; Accession: S31116
A.; Accession: S31116
A.; Status: preliminary; nucleic acid sequence not shown; translation not shown
A.; Status: preliminary
A.; Residues: 1-118 < RAA>
A.; Residues: 1-118 < RAA>
A.; Cross-references: RMSL:X62966
A.; Cross-references: RMSL:X62966
A.; Oross-references: RMSL:X62966
A.; Oross-references: RMSL:X62966
C.; Superfamily: immunoglobulin V region; immunoglobulin homology
C.; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31603
C;Accession: S31603
C;Accession: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Description that generate human immunoglobulin diversity operate from A;Description that generate from A;Description that generate from A;Description that generate from A;Description that generate from A;D
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A;Molecule type: mRNA
A;Residues: 1-132 <CUI>
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A; Accession: $31603
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Best Local Similarity
Matches 98; Conserv
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Pred. No. 3.6e-40;
5; Mismatches 14;
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US-09-540-018-10
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                                                                   Sequence 1
Patent No.
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Best Local Similarity
Matches 87; Conserv
                                                     GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acide
TOPOLOGY: liner-
WOLECUT -
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NAME: DeConti, Giulio A., J
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
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LENGTH: 121 amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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FRAGMENT TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
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STATE: Massa
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                                                                     10, Application US/09540018
o. 6509015
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Salfeld, Jochen G.
Allen, Deborah J.
Hoogenboom, Hendricus R.J.M.
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ilarity 69.0%;
Conservative 17
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internal
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Pred. No. 1.4
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; MOLECULE TYPE:
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US-09-540-018-10
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                                                                     ; GENERAL INFORMATION:
                                                                                    Sequence 80, Application US/09315926A Patent No. 6498027
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
              APPLICANT: Havenga, Menzo APPLICANT: Verlinden, Stei
                                                  APPLICANT: Es van, Helmuth
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APPLICANT:
APPLICANT:
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APPLICANT:
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REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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ADDRESSEE: LAHIVE & (
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acide
TOPOLOGY: line-
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INVENTION: Human Antibodies that Bind Human TNFa
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White, Michael
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Mankovich, John A.
McGuinness, Brian T.
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internal
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                    Stefan
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RESULT 12
US-08-599-226-10
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Sequence 10, Application US/08599226
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 residues
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DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: OC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
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NAME: Mary M. Krinsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB:
FILING DATE: June 28, 1996
CLASSIFICATION: 435
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APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: DM414 scFv antibodies obtained from LIBRARY: fUSE5 fusion phage construct CLONE: V13
                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/983,607 FILING DATE: April 27, 1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America ZIP: 06520-8114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Department of Molecular Biophysics ADDRESSEE: and Biochemistry, Yale University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                              111 PVTVSS 116
                                                                                                                                 121 MVTVSS 126
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                                                                                                                                                                                                                                                                                                                       92; Conservative
                                                                                                                                                                                                                                                                                  1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
                                                                                                                                                                    ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                                                                                                                                                                               EVQLVQSGGGLVQPGGSLRLSCAASGFTESSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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                                                                                                                                                                                                                                                                                                                   70.5%; Score 469; DB 3; Length 131; 73.0%; Pred. No. 1.1e-37; ative 11; Mismatches 13; Indels
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RESULT 13
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GENERAL INFORMATION:
APPLICANT: Salfeld
APPLICANT: Allen,
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Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                           TRLEPAX: (617)227-10:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1-ENGTH: 121 mino acids
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                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: DECONTI, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sakorafas, Paul
APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Tristan J.
APPLICANT: White, Michael
APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
NUMBER OF SEQUENCES: 37
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STATE: Massachusetts
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                                                  116 LVTVSS 121
                                                                              121 MYTYSS 126
                                                                                                              61 ADSVEGRPAVSRDNAKNALYLQMNSLRPEDTAVYYC----TKASYLSTSSSLDNWCQGT 115
                                                                                                                                    61 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                                                                                                                               1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
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Mankovich, John A.
McGuinness, Brian T.
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                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                          70.3%; Score 467.5; DB 3; 69.0%; Pred. No. 1.4e-37; ative 17; Mismatches 17;
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US-09-125-098-10

Sequence 10, Application US/09125098 Fatent No. 6258562 GENERAL INFORMATION: APPLICANT: Salfeld, Jochen G. APPLICANT: Allen, Deborah J.

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APPLICATION NUMBER: US/08/652,816A
PILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                         FILING DATE: 23-SEP-1992
PRIOR APPLICATION UNMBER: GB 9:
APPLICATION UNMBER: GB 9:
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: GB 920031...
PILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: GB 9206372.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5:
                                                                                         FILING DATE: 23-MAY-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 71.1%;
Local Similarity 73.8%;
les 93; Conservative 1
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                                                    APPLICATION NUMBER: PCT/CFILING DATE: 02-DEC-1992
                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 LVTVSS 123
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MBER: US 08/244,597
01-JUN-1994
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                                                                     PCT/GB92/02240
                                                                                                                                                                                    GB 9525004.9
                                                                                                                             GB 9610824.6
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Pred. No. 4.7e-38;
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RESULT 11
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CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 75
LENGTH: 245
TYPB: PRT
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Best Local Similarity
Matches 93; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 312-474-6300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Adams, Camellia APPLICANT: W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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TOPOLOGY: lines-
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LENGTH: 116 amino acid
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NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28
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                                                    MVTVSS 120
                                                                                   MVTVSS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SALAT
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                                                                                                                  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA-----RWSGEDAFDIWGQGT 114
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                                                                                                                                                                                                                                                70.7%; Score 470; DB 4; 73.8%; Pred. No. 1.7e-37; ative 12; Mismatches 13
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                                                                                                                                                                                                                                                                              Length 245;
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US-08-983-607-28

Sequence 28, Application Patent No. 6140470 GENERAL INFORMATION:

US/08983607

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US-08-665-202-30
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TELEFAX: 6491103
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide -07-942-245-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOPTWARE: IN house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
PILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10FORMATION:
TELECOMMUNICATION 10FORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/665,202
FILING DATE: 13-UN-1996
CLASSIFICATION: 424
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MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                             FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (204) 25
TELEPHONE: (202) 293-7860
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oh 71.3%; Score 474; DB 1; Length 117; Similarity 75.6%; Pred. No. 3.2e-38; 90; Conservative 11; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQLVESGGGLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSGISWDSSSIGY 60
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                                                                                                           US 60/000,250
    02307B-061410
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TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6512097
GENERAL INFORMATION:
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STRANDEDNESS:
TOPOLOGY: line-
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
                                                                                                                                  APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Four Embarca
CITY: San Francisco
STATE: California
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ZIP: 94111-4106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 LVTVSS 123
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93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09315574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.1%; Score 472.5; DB 2
73.8%; Pred. No. 4.7e-38;
tive 11; Mismatches 19
                                                                                         02307E-061411
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SEQUENCE CHARACTERISTICS:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,226
                                                                                                                                                    GENERAL INPORMATION:
APPLICANT: Salfeld
APPLICANT: Allen,
APPLICANT: Hoogenb
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 73.0 Matches 92; Conservative
                                                                                                                                                                                                                      Sequence 2, Application US/09540018
Patent No. 6509015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227,7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THIEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human
                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
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                                                                                                                                                                                                                                                                                                                                  116 LVTVSS 121
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                                                          Labkovsky, Boris
Mankovich, John A.
McGuinness, Brian T.
Roberts, Andrew J.
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60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                             Sakorafas, Paul
                                                                                                                                  Hoogenboom, Hendricus
Kaymakcalan, Zehra
                                                                                                                                                                    Allen, Deborah J.
                                                                                                                                                                                       Salfeld,
Schoenhaut, bu. Schoenhaut, bu. Tristan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.2%; Score 486.5; DB 3; Length 121; 73.0%; Pred. No. 2.2e-39; tive 14; Mismatches 15; Indels 5
                                                                                                                                                                                     Jochen G.
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                                                                                                                                                        R.J.M.
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US-07-942-245-24
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                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                       Sequence 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                             APPLICANT: PEDERS
APPLICANT: SEARLE
APPLICANT: REES,
APPLICANT: ROGUSK
APPLICANT: GUILD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICATION NUMBER: US/09/540 CLASSIPTOTE 31-MARC.
                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BEI-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/01
APPLICATION NUMBER: US/01
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
PRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
             ADDRESSEB: Sughrue, Mion, Zinn, I
STREET: 2100 Pensylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                          121 MVTVSS 126
                                                                                                                                                                                                                                                                                                   116 LVTVSS 121
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                                                                                                                                                                                                                                                                                                                                                                                      61 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Washington
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                                                                                                                        ROGUSKA,
                                                                                                                                                    SEARLE,
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internal
                                                                                         Stephen M.J.
Anthony R.
Anthony R.
Michael A.
Braydon C.
SURFACE RESIDUE VENEERING
                                                             ANTIBODIES
522
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                                                                                                                                                                        Jan T.
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                Zinn, Macpeak & Seas
venue, N.W.
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RESULT 2
US-08-958-201-8
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                                                     Sequence 2, Application
Patent No. 6990382
GENERAL INFORMATION:
APPLICANT: Salfeld,
APPLICANT: Allen,
APPLICANT: Hoogenby
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                                                                                                                                                                           US-08-599-226-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/0
PILING DATE: 21-OCT-1996
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08958201
Patent No. 5977319
GENERAL INFORMATION:
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Best Local (
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APPLICANT: Pritchard, Kevin
APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific binding members for estradiol;
TITLE OF INVENTION: materials and methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
CLONE: 2D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                         APPLICANT:
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                     Application US/08599226
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6300 Sears Tower, 233 South Wacker Drive
Allen, Deborah J.
Hoogenboom, Hendricus I
Kaymakcalan, Zehra
Labkoveky, Boris
Mankovich, John A.
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                                                                                              Salfeld, Jochen G.
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; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-599-226-2
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US-09-125-098-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Matches 9
                              GENERAL INFORMATION:
APPLICANT: Salfel, I
APPLICANT: Allen, I
APPLICANT: Hoogenbo
APPLICANT: Kaymakc:
APPLICANT: Labkovsi
APPLICANT: Mankovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/599,226
FILING DATE: 08-FEB-196
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31.503
REFERENCE/DOCKET NUMBER: BBI-043
TELEPHONE: (617)227-7400
                                                                                                                                                    Sequence 2, Applic
Patent No. 6258562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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APPLICANT:
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                 APPLICANT:
 APPLICANT:
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92; Conser
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                                                                                                                                                                      Application US/09125098
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Schoenhaut, Dav
              Labkovsky, Boris
Mankovich, John A.
McGuinness, Brian T.
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Roberts, Andrew J.
                                                                 Kaymakcalan, Zehra
                                                                                 Allen, Deborah J.
Hoogenboom, Hendricus R.J.M.
                                                                                                                     Salfeld,
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                                                                                                   Deborah J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.2%; Score 486.5; DB 3 73.0%; Pred. No. 2.2e-39;
                                                                                                                      Jochen
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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665
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-959-226-2
US-09-540-018-2
US-09-540-018-2
US-09-315-574-30
US-08-918-148-7-2
US-08-918-148-7-2
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US-09-315-398-46
US-09-315-398-46
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US-08-311-3988-46
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146, Appl
46, Appl
47, Appl
48, Appl
48, Appl
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452.5 68.0 125 3 US-09-240-274-151 452 68.0 120 2 US-07-934-373°C-4 452 68.0 120 3 US-08-437-642B-4 452 68.0 120 4 US-08-146-206°C-4 452 68.0 120 4 US-08-146-206°C-4 451.5 67.9 127 3 US-09-240-274-4 451.5 67.9 249 4 US-10-039-785-53 451.5 67.7 125 5 PCT-US93-10555-1 450.5 67.7 125 5 PCT-US93-10555-1 450.5 67.7 245 4 US-08-988-198-2 449 67.5 120 4 US-09-260-198A-2 449 67.5 120 4 US-09-25-7698-38 449 67.5 120 4 US-09-25-7698-63 449 67.5 120 4 US-09-025-7698-63 449 67.5 120 4 US-09-025-7698-63 449 67.5 120 4 US-09-025-7698-18	45	44	43	42	41	40	39	38	37	36	35	4	ω W	32	31	30	29	6
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US-09-240-274-151 US-07-934-373C-4 US-08-437-642B-4 US-08-146-206C-4 US-08-146-206C-4 US-09-240-274-4 US-09-240-274-2 US-09-983-607-32 US-08-983-607-32 US-09-256-769B-63 US-09-025-769B-63 US-09-025-769B-63 US-09-025-769B-63 US-09-025-769B-63 US-09-025-769B-178 US-09-025-769B-178	ب	4	w	4	4.	4	4	v	N	w	4	w	w	4	W	N	w	
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	36,	178	,	63,	38,	,	78,	,	-	32,	53,	27,			4	٠,	151	
W1153244445151	App	178, App	App1 i	Appl	App	App1 i	78, Appl	Appli	, Appli	Appl	App	App	Appli	Appli	Appl	Appli	, Ap	44.

ALIGNMENTS

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US-08-958-201-10
US-08-958-201-10
Sequence 10, Application
Sequence 10, S977319
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                   US-08-958-201-10
                                                                                                                                                                                                                                                                                                                                                    PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/02
APPLICATION NUMBER: US 60/02
FILING DATE: 21-OCT-1996
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                      Query Match
Best Local S
                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
COMPUTER READABLE FLORM:
MEDIUM TYPE Florpy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pope, Anthony R
APPLICANT: Pritchard, Kevin
APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific binding members for estradiol;
TITLE OF INVENTION: materials and methods
                                                                                                                                                                                                                                                                       TOPOLOGY: line
IMMEDIATE SOURCE:
CLONE: 2Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                 LENGTH: 120 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
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61
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5977319
                                                                                                                                                                                      Similarity
                        ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAPDIWGQGT
                                                                                 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
                                                                                                                        QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARPL----YPKG-TQYDFWGQGT
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                76.5%; Score 509; DB 2; Length 120; 76.2%; Pred. No. 1.5e-41; tive 14; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            US 60/028,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/958,201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.25 (EPO)
                                                                                                                                                                  6
                                                                                                                                                                Gaps
                                                                                   60
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Sequence 76, Application US/09972656

Publication No. US20030099647A1

GENERAL INFORMATION:
APPLICANT: Deshpande, Rajendra
APPLICANT: Teai, Mei-Mei

ITILE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
ITILE OF INVENTION: Neutralizing Activity

FILE REFERENCE: A-799

CURRENT APPLICATION NUMBER: US/09/972,656

CURRENT FILING DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 135

SOFTWARE: PatentIn version 3.0

SEQ ID NO 76
LENGTH: 227

TYPE: PRT

ORGANISM: Homo sapiens

US-09-972-656-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOPTWARE: PATENTIN VET: 2.0
SEQ ID NO 1324
LENGTH: 246
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US-09-972-656-76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 73.1%; Score 486; DB 11; Length 246; Best Local Similarity 73.8%; Pred. No. 7e-40; Matches 96; Conservative 11; Mismatches 9; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111
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 119
                                   121 MVTVSS 126
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                                                                                                     61 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                                                                                   1 QVQLVESGGGLVQPGRSLRLSCTASGFTFGDYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COCTMVTVSS 120
                                                                         ADSVXGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASDLVLTMTSRR--AAFDIWGQGT 118
 MVTVSS 124
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Search completed: December 30, 2003, 11:45:24 Job time : 28.0219 secs

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US-10-133-715-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10133715 Publication No. US20030206898A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                                                    SEQ ID NO 2
LENGTH: 121
                                                                                    Matchea
                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                      APPLICANT: Fischkoff, Steven
APPLICANT: Chartash, Elliot
TITLE OF INVENTION: Use of TNF-a Antibodies and
FILE REFERENCE: BBI-186
CURRENT APPLICATION NUMBER: U$/10/133,715
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                  OTHER INFORMATION: D2E7 heavy chain variable region -10-133-715-2
                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31.503
REFERENCE/DOCKET NUMBER: BBI-043CPUSCN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/599,226
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: US 60/031,476
FILING DATE: 25-NOV-1996
APPLICATION NUMBER: US 09/125,098
FILING DATE: 07-AUG-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 MVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                    Similarity 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSAITWNSGHIDY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADSVEGRETISRDNAKNSLYLQMNSLRAEDTAVYYCA-----KVSYLSTASSLDYWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 121 amino acids
TYPE: amino acid
TYPE: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.2%; Score 486.5; DB 1 ilarity 73.0%; Pred. No. 2.8e-40; Conservative 14; Mismatches 15
                                                                                    Conservative
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                                                                                                   73.2%;
73.0%;
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                                                                                Score 486.5; DB 12; Length 121;
Pred. No. 2.8e-40;
4; Mismatches 15; Indels 5;
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                                                                                                                                                                                                                                                                                                                                                                                                           Another Drug
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RESULT 14
US-09-880-748-1324
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                                                                        ; Sequence 1324, Application US/09880748 ; Publication No. US20030059937A1 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-302-356A-2
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US-10-302-356A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-03-18
PRIOR APPLICATION NUMBER: 08/599226
PRIOR FILING DATE: 1996-02-09
NUMBER OF SEQ ID NOS: 37
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10302356A Publication No. US20030219438A1 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WILTON, Alison, J.

TITLE OF INVENTION: Human Antibodies That Bind Human
TITLE OF INVENTION: TWFALPHA
FILE REFERENCE: BBI-043CPACN2
CURRENT APPLICATION NUMBER: US/10/302,356A
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 09/540018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SALFBLD, Jochen G. APPLICANT: ALLEN, Deborah J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Mutated human antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                   116
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                                                                                                                                                                                                                                                                                                                                                                     1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
                                                                                                                                                                                                                                                                                                                                                                                                                     92; Conservative
                                                                                                                                                                                                   LVTVSS 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LABKOVSKY, BOTIB
MANKOVICH, John A.
MCGUINNESS, Brian T.
ROBERTS, Andrew J.
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SCHOENHAUT, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOOGENBOOM, Hendricus
KAYMAKCALAN, Zehra
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WHITE, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                    73.2%; Score 486.5; DB 1
73.0%; Pred. No. 2.8e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                     14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 66
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 59, Application US/09791153A Publication No. US20030103978A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/791,153A CURRENT FILING DATE: 2001-07-17 PRIOR APPLICATION NUMBER: 09/511,139 PRIOR FILING DATE: 2000-02-23 NUMBER OF SEO ID NOS: 154 SOFTWARE: Patentin version 3.0 SEO ID NO 59 LENGTH: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
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PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 154
                                                                                                                             Matches
                                                                                                                                                                     Query Match
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
-09-791-153A-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN FILE REFERENCE: A-633A
CURRENT APPLICATION NUMBER: US/09/791,153A
CURRENT FILING DATE: 2001-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sullivan, John
TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING
FILE REFERENCE: A-633A
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APPLICANT: Hitz, Anna
APPLICANT: Boyle, William
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Local Similarity 73.8%; Pred. No. 1.8e-40;
198 93; Conservative 13; Mismatches 17
                                                                                                                                                   Local
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:|||::||||||||::|: ||:
                                                                                                                             l Similarity
93; Conserv
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                                                                  QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
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Sullivan, John
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                                         EVQLLESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGRIGY 61
  ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                                                             Conservative
                                                                                                                         73.5%; Score 488.5; DB 11; Length 227; 73.8%; Pred. No. 3.6e-40; tive 13; Mismatches 17; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 123;
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOPTWARE: PATENTIN VET. 2.0
SEQ ID NO 1416
LENGTH: 252
TYPE: PRT
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US-09-880-748-1416
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US-09-801-185A-2
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09801185A publication No. US20030092059A1 GENERAL INFORMATION:
APPLICANT: BASF Aktiengesellschaft
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.3%; Score 487.5; DB 11; Local Similarity 71.2%; Pred. No. 5.1e-40; nes 94; Conservative 14; Mismatches 15;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                    TITLE OF INVENTION: Human Antibodies that Bind Human TNFalpha
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 LVIVSS 124
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                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                    STREET: 28 State Street
                                                                                                                                   COUNTRY: USA
                                                                                                                                                                          CITY: Boston
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLy
FILE REFERENCE: PF523
CURRENT APPLICATION UMMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/210,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
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US-09-880-748-1427
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US-09-880-748-1427
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1427
LENGTH: 254
TYPE: PRT
                                                                                                                                   Sequence 6, Application US/10447331
Publication No. US20030219434A1
GENERAL INFORMATION:
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Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
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Best Local
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FILE REFERENCE: GENENT.122A
CURRENT APPLICATION NUMBER: US/10/447,331
CURRENT FILING DATE: 2003-05-28
                                                     APPLICANT: Carter, Paul J.
APPLICANT: Ridgway, John B.
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: DIAGNOSIS
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111 RGTLVTVSS 119
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;; Pred. No. 2.3e-40;
16; Mismatches 18;
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                                                                              FOR
                                                                              CANCER THERAPY
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PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PACENTIN Ver. 2.0
SEQ ID NO 922
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NUMBER OF SEQ ID NOS: 6
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 922, Application US/09880748 Publication No. US20030059937A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                   Query Match
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/515,825
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 60/122262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ruben et al. TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLySFILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                   Local
                                                         108 RGVAAFDIWGQGTMVTVSS 126
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                                                                                                                           61 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCA------LPYINSSNYR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCARDAPSGSYGY-----WFDPWGQG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95;
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                                                                                                                                                                                                                                                              94;
                                                                                                                                                                                                                                                                                                                                                                                                    251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                QVQLVQSGGGVVQPGRSLRLSCAASGFNFNDYGMHWVRQAPGKGLEWVSGISWNSGTIGY
                                                                                                AESVKGRFTISRDNAKNSLSLOMNSLRAEDTAVYYCARVSPSYDILTGYYLPH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                               73.5%; Score 489; DB 11; 67.6%; Pred. No. 3.6e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.5%; Score 489; DB 12; 74.8%; Pred. No. 1.6e-40;
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                                                                                                                                                                                                                                                              14; Mismatches
                                                                                                                                                                                                                                                                                                   DB 11; Length 251;
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                                                                                                                                                                                                                                                              Indels 24;
                                                                                                                                                                                                                                                              Gaps
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US-09-840-459-88

Application US/09840459

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PRIOR FILING DATE: 2000-02-03
PRIOR PELING DATE: 2000-02-03
PRIOR PILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 88
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 88,
Patent No. U
                                                                                                                                                                                                                                                                                                                                                     Sequence 50, Application US/08779457 Publication No. US20020193571A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Reefe, Theress
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USB THEREFOR
FILB REFERENCE: 1855.1052-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US01/03537 PRIOR FILING DATE: 2001-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LaRosa, APPLICANT: Horvatl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                               APPLICANT: Chiang, Nancy Y.
APPLICANT: Kyung, Jin Kim
APPLICANT: Matthews, William
APPLICANT: Rodrigues, Maria L.
TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                APPLICANT: Carter, Paul J. APPLICANT: Chiang, Nancy Y
                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                    94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVOLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
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Newman, Walter
Jones, S. Tarran
                                                                                                         California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.0%; Score 505.5; DB 10; Length 119; 77.0%; Pred. No. 3.8e-42;
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RESULT 4
US-09-880-748-1926
J Sequence 1926, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
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                                          US-09-880-748-1926
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CURRENT PILLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILLING DATE: 2000-06-15
PRIOR PILLING DATE: 2000-10-17
PRIOR PILLING DATE: 2000-10-17
PRIOR PILLING DATE: 2000-10-17
PRIOR PILLING DATE: 2001-03-16
PRIOR PILLING DATE: 2001-03-16
PRIOR PILLING DATE: 2001-03-16
PRIOR PILLING DATE: 2001-03-21
PRIOR PILLING DATE: 2001-03-21
PRIOR PILLING DATE: 2001-03-21
PRIOR PILLING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 50
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
                                                                                                                              SOPTWARE: PatentIn Ver. 2.0 SEQ ID NO 1926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/667
PILING DATE: 06/20/96
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: 08/585
PILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,457
FILING DATE:
                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
08/667197
                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 LVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 MVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTD-----AFDIWGRGT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Score 503.5; DB 11; Length 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 241;
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Query Match

75.74;

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Database
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                     Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US00C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US00C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US00_REW_PUB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US00_REW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US00_REW_PUB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US00_REW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US00_REW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US00_REW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
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665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVQLVQSGGGLVQPGKSLRL.....RRGVAAFDIWGQGTMVTVSS 126
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Result No.	Score	* Query Match Length	Length	DB	ID	Description
1	512	77.0	132	11	US-09-791-153A-65	
N	505.5	76.0	. 119	10	US-09-840-459-88	Sequence 88, Appl
w	505.5	76.0	241	8	US-08-779-457-50	•
4	503.5	75.7	245	H	US-09-880-748-1926	Sequence 1926, Ap
Ç	491	73.8	254	11	US-09-880-748-1427	Sequence 1427, Ap
σ.	489	73.5	122	12	US-10-447-331-6	Sequence 6, Appli
7	489	73.5	251	11	US-09-880-748-922	
8	488.5	73.5	123	11	US-09-791-153A-66	
9	488.5	73.5	227	11	US-09-791-153A-59	
10	487.5	73.3	252	1	US-09-880-748-1416	Sequence 1416, Ap
11	486.5	73.2	121	11	US-09-801-185A-2	Sequence 2, Appli
12	486.5	73.2	121	12	US-10-133-715-2	Sequence 2, Appli
13	486.5	73.2	121	12	US-10-302-356A-2	Sequence 2, Appli
14	486	73.1	246	Ľ	US-09-880-748-1324	
15	483	72.6	227	11	US-09-972-656-76	Sequence 76, Appl

45	44	4	42	41	40	39	9	37	36	35	34	ω U	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
467.5	467.5	467.5	467.5	467.5	467.5	₽	467.5	468	468	468	469	469	469	469	469.5	469.5	471	472	472.5	472.5	472.5	472.5	473	474	475	475	476	481
70.3	70.3	70.3	70.3	70.3	70.3	70.3	70.3	70.4	70.4	70.4	70.5	70.5	70.5	70.5	70.6	70.6	70.8	71.0	71.1	71.1	71.1	71.1	71.1	71.3	71.4	71.4	71.6	72.3
244	244	244	225	121	121	121	119	367	248	136	249	122	122	116	259	121	239	239	296	296	290	290	239	239	239	128	248	251
11	11	11	11	12	12	11	15	12	11	12	11	15	15	15	11	12	11	11	12	12	12	12	11	11	11	15	11	11
-09-880-	US-09-880-748-164	US-09-880-748-82	US-09-453-234-68	US-10-302-356A-10	US-10-133-715-10	-09-801	US-10-073-644C-6	US-10-045-674-453	US-09-880-748-1974	US-10-045-674-487	US-09-880-748-1109	US-10-269-805-11	US-10-269-805-7	US-10-091-300-24	US-09-880-748-1664	US-10-010-942B-9	US-09-880-748-937	US-09-880-748-2023	US-09-949-039-75	US-09-969-748C-12	US-09-949-039-2	US-09-969-748C-2	US-09-880-748-2022	US-09-880-748-2015	US-09-880-748-2038	US-10-269-805-29	US-09-880-748-1890	US-09-880-748-1542
Sequence	Sequence				Sequence				Sequence	Sequence	Sequence							Sequence	Sequence	Sequence	Sequence	Sequence		æ		Sequence	Sequence	Sequence
•	164, App	82, Appl	•	•	10, Appl	10, Appl	6, Appli	453, Ap	1974, Ap	487, App	1109, Ap	11, Appl	7, Appl	24, Appl	1664, Ap	9, Appli	937, Ap	2023, Ap	75, Appl	12, Appl	2, Appl	Appli	2022, Ap	2015, Ap	2038, A	29, Appl	1890, A	1542, Ap

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; ORGANISM: Homo sapiens
US-09-791-153A-65
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; Sequence 65, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/791,153A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/511,139
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin version 3.0
SEQ ID NO 65
LENGTH: 132
                                                                                                                                                                                                                                                       Query Match 77.0%; Score 512; DB 11; Best Local Similarity 75:0%; Pred. No. 9.9e-43; Matches 99; Conservative 12; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Deshpande, Rajendra
APPLICANT: Hitz, Anna
APPLICANT: Boyle, William
APPLICANT: Boyle, William
APPLICANT: Sullivan, John
TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
FILE REFERENCE: A-633A
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121 YWGQGTLVTVSS 132
                                          115 IWGQGTMVTVSS 126
                                                                                       61
                                                                                                             61 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAA-----FD 114
                                                                                                                                                                                             1 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
                                                                                       ADSVKGRPTISRDNAKNSLYLQMNSLRAEDTALYYCAKDGYSSGWYGIAVAGVQWLVYFD
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RESULT 15
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Matches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                              Key
Region
                                                                 Region
                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LU20; human; antibody; VH domain; decay accelerating factor; DAF; phage display; subtractive panning; lung cancer; lung carcinoma; lung adenocarcinoma; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human anti-DAF antibody LU20 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel antibodies that immunospecifically bind of B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96065 standard; protein; 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADSVKGRFTISRDNSKNTLYLQWNSLRAEDTAVYYCTRGYEYYDILTGYNELGAFDIWGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                               /note= "hypervariable loop 50..66
                                                                                                                        /note= "complementarity determining region
53..56
                                                                                      /note=
                                                                                                                                                                                                                                                                                                   note= "complementarity determining
                                                                                                                                                                                                                                                                                                                                  /label= CDRI
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"complementarity determining region
                                                                                         "hypervariable loop residues
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                                                                                                                                                                                                                                                                                             The present sequence is that of the heavy chain variable region (VH) of the anti-decay accelerating factor (DAF) human antibody LU20. The VL region is given in AAY06062. LU20 was produced using a Covel method for making antibodies which can be used for cancer antibody phage from a naive antibody phage library to a live cancer cell; (b) selecting an antibody phage or antibody which binds cell; (b) selecting an antibody phage or antibody which binds to which the antibody phage or antibody binds. To obtain LU20, a counter-selecting with a non-tumour bronchial epithelial cell line, and counter-selecting with a non-tumour bronchial epithelial cell line, antigens by panning the lung adenocarcinoma cell cell cell line, antigens by panning the lands odescribes a method for identifying an antigen because the surface of composition comprising the antibody, is useful for in vivo cancer diagnosis or therapy. In particular, the antibody is useful for diagnosing or treating lung cancer, e.g. small-cell lung cancer, con-small cell lung cancer, large cell lung carcinoma (all claimed).
                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Making antibodies (e.g. anti-decay accelerating factor antibody) for diagnosing or treating e.g. lung cancer comprises identifying an antigen that is differentially expressed on the surface of two or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1999;
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                               TMVTVSS 126
                                                                                   ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSS-NYRRGVAAFDIWGQG 119
                                                                                                                                   EVOLVETGGGLVQPGRSLRLSCAASGFTFEDYGMHWVRQAPGKGLEWVSGINWNGGSTGY
                                                                                                                                                      QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
SSALATE
                                                                 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCARDAPSGSYGY----WFDPWGQG
                                                                                                                                                                                                                                                                         122 AA;
                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                  73.5%; Score 489; DB 21; 74.8%; Pred. No. 2.3e-39; tive 12; Mismatches 14
                                                                                                                                                                                                                                  Length 122;
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Search completed: December 30, 2003, Job time: 41.6162 secs

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus crythematones, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-2000
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AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST) sequences, corresponding to human secreted proteins. AAY64651 to AAY66538 represent the EST-related proteins corresponding to AAZ42265 AAZ43052. The 5' ESTs can be used for producing secreted human gene
                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                      Dumas Milne Edwards
                                                                                                                                                                                                                                                                                  09-APR-1998;
                                                                                                                                                                                                                                                                                                             09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                            WO9953051-A2
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                           Claim 3;
                                                                                                        Novel secreted protein 5' expressed diagnostic, forensic, gene therapy,
                                                                                                                                                                                                                                     (GEST ) GENSET
                                                                                                                                                                       2000-038446/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST related polypeptide SEQ ID NO:898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                          Page 627; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 AA;
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98US-0069047.
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                                                                                                                                                                                                      Giordano
                                                                                                        sequence tag sequences used in and chromosome mapping procedures
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC products. They can be used to identify and isolate 5' untranslated cc regions (UTRs) and upstream regulatory regions which control the clocation, development stage, rate, and quantity of protein synthesis, as cc well as stability of mRNA. The ESTs are also useful as probes for cc chromosome mapping, and to obtain full length cDNA clones. The ESTs can calso be used in forensic procedures to identify individuals, or in cdiagnostic procedures to identify individuals, or in consulting from abnormal gene expression. The products may also be used in cc gene therapy protocols. The nucleic acids encoding signal peptides can be cc used for directing extracellular secretion of a polypeptide into a membrane, or importing a polypeptide control a cell. The proteins encoded by the EST sequences may be useful in cc therappetic value, and the identification of new secreted proteins is caluable. AAZ42249 to AAZ42264 and AAX64644 to AAX64650 represent cx sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                         BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                               16-JUN-2000;
17-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human BLyS binding scFv SEQ ID 1427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP45416;
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WPI; 2002-114799/15
                                Ruben SM,
                                                                                                                                                                                                                15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                                                               10-JAN-2002.
                                                                                                                                                                                                                                                                                WO200202641-A1.
                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                             common variable immunodeficiency; acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP45416 standard; Protein; 254
                                                                                                                              16-MAR-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132
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                                                               HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMDVWGQGTTVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADSVKGRPTISRDNAKNSLYLQMNSLRTEDTAFYFCAKARGLFSDTWPYXH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 AA;
                                Barash SC,
                                                                                                             ); 2000US-212210P.

); 2000US-240816P.

); 2001US-276248P.

); 2001US-277379P.

); 2001US-293499P.
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70.4%; Pred. No. 1.3e-39;
tive 11; Mismatches 12
                                Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146
                                                                 TECHNOLOGY.
                                Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                   Hilbert
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The present sequence is an agonist antibody clone to the human WSX creceptor, which can be used to identify and purify ligands and cactivators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor, leading to enhanced proliferation or differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to cenhance proliferation or differentiation of lymphoid, myeloid or cenhance proliferation or differentiation of lymphoid, myeloid or cerythroid blood cell lineages. This is useful when a mammal. Cespecially a human, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone commartow transplantation tharapy. It can also be used to treat, composition of the composition 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; WSX receptor; clone #17; identification; purification; ligand; activator; antibody; agonist; proliferation; obesity; differentiation; anaemia; treatment; neoplasia; arteriosclerosis; Type I diabetes; polycystic ovarian disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WSX receptor and related antibodies and ligands - used products for diagnosis and therapy, e.g. for improving haematopoiesis or for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiovascular disease; osteoarthritis; dermatological disorder; hypertension; insulin resistance; hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 14; Pages 122-123; 219pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-372864/34.
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96US-0585005
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Pred. No. 5.8e-41;
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RESULT 12
ABP45915
ID ABP45
XX ADP45
XX ADP45
XX ADP45
XX ID-AU
XX BLy8;
KW ELUMOU
XW LUMOU
XW IMMUN
AMITIA
KW Syste
KW COMMO
XX HOMO
XX ADP1;
XX HOMI
XX ADP1;
XX ANTII
PR 25-MJ
XX HOMI
XX CHNMJ
PR 25-MJ
XX HOMO
XX CHNMJ
PR 25-MJ
XX HOMO
XX CHNMJ
R 25-MJ
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R CC TNia
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CC CYTO
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
                                                                                                        Claim
                                                                                                                                     Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                       16-JUN-2000; 2000US-212210P
17-OCT-2000; 2000US-240816P
16-MAR-2001; 2001US-276248P
21-MAR-2001; 2001US-277379P
25-MAY-2001; 2001US-293499P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human BLyS binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP45915;
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                                                                                                                                                                                                                                                                                                                                                                                                                   10-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiAIDS; vacci
systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP45915 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200202641-A1
                                                                                                                                                                                                                                              (CAMB-)
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                                                                                                                                                                                                                                               CAMBRIDGE ANTIBODY
                                                                                                                                                                                                                                                              HUMAN GENOME SCI INC
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                                                                                                                                                                                                                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                        2699-2700; 3148pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erythematosus; rheumatoid arthritis; CVID; A: erythematosus; rheumatoid arthritis; CVID; A: eimmunodeficiency; acquired immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCFV SEQ ID
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77.0%;
                                                                                                                                                                                                                Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                 TECHNOLOGY.
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Pred. No. 1.2
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                                                                                                                                                                                                                Vaughan T,
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                                                                                                                                                                                                                 Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIDS;
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This invention describes novel antibodies that immunospecifically bind to E Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

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antirheumatic

immunosuppressive, lc and antiAIDS act

activity and

can be used in

VH3-4 amino acid sequence SEQ ID NO:1.

24-MAY-2002

(first

entry)

Human heavy chain variable

(H)

region,

UBI-24.

16-OCT-2001

(first entry

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Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                              fused to a fluorescent protein. The method comprises constructing a scPv antibody library composed of phage clones expressing scPv antibody on their surface, screening this library with an antigen, extracting the gene for scPv antibody from the selected phage clones and inserting it into an expression vector that expresses the gene fused to a fluorescent protein. Also described are: (1) a fusion protein comprising the scPv antibody fused to a fluorescent protein; (2) immunological assays using the fusion protein of (1); (3) an expression vector encoding the fusion protein of (1); and (4) a kit for producing the fusion protein of (1). The fusion protein can be used in immunoasys and immunobtaining.

The fusion protein can be used in immunoasys and immunostaining. The fusion protein do not require a secondary or tertiary antibody. Direct intracellular and even in vivo assays are possible. ABJ49521 to ABJ49591 and ABB06286 to ABB06276 represent
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing scFv antibody fused to a fluorescent protein, useful for immunoassay and immunostaining, comprises expressing a scFV gene (extracted from selected clones) fused to a fluorescent protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-098058/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for producing a scFv antibody fused to a fluorescent protein. The method comprises constructing a sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunological assay.
                                                AAE07025 standard; Protein; 119 AA
                                                                                                                                     115
                                                                                                                                                                      121 MVTVSS 126
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                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 82-83; 105pp; Japanese
                                                                                                                                                                                                                                                                           EVOLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
                                                                                                                                                                                                          ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKGPSGSFD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the exemplification of the present invention
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                              Score 508; DB 23;
Pred. No. 3.4e-41;
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                                                                                                                                                                                                                                                                                                                                                                              Length 120;
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AAE07025

Sequence

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CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin CC (CCR2), comprising an antigen binding region of non-human origin CC and at least a portion of an immunoglobulin of human origin. The CC and at least a portion of an immunoglobulin of human origin. The CC humanised antibodies are useful for inhibiting or treating CC HIV infection. The proteins of the invention are useful for inhibiting CC (CC HIV infection. The proteins of the invention are useful for inhibiting CC (CC arthritis and multiple sclerosis, atterogenesis and atterosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, CC and for inhibiting restenosis. They are useful in therapy or diagnosis, CC and in the manufacture of a medicament for treating CCR-2 mediated CC disease. They are also useful for treating allergy, anaphylaxis, CC malignancy, chronic and acute inflammation, histamine and IgE-CC dimune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. CC Humanised antibodies are also useful for inhibiting narrowing of the CC usesel in a mammal, and inhibiting narrowing of the present sequence is human heavy chain variable (VH) region, UBI-24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            multiple scierosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody; neointimal hyperplasia; VH; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488888/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-2000; 2000US-0497625.
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/note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Complementarity determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183pp; English
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                                                                                                                                                                                                                                     This sequence represents a VH domain complementarity determining region CC (CDR) from an antibody specific for estradiol. The invention relates to Specific binding members (abp) comprising a polypeptide that comprises an CC antibody antigen binding domain (ABB) which has a dissociation constant of at CC less than 1.0x10^-8M for estradiol, and a dissociation constant of at CC less tool-fold higher for the steroid hormones selected from estriol, CC testosterone, dihydrotestosterone, progesterone, estriol-3-sulphate and CC estriol 3-betta-di-glucuronide, where the polypeptide comprises an CC antibody VH domain. The sbps can be used in an immunoassay for CC determining the presence or absence of estradiol in a sample. They can be used for monitoring estradiol levels, e.g. during the menstrual cycle, in CC hormone replacement therapy and for disgnosting osetrogen secreting CC tumours. The sbps can provide for disgnosting osetrogen secreting CC other related steroids.
                                                                                                                                                    Best Local
Matches
                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New specific binding partners for estradiol, used for monitoring estradiol levels during the menstrual cycle, in hormone replacement
                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-619713/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY43254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY43254 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy and for diagnosing oestrogen secreting tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Column 23-24; 26pp;
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                                                                                                                                                                   Similarity
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                                                                                                      QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
MVTVSS 126
                                            ADSVKGRPTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                       RVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
                              ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARPL----
                                                                                                                                                                                                               120 AA;
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pope AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of anti-estradiol antibody.
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                                                                                                                                                                 76.4%;
76.2%;
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                                                                                                                                                 14;
                                                                                                                                                                 Score 508;
Pred. No.
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                                                                                                                                                    Mismatches
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                                                                                                                                                                   3.4e-41;
                                                                                                                                                                               DB 20;
                                                                                                                                                   10;
                                                                                                                                                                               Length 120;
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                              - YPKG-TQYDFWGQGT
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RESULT 9
ABB06276
ID ABB0
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AC ABB0
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ARGES 39
ARGES 29
ARGES 20
ARGES XX
ARGES XX
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ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES ARGES A
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Matches
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  ABB06276;
                                                       ABB06276 standard; Protein; 120 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 20; 181pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                producing gene libraries and antibody libraries, involves selecting light chain that binds to a heavy chain product to produce a function formation, and producing a gene library of the light chain variable
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Okuno Y, Sł
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-2000; 2000JP-0050543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-AUG-2001
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115 LVTVSS 120
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                                                                                                                                                                                                                                                                                                                                ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 508; DB 22;
; Pred. No. 3.4e-41;
11; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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Matches 99
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06-JUN-1997;
12-DEC-1997;
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Region
                                                                                                                                                                       This invention describes novel nucleic acid fragments that encode human auto-antibodies and anti-idiotypic antibodies against blood platelet membrane protein, GPIIb/IIIa. The products of the invention are used for diagnosis (including monitoring and determining predisposition), prevention and treatment of autoimmune thrombocytopaenic purpura (AITP) and also for modulating binding of fibrinogen to thrombocytes (particularly to dissolve thrombi and/or prevent their formation, e.g. in cases of cardiac infarction or pulmonary embolism). Unlike murine antibodies, human antibodies (hab) do not induce adverse side effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
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                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                            Disclosure; Page 58-59;
                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding human autoantibodies against platelet glycoprotein IIb/IIIa - used for diagnosis, treatment and pof autoimmune thrombocytopaenic purpura and for modulation fibrinogen binding
                                                                                                                                                                                                                                                                                                                                                                                                              Berchtold P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1998;
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DB; AAV72231.
61
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                                                                                                      Similarity
                                                         QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
              ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINS---SNYRRGVAAFDIWGQ
                                             ADSVKGRFT1SRDNAKNSLYLQMNSLRAEDTALYYCVKDMGSSVVATYN----AFD1WGQ
                                                                                                                                        124 AA;
                                                                                                                                                              for longer
                                                                                           Conservative
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97DE-1023904.
97DE-1055227.
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                                                                                          11;
                                                                                          Score 511; DB
Pred. No. 1.8e-
11; Mismatches
                                                                                           DB 20;
1.8e-41;
hes 12;
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                                                                                                                                                                                                                                                                                                                                          prevention
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                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                           testosterone, dihydrotestosterone, progesterone, estriol-3-sulphate estriol 3-beta-di-glucuronide, where the polypeptide comprises an antibody VH domain. The sbps can be used in an immunoassay for determining the presence or absence of estradiol in a sample. They could for monitoring estradiol levels, e.g. during the menstrual cycl hormone replacement therapy and for diagnosing oestrogen secreting tumours. The sbps can provide for discrimination between estradiol a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody antigen binding domain; steroid hormone; estriol; testosterone; dihydrotestosterone; progesterone; estriol 3-beta-di-glucuronide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a VH domain complementarity determining region (CDR) from an antibody specific for estradiol. The invention relates to specific binding members (sbp) comprising a polypeptide that comprises an antibody antigen binding domain (AABD) which has a dissociation constant of less than 1.0x10 -8M for estradiol, and a dissociation constant of at least 500-fold higher for the steroid hormones selected from estration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New specific binding partners for estradiol, used for monitoring estradiol levels during the menstrual cycle, in hormone replacement therapy and for diagnosing oestrogen secreting tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5977319-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             menstrual cycle; hormone replacement therapy; oestrogen diagnosis; VH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Estradiol, complementarity determining reantibody antigen binding domain; steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VH domain CDR of anti-estradiol antibody.
                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Column 25-26; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                       other related steroids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy and for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                           EVŐLVEŚĠĠĠĹVÓÞĠRŚĹRĹŚĆĄASGFTFDDYAMHMVRQAPGKGLEMVSGISMNSGSIGY
                                                                                                                                           QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
;||||:|||||||||::|: ;||: ;||:
                                  ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT
     ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARPL----
                                                                                                                                                                                                                                                                                                                                    120 AA;
                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                        Score 509; DB 20;
Pred. No. 2.7e-41;
4; Mismatches 10
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                                                                                                                                                                                                                                                                                 DB 20;
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Matches 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant protein which binds to complex vire HIV-1 - contains variable region of antibody decell line, used for detecting HIV-1 antigen
                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                         Heavy chain of 3D6 anti-HIV antibody.
                                                                                                                                                                                                                                                                                                                                                                                                       AAR20057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR20057 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 31; 52pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ20068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Felgenhauer M, Himmler G,
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                                                                               Region
                                                                                                                                                                                                                                                               complementarity
                                                                                                                                                                                                                                                                                Plasmid pUC3D6HC; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1992
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                                                                                                                                                            Peptide
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  /label= CDR-1
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                                                                                                                                                                                                                                                             region.
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Pred. No. 1.3e-41;
1; Mismatches 14
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uct sc3D6 was
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ker. The
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ved from 3D6
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Query Match
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Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis; blood platelet membrane protein; predisposition; prevention; treatment; autoimmune thrombocytopaenic purpura; AITP; fibrinogen binding; thrombithrombocyte; cardiac infarction; pulmonary embolism; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The variable region of the heavy chain is used in a recombinant protein with the variable region from the kappa light chain of 3D6, the two V regions being joined by a linker. The recombinant protein binds to HIV gp160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ20066.
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                                                                  Human anti-GPIIb/IIIa
                                                                                              07-SEP-1999
                                                                                                                                                    AAW90286 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            See also AAQ20067 and AAQ20068.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JUNG/) JUNGBAUER A.
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                                                                                                                                                                                                                                                                                              ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYC--ALPYINSSNYRRGVAAFDIWGQ
                                                                                                                                                                                                                                                                                                                                      EVQLVESGGGLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSGISWDSSSIGY
                                                                                                                                                                                                                        GTMVTVSS 145
                                                                                                                                                                                                                                                                              ADSVKGRFTISRDNAKNSLYLQMNSLRAEDMALYYCVKGRDYYDSGGY--FTVAFDIWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                475 AA;
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86..117
/label= Framework_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118..134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= CDR_3
                                                                                                                                                    Protein; 124 AA
                                                                                                                                                                                                                                                                                                                                                                                           77.6%; Score 516; DB 13; 77.3%; Pred. No. 2.6e-41; ive 11; Mismatches 14
                                                                 antibody heavy chain protein from phagemid AI-X40
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                                                                                                                                                                                                                                                                                                                                                                                            14;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 475;
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Example

8

Fig

9A; 61pp;

English

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X & X S S S S S S S S S S X X
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human factor VIII antibody A3-C1 specific scFv protein B18 which is used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; heavy chain; hemophilia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human FVIII antibody heavy chain variable region B18 protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY50967 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                   New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                  08-MAY-1998;
                                                                                                                                                                                                                                                                                               07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                          WO9958680-A2
This invention describes a novel polynuclectide (I) (and complements and hybridizable polynuclectides) comprising a contiguous nuclectide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the
                                                                                                                                                                                                                                                                                                                           18-NOV-1999
                                                                         Example 8; Fig 9C; 61pp; English.
                                                                                                                                                                                                                                       (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                                                                             2000-053102/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAPDIWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
                                                                                                                                                                                                           'n,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
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                                                                                                                                                                                                           Van Den
                                                                                                                                                                                                                                                                    98EP-0201543
                                                                                                                                                                                                                                                                                               99WO-NL00285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 126
                                                                                                                                                                                                                                                                                                                                                                                                                                antibody; factor VIII; hemostatic; variable region;
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Pred. No. 3.1e-56;
Mismatches 0;
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                                                                                                                                                                                                           Turenhout EAM;
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                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                Plasmid pUC3D6LC; PUC3D6HC; human immunodeficiency virus; AIDS;
                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                       complementarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                         determining region.
                                                                                                                                                                                                                                /label= CDR_2_heavy_chain 68..99
                                                                                                                                                                                                                                                                         /label= CDR_1_heavy_chain 37..50
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                       label= Framework_1_heavy_chain
                                                                                                                                                                                                                                                             label= Framework_2_heavy_chain
                                                                                                                               label=
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                                                                            .191
el= Framework_2_light_chain
                                                                                                                                            . 165
                      CDR_3_light_chain
                                         Framework_3_light_chain
                                                                                                                                                                         Framework_4_heavy_chain
                                                                                                                                                                                            _CDR_3_heavy_chain
                                                                CDR_2_light_chain
                                                                                                                              Framework_1_light_chain
Framework_4_light_chain
                                                                                                                                                                                                                                                                                                                                                                                                       gp160 antibody.
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Pred. No. 3.1e-56;
; Mismatches 0;
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Maximum DB
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Perfect score:
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Maximum Match 10
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and is der
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seq length: 2000000000
                                                                                                                                                                                                                                                                                                              No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein search, using
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665
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493.415 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                             Length
    126
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Human PVIII antibo
Human FVIII antibo
Recombinant 8c3D6
Heavy chain of 3D6
Heavy chain of 3D6
Human anti-GPIIb/I
VH domain CDR of a
VH domain CDR of a
Amino acid sequenc
VH3-4 amino acid s
                                                                                                                                                                                                             Description
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Human BLyS binding	ABP46012	23	239	71.0	472	u
Human secreted pro	AAU81993	23	519	71.1		4
Immunoglobulin rel	ABG60637	23	296	71.1	472.5	ω
Immunoglobulin rel	ABG60632	23	291	71.1		N
Pelb/5AF/myc/6His	ABP55318	24	290	•		-
n antibody	AAW08582	18	123		-1	0
Dig3 antibody heav	AA015187	23	117		472.5	9
n BLyS	ABP46011	23	239	71.1	473	8
BLyS	ABP46004	23	239	71.3	474	7
3	AAR52053	15	117	71.3	474	σ
	ABP46027	23	239	71.4	475	ر.
Human BLyS binding	ABP45879	23	248		476	•
Anti-adipocyte mon	AAU02501	22	120	٠	476	ω
Anti-adipocyte mon	AAU02593	22	118		479	N
Anti-adipocyte mon	AAU02605	22	118	٠	480	-
	AAR88848	17	121	٠	480.5	0
Human BLyS binding	ABP45531	23	251	٠	481	Φ
HCV E1 antigen mon	ABG76547	23	131	٠	481	œ
HCV El antigen mon	ABG76513	23	127	72.3	481	7
ш	ABP45309	23	251	72.6	483	σ
Human BLyS binding	ABP45313	23	246	73.1	486	u
anti-	AA016460	24	121	73.2	486.5	4
Anti-TNF-alpha ant	AAW27569	18	121	73.2	486.5	ω
adipoc	AAU02560	22	118	73.2	487	N
Human BLyS binding	ABP45405	23	252	73.3	487.5	_
Anti-hEDRF antibod	AAG65590	22	248	73.3	487.5	0
3	ABJ36923	24	146	73.3	487.5	φ
Anti-adipocyte mon	AAU02623	22	126	٠	487.5	œ
Anti-OPGbp antibod	AAU08385	22	227	٠	488.5	7
Human BLyS binding	ABP44911	23	251		489	σ
Human anti-DAF ant	AAY96065	21	122	73.5	489	U
Human BLyS binding	ABP45416	23	254	73.8	ø	•
	AAY64737	21	149	•	•	ω
LyS b	ABP45915	23	245	•		N
Human WSX receptor	AAW24063	18	241	76.0	505.5	_
Human heavy chain	AAE07025	22	119	76.0		0

ALIGNMENTS

AAY50961 standard; Protein; 126

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RESULT 1
AAY504

New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                            WPI; 2000-053102/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; heavy chain; antibody; factor VIII; hemostatic;
hemophilia A; scFv; A3-C1.
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                                                                                                                                                                                                                                                                                                   Voorberg JJ, Van Den Brink EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human FVIII antibody A3-C1 scFv heavy chain protein B18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY50961;
                                                                                                                                                                                                                                                                                                                                                                                                    (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98EP-0201543.
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135 121

LVTVSS 140 MVIVSS

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Q9UL72
ID UC72
Q9UL72
Q9
DT O11
DT O1
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Q96K68
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Best Local Similarity
Matches 88; Conserv
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Q9UL72;
Q1-MAY-2000
                                                                                                                                                Q96K68 PRELIMINARY; PRT; 494 AA.
Q96K68;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ14473.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eur leostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hor!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_M3C.
InterPro; IPR003506; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clin. Immunol. Immunopathol. 87:184-192(1998). EMBL; AP035042; AAD56278.1; -. HSSP; P01772; 2F84.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
TISSUE=Mammary gland;
Isogai T., Ota T., Hayashi K.,
Nishikawa T., Nagai K., Sugano
                                                                                                                                  NCBI_TaxID=9606;
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NON_TER 1 18
NON_TER 118 118
SEQUENCE 118 AA; 12872 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAFYYCA----RDRFGEFLFDYWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.0%; ilarity 69.8%; Conservative 11
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                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
  Sugiyama T., Otsuki T., S., Shiratori A., Sudo P
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                               Suzuki Y.,
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Search completed: I
Job time : 31.7067
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Best Local Similarity
Matches 83; Conserv
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SMART; SM00406; IGv; 1.

PROSITE; P850835; IG_LIKE; 4.

PROSITE; P800290; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 494 AA; 53088 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watcanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO27379; BAB55072.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003056; Ig_MHC.
                                                                 136
                                                                                              121 MVTVSS 126
                                                                                                                               80
                                                                                                                                               61 ADSVKGRPTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT
                                                                                                                                                                                              20
                                                                                                                                                                                          1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
|||||:||||||||::
20 EVQLVESGGGLVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGKGLEWVSSISSRSDYIYY
                                                                 LVIVSS
                                                                                                                               RDSVKGRPTISRDNAKNSLYLQMNSLRVDDTAVYYCARDSCNGAI----CYGPSPWGQGT
                                                                                                                                                                                                                                                              Conservative
 December 30,
7 secs
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                                                                                                                                                                                                                                                                         62.7%;
65.9%;
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                2003, 11:01:08
                                                                                                                                                                                                                                                                           Score 417; DB 4; Length 494; Pred. No. 4e-34;
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RESULT 12
Q9UL84
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Best Local S
Matches 84
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Q9Y509;
01-NOV-1999
01-NOV-1999
01-MAR-2003
                                                                             (1)
SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
MEDLINE-98277139; PubMed=9614934;
                                                                                                                                                                          Q9UL84 PRELIMINARY; PRT; 122 AA.
Q9UL84;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                           fetus.";
Clin. Im
                                                                                                                                      Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers. Leukemia 9:1948-1953(1995).
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MEDLINE-96071149; PubMed-7475288;
Cao J. Vescio R.A., Rettig M.B.,
Lichtenstein A.K., Berenson J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S80860; AAD14339.1; -. HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                     Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035030; AAD56266.1; -.
HSSP; P01772; 2FB4.
                                                            Wu X., Liu B., Van der Merwe P.I
Young D.C.;
"Myosin-reactive autoantibodies
                                                                                                                            NCBI_TaxID=9606;
           interPro;
                                                                                                                                                                      Fragment).
                                                                                                                                                                                                                                                                                           119
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                   QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
                                                                                                                                                                                                                                                                                                                                                                           QVHLVESGGGVVQPGKSLRLSCEASGFTFSTYGMSWVRQAPGKGLDV\\LISYDGSTQYY
                                                                                                                                                                                                                                                                                           GTLVTVSS 126
                                                                                                                                                                                                                                                                                                              GIMVIVSS 126
IPR007110; Ig-like IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 AA; 15768 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                64.2%;
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12,
23,
                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 427; DB
Pred. No. 8.3e-
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                       Craniata; Vertebrata; Eute
Catarrhini; Hominidae; Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                              rheumatic
                                                                                   Kalis N.N., Berney
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                                                                carditis
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                                                                                                                                                                                    Query Match
Best Local S
Matches 83
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Best Local S
Matches 82
                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 4.

SMART; SM00409; IG; 4.

SMART; SM00409; IG; 1.

SMART; SM00406; IGv; 1.

SMORT; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS508290; IG—MHC; 1.

Hypothetical protein.

SEQUENCE 493 AA; 53224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1
NON TER 122 122
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01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ90170.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE-Mammary gland;

TISSUE T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Yamamoto J., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Masuho Y., Ono T., Ukayanagi T., Ninomiya K.;

**REDO human cDNA sequencing project.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

**EMBL; AK074651; BAC11114.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8NCL6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003599; Ig.
InterPro; IPR007510; Ig-1ike.
InterPro; IPR003597; Ig-ci.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
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                                                                                               20
                                                                                                                                                                                       83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 63.2%; Score 420; DB 4; Similarity 65.1%; Pred. No. 3.4e-35; 82; Conservative 16; Mismatches 24
                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVTVSS
SSALAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT
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122 AA; 13579 MW;
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
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                                                                                                                                                                                                                                                                                    53224 MW; 12ECD7E094777101 CRC64;
                                                                                                                                                                                                               63.1%; Score 419.5; 65.9%; Pred. No. 2.2
                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           493
                                                                                                                                                                                       1.2e-34;
1es 25;
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                                                                                                                                                                                                                                   DB 4; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 122
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable

region

(Fragment)

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QRESULT
QRESUL
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A Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC032249; AAH32249.1; -.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003597; Ig.
R InterPro; IPR003597; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R SMART; SM00407; IG.
R SMART; SM00407; IG.
R SMART; SM00407; IG.
R SMART; SM00407; IG.
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
"Myosin-reactive autoantibodies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8N5K4;
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8N5K4
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P01772; 2FB4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Blood;
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116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%; Score 443.5; larity 68.0%; Pred. No. 1.3e Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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n der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
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22, Last sequence 23, Last annotations
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local Similarity
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InterPro; IPR003006; Ig_MCC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Tin B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF035024; AAI
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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EMBL; AF035024; AAD56260.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fetus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coung D
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   108
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                                                                                                                                                                                                                                                       GKGTTVTVSS
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                                                                                                                               ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA---
                                                                 SSALAW
                                                                                                                                                                                            ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12437 MW; ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53376 MW;
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66.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                Score 437.5; DB 4
Pred. No. 5.1e-37;
.4; Mismatches 14
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Catarrhini; Hominidae;
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Best Local S
Matches 86
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Strausberg R.;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024289; AAH24289.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                      QBTC77; PRELIMINARY;
QBTC77; CTEMBLrel. 21,
01-JUN-2002 (TTEMBLrel. 21,
01-JUN-2003 (TTEMBLrel. 23,
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Q9HCC1;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Single chain Fv (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
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Mammalia; Eutheria; Primates;
                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-Spleen;
                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                Hypothetical protein. Homo sapiens (Human).
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112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;
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                                                                                                                                                                                                                                                                Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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Pred. No. 6
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                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                471
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RESULT Q9UL93 ID Q9 AC Q9

Q9UL93 Q9UL93;

PRELIMINARY;

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Best Local S
Matches 88
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Best Local S
Matches 90
                                                                                                                                                                            EMMI; BC015760; AAH15760.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR0030596; Ig_v.
Pfam; PP00047; Ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         Q96BB9;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 471 AA; 51791 MW;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96BB9
                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    CISSUE=B-ce
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                                                                                                                                             Similarity
                                                        ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALP---YINSSNYRRGVAAFDIWG
                                                                                       EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                  QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTMVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRQLTSYMY-----FDLMGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCA--LPYINSSNYRRGVAAFDIWGQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVQLVESGGGLVXPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSMSSSSSYIYY
                     OCTMVTVSS
                                            ADSVKGRFT1SRDNSRDTLYLQMNSLRAEDTAVYYCAKDPRGYSASGNYTRE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTLVIVSS 141
QGTLVTVSS
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                      126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.7%;
                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                              65039 MW;
                                                                                                                                            67.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                 Score 446.5; DB 4;
Pred. No. 4.9e-37;
L7; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 450; DB 4;
Pred. No. 1.6e-37;
                                                                                                                                                                              4FCA3AD8ECE263D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388F7F4CF588660E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                              databases
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                                                                                                                                                                               CRC64;
                                                                                                                                   Indels
                                                                                                                                                        Length
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                                                                                                                                  Gape
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                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 6491103
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7860
TELEPAX: (202) 293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                             NUMBER OF SHADLESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
ADDRESSEE: Townsend plaza, Steuart Street Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                         APPLICANT: Willingham, Mark APPLICANT: FitzGerald, David
                                                                                                                                                                                   TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins TITLE OF INVENTION: and Their Uses (as amended)
                                                                                                                                                                                                                       APPLICANT: Brin
                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                         COUNTRY:
                                                                        CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ADSVKGRFAISRDNAKWTLYLOMNSLTIEDTAVYYCAKDLIESNIAEAL---WGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
                                        94105-1492
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    Sughrue, Mion, Zinn, Macpeak & Seas
    Pensylvania Avenue, N.W.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.9%;
79.5%;
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SURPACE RESIDUB VENEERING
ANTIBODIES
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Michael
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Pred. No. 1.1e-41;
7; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 120;
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-331-398A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-331-397B-46
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46, Application US/08331397B
Patent No. 5981726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 543-504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAMB: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 0153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9603
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/767,331
PILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
       COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/331,398A FILING DATE: 28-OCT-1994
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                                                                                                                              COUNTRY: USA
ZIP: 94105-1492
                                                                                                                                                                 STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                     CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARRSARTYYFD-YWGQGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 amino acids
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                                                                                                                                                                                                                                                                                                                                         Pastan, Ira
Benhar, Itai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.2%; Score 486.5; DB 1; 78.3%; Pred. No. 2.7e-41;
                                                                                                                                                                                                                                                                                    Chimeric
Specific
Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Human fetal immunoglobulin
56P1'CL Variable Heavy chain (V-H)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 07/596,289
US/08/331,397B
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                                                                                                                                                                                                                                                                                                      Antibody Fragments,
                                                                                                                                                                                                                                                                                                                          and Mutationally Stabilized Tumor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 119;
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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 8
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Maximum DB seq length: 200000000
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      number of hits satisfying chosen parameters:
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   469
468
467.5
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Gapop 10.0 , Gapext 0.5
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622
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   Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                             Length
   DB
US-09-315-926A-80
US-07-942-245-35
US-08-331-397B-46
US-08-331-397B-46
US-08-331-397B-46
US-08-759-804A-46
US-09-250-198A-1
US-09-260-198A-1
US-09-260-198A-1
US-09-240-274-2
US-09-240-274-6
US-09-240-274-5
US-09-240-274-26
US-09-240-274-150
US-09-240-274-150
US-09-240-274-160
US-09-240-274-150
US-09-240-274-150
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            Sequence 80, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 10, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 27, Appl
Sequence 28, Appl
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		Query M Best Lo Matches	0	NAME	TYPE:	SEQ ID NO	NUMBER OF SOFTWARE:	PRIOR	PRIOR	PRIOR	CURRE	HITLE	APPLI	ENERA APPLI	equen	RESULT 1		4 4 5	43	4 4	40	ب 8 م	37	35	ω (μ 4-	32	ט ני	29	28
61 AI 83 AI	1 EV 23 QV	atch cal	INFC	NAME/KEY: misc fea OTHER INFORMATION:	ij	NO 80		PRIOR FILING DATE:	PILING DATE: 1999-05-20		CURRENT APPLICATION NUMBER:	33		ENERAL INFORMATION: APPLICANT: ES van.	80,	926A-		458.5 458.5	459	459.5	459.5	461 461	461.5	462	462 462	462	462	462	464
SVKG	Ordo Orde	Similarity 4; Conser	(1)(248) RMATION:	misc f	Artificial		PatentIn ve	DATE	DATE	TION	CATI	NIIO	Havenga, M Verlinden,	RMATION:	ppli 2007	8		73.		73			74	٠			74	4.	74.
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RAED	SLTFS - -	495; No. matc	a C	Artificial				ì		Ü	5,926A						AL I GNMENTS	28-1	240-2	240-2	74-8	983-6	02-1	3-07	146-2	34-3	146-2	34-3	240-2
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RESULT 2
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; Sequence 35, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.

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Q99LCA
ID Q99LC
AC Q99LC
AC Q99LC
AC Q99LC
DT 01-JU
DT 01-JU
DT 01-MA
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GN IGH-14
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InterPro; IPKUULL.
InterPro; IPKUULL.
Pfam; PF00047; 19; 4.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 463 AA; 51007 MW; E
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Q99LC4;
Q99LC4;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Shang S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Theng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Theng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Theng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Index regulated in colorectal cancer.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF283666; AAL36987.1; -.

InterPro; IPR003196; Ig-11ke.

InterPro; IPR003196; Ig_MHC.

InterPro; IPR003196; Ig_v.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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cl Similarity 59.0%;
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Last annotation update)
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                                                                                                                                                                 74;
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                                                                  AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCE------LDWFYIWGQGTM 109
                                                                                                                         QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY 60
                        VIVSS 114
                                                    AQKFQGRLTFSRDTSINTAYMYLSSLSTEDSAIYFCARGNLRGGRGFGYNWFDPWGHGTL 139
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Search completed: December 30, 2003, 11:01:09
Job time: 27.7823 secs

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RESULT
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AC Q8
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"Direct Estimation of Relative Affinity by Flow Cytometry I 
"Direct Estimation of Relative Affinity by Flow Cytometry I 
The stimation of B Cell Antigen Receptors in Response 
I Hydroxy-3-Nitrophenyl)Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. 
REMBL; AB069915; BAB63931.1; -

RINCEPTO; IPR007110; Ig-like. 
RINCEPTO; IPR003006; Ig-MHC. 
RINCEPTO; IPR003006; Ig-MHC. 
RINCEPTO; IPR003596; Ig-V. 
REFAMP PPR0047; 1g; 1. 
R SMART; SM00406; IGv; 1. 
R PROSITE; PS50835; IG_LIKE; 1.
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Q924Q0; O1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 23, Last sec
01-MAR-2003 (TrEMBLrel. 23, Last and
V165-D-J-C Mu protein (Fragment).
V165-D-J-C Mu protein (Fragment).
W165-D-J-C MU
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Crani,
Mammalia, Eucheria; Rodentia; Sciur.
SEQUENCE FROM N.A.
STRAIN-BALB/c;
Chernajoveky Y.;
Submitted (OCT-2001) t
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Q8VDC9;
01-MAR-2002
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
Anti-MOG Z12 variable gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELD-----WFYIWGQGTMVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCEL---DWFYIWGQGTMVTVSS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEMMGDIIPILGTGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAPDSNHLYFDYWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAPGKGLEWVGSFDPESGESIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A
                                                                                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.5%; Score 385; DB 11; 62.7%; Pred. No. 1.6e-32;
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                              the
                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
2a (Fragment).
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Last annotation updat
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                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C99D2433F2BAD8A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                   168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143
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                              databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4:
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                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
Q9BRV0
ID Q9BRV
AC Q9BRV
DT 01-JU
DT 01-JU
DT 01-MJ
DE HYPOT
OS HOMO
OS ELMAN
OC ELMAN
OC MAMMMA
OC MAMMA
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                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Targeting T cells to the CNS."
Submitted (JAN-2002) to the EMB
EMBL; AJ416332; CAC94867.1; -.
InterPro; IPR007110; Ig 1ike.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
pfam; pP00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON TER
168 168
SEQUENCE 168 AA; 18293 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 4.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N
STRAIN=BALB/c;
Sembi P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BRV0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (APR-2001) to the
EMBL; BC005951; AAH05951.1;
HSSP; P01789; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
SEQUENCE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                       Local Similarity
                              140
                                                                          107
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                                                                                                                                                                                                                                                                                               76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
                                                            GIMVIVSS
                                                                                                                 AKKPOGRVTLTTDTSTSTVYMELRSLRSDDTAVYYCARRYCSYSSCONDYYYYYMDVWGK
                                                                                                                                             AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYY--------
                                                                                                                                                                                                          CITVIVSS
                                                                                                                                                                                                                                                                                                                                                                                     al protein.
500 AA; 5
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ilarity 60.5%;
Conservative 2
                                                                                                                                                                                                                                                                                                  Conservative
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                              147
                                                                                                                                                                                                                                                                                                                                                                                     54154 MW;
                                                                                                                                                                                                                                                                                                                    63.3%;
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he EMBL/GenBank/DDBJ
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Last sequence
Last annotation
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Pred. No. 5.8e-32;
?1; Mismatches 21;
                                                                                                                                                                                                                                                                                             Score 378; DB 4;
Pred. No. 4.2e-31;
5; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                             4.2e-31;
ches 23;
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                                                                                                                                                                                                                                                                                                                                         Length 500;
                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
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                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                           -CELDWFY----IWGQ 106
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                                                                                                                                                                                                                                                                                               Gaps
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79 60

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GQGTTVTVSS 149

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RESULT 9
Q8VCX7
ID Q8VC
AC Q8VC
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DT 01-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; 1:... 1g; 4.
Pfam; PF00047; 1g; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKB; 4.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
   Q8VCX7;
Q8VCX7;
01-MAR-2002 (
01-MAR-2002 (
01-MAR-2003 (
Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=C57BL/6J; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK007918; BAB
HSSP; P01842; 7FAB.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:96443; Igh-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Pancreas;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1810060009Rik protein.
IGH-1 OR 1810060009RIK.
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                                                                                                                                                            PRELIMINARY;
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Last sequence update)
Last annotation update)
                                 Last sequence update)
Last annotation update)
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Pred. No. 2.2e
22; Mismatches
                                                                                                  Created)
                                                                                                                                                            PRT;
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Query Match
Best Local S
Matches 79
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MGD; MGI:96448; Igh-6.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MCC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 5.
SMART; SM00406; IGv 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS508290; IG_MIC; 3.
                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=98322155; PubMed=9657749;

Jacquemin M.G., Vander Elet L.P.L.;

Jacquemin M.G., Vander Elet L.P.L.;

"Mechanism and kinetics of factor VIII inactivation: study with

"Mechanism and kinetics of factor a hemophilia A patient with
                                                                                                                                                                                                                                                                                                                                                                                                      Q9Y298
Q9Y298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                      Signal.
                                                                                                                                                                Blood 92:496-506(1998)
EMBL; AJ224083; CAA118
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                           196 VH.
                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein SEQUENCE 613 AA;
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                                                SEQUENCE
                                                            NON TER
                                                                                              PROSITE;
                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Salivary gland;
                                                                                                                             InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                      protein precursor (Fragment).
19; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVQLQQSGAELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGSGSTNY
                                                                                            PS50835; IG_LIKE;
                                                 150
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                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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150
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                                                16031 MW; 563D164AB22802D5
 65.2%; Score 389.5; DB 4
67.5%; Pred. No. 5.8e-33;
tive 11; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 390; DB 1
Pred. No. 3e-32;
                                                                         POTENTIAL
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                         DB 4;
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                                                  CRC64;
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                        Length 150;
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Gaps

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RESULT
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ID Q9
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DT 01
DT 01
DT 01
DT 01
RN 0C Bu
OCC MM
OCC MM
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TRA 16
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Best Local S
Matches 85
                                                                                                                                                                                                                                          Q96DKO;
Q96DKO;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ25298.
Homo sapiens (Human).
Homo sapiens (Human).
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Q9UL95;
01-MAY-2000
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SMART; SM00406; IGV; 1.

PROSITE; PS50835; IGLIKE; 1.

NON TER 125 125
SEQUENCE FROM N.A.

TISSUB-Gastric mucosa;
TISSUB-Gastric mucosa;
Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
Ishibashi T., Kanehori K., Yosida M., Takiguchi S., Kusano J.,
Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035019; AAD56255.1; -.
HSSP; P01810; 2FB1.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
DF8m. DF0047. ic. 1g_v.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96DK0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
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125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                            Chordata;
Primates;
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Pred. No. 2.9e-35;
                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local S
Matches 82
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Best Local :
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"MEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKOS8027; BAB71633.1; -.
InterPro; IPR003006; Ig_HC.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003956; Ig_v.
Pfam; PF00047; ig; 4.
PROSITE; PS00406; IG, ILKE; 4.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 496 AA; 53532 MW; C72EE1E247C86FED CRC64;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
SEQUENCE 159 AA; 17497 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Homo sapiens putative microfibrillar protein with Ig-like mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3)."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AV039025, AAX082649.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative matrix cell adhesion molecule-3.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q96QS0
Q96QS0;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                             105
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                                                                                                                                                                                                                                                                                      82;
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Similarity 65.3%;
                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                GOGTMVTVSS 114
                                                                                                     SSVT
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                                                                                SOKFOGRLIMIRDISTSTVYMDLSSLRSDDTAVYFCAREMEITFGGAVSKGFYYYGMDVW
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                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                              67.7%; Score 404; DB 4; Length 159; 63.1%; Pred. No. 1.9e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
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Pred. No. 3e-34;
                                                                                                                                                                                                                                                                                                                                                                                            5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ξ
                                                                                                                                                                                                                                                                                      14; Indels
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                                                                                                                                                                                                                                                                                      16;
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RESULT 3
29TU-94
ID 29UL
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NON_TER 1 1 1.

NON_TER 124
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
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01-MAY-2000
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
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MEDLINE=98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N.,
Young D.C.;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                    Chordata;
Primates;
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                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC009851; AAH09851.1; -.

InterPro; IPR000005; HTHATAC.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003396; Ig_wHC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 5.

RMART; SM00406; IGv; 1.

RPROSITE; PS00041; HTH APAC_FAMILY_1; 1.

RPROSITE; PS00031; IG_LIKE; 5.

RPROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q96GA6 PRELIMINARY; PRT;
Q96GA6;
01-DEC-2001 (TEMBLrel. 19, Created)
01-DEC-2001 (TEMBLrel. 19, Last seq
01-MAR-2003 (TEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata,
Mammalia; Eutheria; Primates;
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NON_TER 1 1
NON_TER 119 119
SEQUENCE 119 AA; 13205 MW;
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SMART; SM00406; IGv; 1.
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HSSP; P01810; 2FBJ
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Young D.C.;
"Myosin-reactive autoantibodies in
                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                         AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCEL-----DWFYIWGQGTMVTVS
                                                                                       OMOLVOSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMGWITPFNGNTNY
                                                                                                           QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQKFQGKVTMTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLWFDPWGQGTLVTVSS
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AQKFQDRVTITRDRSMNTAYMELSSLRSEDTAMYYCARGYSSSWDDAFDIWGQGTMVTVS
                                                                                                                                                                                                                                                                al protein. 614 AA; 6
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Conservative
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13205 MW; 13E64F5345F4A16E CRC64;
                                                                                                                                                                                                                                                                  67921 MW;
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                                                                                                                                                                                                69.3%;
71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                           Score 413.5; DB 4; Length Pred. No. 1e-34; 6; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                  55EF536E77AA9BBB CRC64;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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                                                                                                                                     SPTREMBL 23:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
7: sp_mhc:*
8: sp_phage:*
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Gapop 10.0 , Gapext 0.5
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597
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                    sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
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sp_phage:*
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sp_bacteria:*
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

13 14 16	10 11 12	7654227	Result
378 376 373.5 372.5	399.5 389.5 385.5	482 416.5 413.5 410.5 410.5	score
63.0	64.5 63.3	80.7 70.7 69.8 69.3 68.8 68.3	Query Match
500 463 497 119	473 613 150 143	116 124 119 614 125 496	Query Match Length
5414	11411	44444	DB
Q9BRV0 Q99LC4 Q8WY24 Q8WYZ2	Q9D8L4 Q8VCX7 Q9Y298 Q924Q0 Q8VDC9	Q9UL89 Q9UL92 Q9UL94 Q96GA6 Q96GA6 Q9UL95 Q96DK0	ij
Q9brv0 homo Q991c4 mus Q8wy24 homo Q9gyz2 schis	Q9d814 mus Q8vcx7 mus Q9y298 homo Q924Q0 mus Q8vdc9 mus	Q9ull8 homo Q9ull94 homo Q9ul94 homo Q9ug96 homo Q9ul95 homo Q9ul95 homo Q96dk0 homo Q96dk0 homo	Description
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58.0	58. 9	59.0	59.0	59.1	59.1	59.2	59.3	•	59.5	•	•	•	59.8	59.8	60.1	60.3	60.3	60.3	60.4	60.6	•	•	•	•	•	61.6	•
145	142	145	489	278	141	144	145	482	137	146	123	145	473	145	480	143	139	118	117	147	481	140	142	120	117	143	143
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Q924Q9	Q924Q2	Q924Q7	Q8VCX4	Q921K1	Q924Q4	Q924P5	Q924Q6	Q8K172	Q924R6	Q924R8	Q8VIJ1	Q924R4	Q99L25	Q924R3	Q8K0Z4	Q924Q5	Q924R5	Q9Z1C4	Q9QXF0	Q925S3	Q91WT1	Q924P8	Q924Q1	Q920E8	Q9QXE9	Q924P9	Q91V67
Q924q9 mus	Q924q2 mus	Q924q7 mus	Q8vcx4 mu	Q921k1 mus	Q924q4 mus	Q924p5 mus	Q924q6 mus	Q8k172 mus	Q924r6 mus	Q924r8 mus	Q8vij1 mus	Q924r4 mus	Q99125 mus	Q924r3 mus	Q8k0z4 mus	Q924q5 mus	Q924r5 mus	Q9z1c4 mus	Q9qxf0 mus	Q92583 mus	Q91wt1 mus	Q924p8 mue	Q924q1 mus	Q920e8 mus	Q9qxe9 mus	Q924p9 mus	Q91v67 mus
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ALIGNMENTS

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A Zakut R., Cohen J., Givol D.;

C --- MISCELLANGOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED

FROM A MYELOMA THAT SECRETES IGG2B.

C --- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR, A93708; GVMS11.

R PIR; A93708; GVMS11.

R PIR; A93708; GVMS11.

R HSSP; P01810; 2FBJ.

R InterPro; IPR003106; Ig-NEC.

R InterPro; IPR003196; Ig-V.

R InterPro; IPR003196; Ig-V.

R Ffam; PP0047; ig; 1.

R PROSITE; PS50835; IG_LIKE; 1.

R PROSITE; PS50835; IG_LIKE; 1.

R Inmunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P01745;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V region MPC 11.

Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE=81053741; PubMed=6253904; Zakut R., Cohen J., Givol D.; Cakut R., Cohen J., Givol D.; "Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPC11."; Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                        114 S 114
                                                                                                                             121 S 121
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                                                                                                                                                                                                                                                  61 NDNLKGKATITADTSSSTAYIQLSSLTSEDSAIYHCARGIYYNSSPYFDSWGQGTTLTVS
                                                                                                                                                                                                                                                                                  55 TDPFQGVYIKWERVTVSLKPSFNQAYMELVNLFNEDGAVYYCAREWKGQVNVNPFDYWGQ 114
                                                                                                                                                                                                                                                                                                                                                                         ch 57.9%; Score 345.5; DB 1; Length 121;
l Similarity 53.7%; Pred. No. 1.9e-28;
65; Conservative 24; Mismatches 25; Indels 7
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121 121
121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
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RESULT 13
HV51_MOUSE
ID HV51_MOUSE
AC P06330;
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    REAL REAL COLUMN TERM OF THE PROPERTY OF THE P
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Matches 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibodies: somatic mutation evident in a gamma 2d variation (1981).

Cell 24:625-637(1981).

-I- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)
                                                                                                                                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
Ig heavy chain V region AC38 205.12.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=81234548;
Bothwell A.L.M.,
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQÜENCE
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J00529; AAA38170.1; -.
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MEDLINE-84182519; PubMede-6201362;
Dildrop R., Bovens J., Siekevitz M.,
"A V region determinant (idiotope) ex
lymphocytes is encoded by a large set
                                                                                     SEQUENCE
                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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1A6U; 27-MAY-98.
1A6W; 15-JUL-98.
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bulin V region; Sign
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Paskind M., Reth
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D SEGMENT.
JH2 SEGMENT.
BY SIMILARITY.
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Pred. No. 4.9e-29;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1B57DD4FD0C9F465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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M., Beyreuther K., Rajewsky K.; 
) expressed at high frequency i 
set of antibody structural gen
                                                                                                                                                                                                                                                                                                                    118
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                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 139;
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    genes.";
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RESULT 14
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                                                                                                                          SOFTITERRED DREED 
Query Match 58.0
Best Local Similarity 56.3
Matches 72; Conservative
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Best Local
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PEAM; PE00047; 1g; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 1

Immunoglobulin v region; Pyz

DOMAIN

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InterPro; IPR003006; Ig_MIC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                       MOD_RES
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SEQUENCE
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21-JUL-1986 (Rel. 01, Last sequence up. 15-SEP-2003 (Rel. 42, Last annotation Ig heavy chain V-I region SIE.
Homo sapiens (Human).
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NON TER
SEQUENCE
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PIR; A02040; MHMS38.
HSSP; P01789; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 20:5822-5830(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andrews D.W., Capra J.D.; 
"Amino acid sequence of the variable regions of heavy chains 
idiotypically cross-reactive human IgM anti-gamma-globulins (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
MEDLINE=82046599; PubMed=7028111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986
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                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activ
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                          124
124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104
118
96
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                                                                                                                             13732 MW;
                                58.0%;
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                                                                                                                                                                                                                                                    Pyrrolidone carboxylic
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Pred. No. 5.2e-29
                                   Score 346;
Pred. No. 1
                                                                                                                                                                                       PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                       IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                             62CED4573BDEF59F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124
                                   1.8e-28;
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                                                                                                                                CRC64;
                                                                                                                                                                                                                                                        acid
                                                                Length 124;
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         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118
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12;

Mismatches

24;

20;

Gape

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RESULT 10
HV03_MOUSE
                                                                                                    A POR DE DE COCOCCERTE DE COCCCERTE DE COCCC
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Best Local S
Matches 70
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Best Local S
Matches 7.1
                                                                                            SEGMENT, JH2.

SEGMENT, JH2.

-i- SIMILARITY: Contains 1 immunoglol HSSP; PO1789; 1MCP.

InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; ig; 1.

SMART; SM00406; IGy; 1.

PROSITE; PS50835; IG LIKE; 1.
IMMUNOGlobulin V region; Hybridoma.
DOMAIN 11 11 IG-LIKE
NON TER 120 120
SEQUENCE 120 AA; 13307 MW; FF04E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain v region 36-65.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Verte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IOv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=83131846; PubMed=6186498;
Siekevitz M., Gefter M.L., Brodeur P.,
                                                                                                                                                                                                                                                                                                                                                                                                       "The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";

Bur. J. Immunol. 12:1023-1032[1982].

-i- mISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME (CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marshak-Rothstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HV03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A94264; HVMSG7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J00493; AAA38128.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 60.7%;
| Similarity 58.7%;
| 71; Conservative 2
  Similarity 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114
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140
       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                              Contains 1 immunoglobulin-like domain
                                                                           120
13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15514 MW;
59.7%; Score 356.5; DB 1
58.3%; Pred. No. 1.4e-29;
tive 20; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 362.5; DB 1;
Pred. No. 4.2e-30;
1; Mismatches 22;
                                                                                                                                              IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG HEAVY CHAIN V REGION 93G7 IG-LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25A4CBBE31DA5CE8 CRC64;
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                                               DB 1;
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                                               Length
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                                                  120;
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  7;
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  Gaps
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RESULT 12
HV07_MOUSE
RRROCOSBATAN
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Best Local S
Matches 70
                              HV07_MOUSE STANDARD; PRT; 139 AA.

p01751; p01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V region B1-8/186-2 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebr:
Mammalia; Butheria; Rodentia; Sciurognathi; Mur:
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WOUSE
IV50 MOUSE
STANDING
IV50 MOUSE
P6329;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A02037; MHNS15.
HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=84182519; PubMed=6201362;
Dildrop R., Bovens J., Siekevitz M.,
"A V region determinant (idiotope) e:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                     70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                              AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELD-WFYIWGGGTMVTVSS
                                                                                                                                                                                                                                                                                      QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIFILGTGNY
                                                                                                                                                                                                                  NEKFKSKATLTVDKSSSATYMQLSTPTSEDSAVYYCARWDYEGDRYFDVWGTGTTVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLLQPGTELVKPGASVNLSCKASGYTFTSYWMHWIRQRPGQGLEWIGGINPSNGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQLVQSGAEVKXPGSSVKVSCKASGGTESSHAISWVRQAPGQGLEWMGDIIPILGTGNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN
                                                                                                                                                                                                                                                                                                                                                                           120 AA;
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106
22
120
                                                                                                                                                                                                                                                                                                                         Conservative
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105
120
96
                                                Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                           13311 MW;
                                                                                                                                                                                                                                                                                                                                    59.1%;
                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                   V SEGMENT.
D SEGMENT.
J SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                    Score 353; DB 1;
Pred. No. 3.3e-29;
                                                                                                                                                                                                                                                                                                                                                                           914453F426F09834 CRC64;
                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                Length 120;
                                                                                                                                                                                                                                                                                                                         Indels
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Best Local
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HV13 MOUSE
P01757;
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NON_TER
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
-!- SIMILARITY: Contains 1 immunoglobulin-like
PIR; A02039; MINS4E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete amino acid sequence of a mouse mu heavy chain constant region domains."; Biochemistry 21:5415-5424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55. MEDLINE=83075344; PubMed=6816276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region MOPC 104E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HV12 MOUSE
P01756;
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V region J558.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P00047; 15, 1, SM00406; IGV; 1.
SM00406; IGV; 1.
E; P850835; IG LIKE; 1.
2globulin V region; Glycoprotein.
1 116 IG-LIKE.
N 296 BY SIMILARITY.
N 96 N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCEL----DWFYIWGQGTMV
                                                                                                                                                                                                                                                                    AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC--ELDWFY-IWGQGTMVTVSS 114
                                                                                                                                                                                                                                                                                                                                                          QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIFILGTGNY 60
                                                                                                                                                                                                                                                                                                                                   EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60
                                                                                                                                                                                                                                             NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDYDWYFDVWGAGTTVTVSS
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59.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 367.5; DB 1
Pred. No. 1.1e-30;
5; Mismatches 20
                                                                                                                                   PRT;
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ches 20;
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Best Local
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Nature 283:35-40(1980).

-I- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS
BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS,
WHICH OCCUR IN THE D AND J SEGMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV02 MOI
P01746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region.
DOMAIN 1 116
              This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute. There are no restrictioned by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.cor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schilling J., Clevinger B., Davie J.M., "Amino acid sequence of homogeneous ant rearrangements in heavy chain V-region of the sequence of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                            "Somatic mutation in genes for the variable immunoglobulin heavy chain."; science 216:309-311(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence upd
15-SEP-203 (Rel. 42, Last annotation u
15-Sep chain V region 93G7 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- MISCELLANEOUS: THIS PROTEIN BINDS
-!- SIMILARITY: Contains 1 immunoglobu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=80078170; PubMed=6765983;
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                                                                                                                                                                                                                                                                                                                        MEDLINE=82152818; PubMed=6801765; Sims J., Rabbitts T.H., Estess P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                Capra J.D.;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                      SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
117
117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13024 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
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59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 363.5; DB 1;
Pred. No. 2.7e-30;
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BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                           Slaughter C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .M., Hood L.; antibodies to dextran
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPRO077110; Ig-like.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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HV1C_HUMAN
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(In) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.1-36,
Marcel Dekker, New York (1978).
-I- MISCELLANEOUS: THIS BPSILON CHAIN WAS ISOLATED FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                 Bell i.O., Gould H.J.; "Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."; Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=83065234; PubMed=6815656;
Kenten J.H., Molgard H.V., Houghton M., Derbyshire R.B., Viney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy, chain 'megion ND precursor (Fragments).
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PIR; S00476; HYHU35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                           InterPro;
P; P01789; IMCP.
GO:0005576; C:extracellular; NAS.
GO:0005823; F:antigen binding activity;
GO:0006825; F:ammune response; NAS.
erPro; IPR007110; Ig-like.
erPro; IPR003006; Ig_MHC.
erPro; IPR003596; Ig_WHC.
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Pred. No. 4.7e-31;
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Matches 76
Query Match
                                                              Pfam; PF00047; 1g; 1
SMART; SM00406; IGv; 1
PROSITE; PS50835; IG LIKE; 1
Immunoglobulin V region.
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02022; G1MSAA.
HSSP; P01772; ZEMSAA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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"Structural studies on induced antibodies with defined idiotypic specificities. VII. The complete amino acid sequence of the heavy chain variable region of anti-p-azophenylarsenate antibodies from mice bearing a cross-reactive idiotype.";

J. Immunol. 123:279-284(1979).
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PROSITE; PS50835; IG LIKE;
Immunoglobulin V region; S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae;
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STRAIN=A/J;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region (Anti-arsonate antibody).
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l Similarity 59.4%;
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                                              114 AA;
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IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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Pred. No. 6
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PYRROLIDONE CARBOXYLIC ACID.
  Score 369;
                                                                                         IG-LIKE
                                              99DD8F0B6A69F4BE
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  ۳,
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  Length 114;
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                                              CRC64;
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RESULT 3
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Best Local S
Matches 76
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PIR; A02024; HVHHHG.
HSSP; P01772; ZPB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding activity; NA:
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR003006; Ig_HHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00356; Ig_V.
HV48 MOUSE
P03980;
23-OCT-1986
23-OCT-1986
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-SEP-2003 (Rel.
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P01743;
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Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
[1]
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene subgroups.";
.Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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                                                                                                                                  AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC 96
                                                                                                                    AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC 115
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(Rel. 02, Created)
(Rel. 02, Last sequence update)
(Rel. 38, Last annotation updat
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el. 01, Last sequence update)
el. 42, Last annotation update)
V-I region HG3 precursor.
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                                                    STANDARD;
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79.2%;
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                                                                                                                                                                                                                                     Score 385; DB 1;
Pred. No. 1.7e-32;
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RESULT 4
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Best Local
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P23083;
P23083;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOMAIN
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003906; Ig_v.
InterPro; IPR003996; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=84248078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
This SWIGS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                     "Dispersed localization of D segments in the human immu heavy-chain locus.";
EMBO J. 7:1047-1051(1988).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=88256408; PubMed=2841108;
Mateuda F., Lee K.H., Nakai S., S.
Ohno H., Fukuhara S., Honjo T.;
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PIR; A02033; HVMST7.
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138 AA;
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Pred. No. 3.1e-31;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                             segments in the human immunoglobulin
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GenCore version (c) 1993 - 2003

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
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Maximum DB
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Gapop 10.0 ,
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597
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C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Caccession: B33548
R;Kipps T.J.; Tomhave, B.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expt
A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: B33548
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-126 <KIP>
A;Experimental source: the sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Ig heavy chain V region (G6+ T-L30) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0960
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Bridence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0960
A;Status: nucleic acid sequence not shown
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F;15-98/Domain: immunoglobu
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79.4%;
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Pred. No. 1.5e-37;
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Pred. No. 8.7e-38;
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F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
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A;Residues: 1-136 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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73.5%;
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Pred. No. 1.6e-37;
6; Mismatches 8
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Search completed: December 30, Job time: 11.9277 secs

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Ig heavy chain V region (G6+ T-L42) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0962
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0962
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C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps. T.J.
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A; Residues: 1-120 < MAR>
C; Superfamily: immunoglo
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A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-132 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin F;1-30/Region: framework 1
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J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
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F;31-35/Region: complementarity-determining 1
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                                                                                                                    framework 2
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                                              complementarity-determining
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Score 501;
  BB
2
Length 132;
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R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Bvidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
Sxp. Med. 175, 983-991, 1992
A;Title: Bvidence for somatic selection of natural a A;Reference number: PH0952; MUID:92202880; PMID:1552
A;Accession: PH0958
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C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
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C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0955
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F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-110/Region: complementarity-determining 3
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                                    A; Molecule type: DNA
A; Residues: 1-127 < MAR>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                               A;Status: nucleic acid sequence not shown
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Local Similarity 80.8%;
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Pred. No. 5e-38;
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PMID:1552291
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A;ACCEBBLUI. A. A. A;ACCEBBLUI. A;MOLECULE type: mRNA
A;Residues: 1-627 <FRI>
A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin; membrane protein
C;Keywords: immunoglobulin; membrane protein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-627/Product: Ig mu chain #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-133 <KIP>
A;Residues: 1-133 <KIP>
A;Experimental source: the sequence was determined from A;Experfamily: immunoglobulin V region; immunoglobulin h C;Keywords: heterotetramer; immunoglobulin P;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
C;Accession: S14683; S08047
R;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A;Title: Complete nucleotide sequence of the membrane form of th
A;Reference number: S14683; MUID:90332450; PMID:2115996
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A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expra;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: C33548
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C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: C33548
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 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----
                                                          OVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
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Pred. No. 1.4
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R; Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A; Title: Evidence for somatic selection of natural autoantibodies
A; Reference number: PH0952; MUID:92202880; PMID:1552291
A; Reference number: PH0953
A; Reference number: PH0953
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C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0953
                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-132 <FIG>
A;Residues: 1-132 <FIG>
A;Cross-references: EMBL: Z31681; NID: g509788; PIDN: CAA83486.1; PID: g1335147
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                             C;Accession: S46394
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
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F;31-35/Region: complementarity-determining
F;36-50/Region: framework 2</pre>
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                                                                                    Matches 102;
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QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIFILGTGNY 60
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                                                                                                       84.1%;
77.3%;
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                                                                                 Score 502; DB 2;
Pred. No. 2.4e-38;
7; Mismatches 5
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Pred. No. 1.8e-38;
2; Mismatches 7
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R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J. Exp. Med. 175, 983-991, 1992
A;Title: Bvidence for somatic selection of natural a A;Reference number: PH0952; MUID:92202880; PMID:1552 A;Accession: PH0957
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E;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
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F;51-67/Region: complementa:
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A. Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Tille: Developmentally restricted immunoglobulin heavy chain variable region A;Reference number: A33548; MUID:89345575; PMID:2503826
                                                                                  Ig heavy chain V-1 region (NEI) - human (Species: Homo sapiens (man) (Species: Homo sapiens (man) (T-Jan-1990 #sequence revision 17-Jan-1990 #text_change 16-Aug-1996 (C) Date: 17-Jan-1990 #sequence revision 17-Jan-1990 #text_change 16-Aug-1996 (C) Accession: A33548; PH0956
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C;Species: Homo sapiens (man)
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Pred. No. 3.8e-39;
5; Mismatches 8
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Pred. No. 1.9e-39;
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PMID:1552291
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R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0952
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A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0952
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F;68-98/Region: framework 3
F;99-117/Region: complementarity-determining
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F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
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A; Residues: 1-129 < Mi
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A;Molecule type: DNA
A;Residues: 1-128 <M
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Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)
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F;36-50/Region: framework 2
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;68-98/Region: framework 3
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Matches
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Similarity 79.8%;
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length: 2000000000
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ALIGNMENTS

RESULT 2 PH0961 R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J. J. Exp. Med. 175, 983-991, 1992 A;Title: Evidence for somatic selection of natural autoantibodies A;Reference number: PH0952; MUID:92202880; PMID:1552291 A;Accession: PH0959 F;31-35/Region: immunoglobulin homology <IMM> C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-30/Region: framework 1 A; Molecule type: DNA A; Residues: 1-116 < MAR> Ig heavy chain V region (G6+ T-L26) - human (fragment) C;Species: Homo sapiens (man) C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996 F;36-50/Region: framework 2 A; Status: nucleic acid sequence not shown C; Accession: PH0959 ;99-104/Region: ;51-67/Region: complementarity-determining ;68-98/Region: framework 3 Query Match Best Local Similarity Matches 102; 13 13 -1 QVQLVQSGABVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY complementarity-determining 3 Conservative 86.4%; 87.9%; Score 516; DB 2; Pred. No. 1.1e-39; 4; Mismatches 8 N œ -: Length 116 Indels 2; Gaps 60 60

R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH9961

A;Molecule type: DNA
A;Residues: 1-119 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology

A; Status: nucleic acid sequence not

Ig heavy chain V region (G6+ T-L33) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0961

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US-08-437-642B-4
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
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APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/7:
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Paul J. APPLICANT: Leonard
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nes 88; Conserv
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CITY: South San Francisco
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                                                                                                APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lee, Wendy M.
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70.4%; Pred. No. 2.9e-37;
tive 14; Mismatches 18; Indels 5
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                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genencech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-NO. 6407213-1993
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICA
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FILING DATE: 14-UNN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 15-JUN-1992 PRIOR APPLICATION DATA:
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FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
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08/146206
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ELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                       REGISTRATION NUMBER: 40,378 REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
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                                                                                                              Lee, Wendy M.
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US-08-379-057-32
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                                                                                                                               RESULT 12
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                          Sequence 32, Application US/08379057 Patent No. 5876950
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     GENERAL INFORMATION:
APPLICANT: Siadak
APPLICANT: Holleni
APPLICANT: Gillil
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TITLE OF INVENTION: W
TITLE OF INVENTION: V
TITLE OF INVENTION: V
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC COMPATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: HOWElls, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: PO
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CORRESPONDENCE ADDRESS:
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CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KBY: Peptide LOCATION: 1..125
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1880 Century Park East - Suite 500
Siadak, Anthony W.
Hollenbaugh, Diane L.
Gilliland, Lisa K.
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                             67.6%; Score 445; DB 5;
67.2%; Pred. No. 2.2e-37;
ative 16; Mismatches 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FD-2630
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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-379-057-32
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US-07-934-373C-4
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,057
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNBY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0133-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 727-36
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                            NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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MEDIUM TYPE: Floppy
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APPLICANT: Bajorath, Jurgen
APPLICANT: Aruffo, Alejandro A.
TITLE OF INVENTION: Monoclonal Antibodies Specific For
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
TITLE OF INVENTION: In Diagnosis and Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
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                                                                        CITY: South San
                                                                                           STREET:
                                    COUNTRY:
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                   ZIP: 94080
                                                                                                             ADDRESSEE:
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                                                       California
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                                                                                         1 DNA Way
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                                      USA
                                                                                                         Genentech, Inc
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727-3601
MO: 32:
                                                                      Francisco
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Pred. No. 2.1e-37;
8; Mismatches 11;
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CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 144
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                                                                                                                                                                                              OTHER INFORMATION: anti-Rh(D) antibody clone US-09-240-274-150
                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver.
SEQ ID NO 150
LENGTH: 126
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 150, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: anti-Rh(D) antibody clone SH24-09-240-274-144
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF FILE REPERENCE: 09596-42U2 CURRENT APPLICATION NUMBER: US/09/240,274 CURRENT FILING DATE: 1999-01-29 EARLIER APPLICATION NUMBER: 60/081,380 EARLIER FILING DATE: 1998-04-10 UNMBER: 60/028,550 EARLIER FILING DATE: 1998-04-10 UNMBER: 60/028,550 EARLIER FILING DATE: 1998-10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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                                                                                                                                               Similarity
ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAAT
                                                                                  EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWV:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDWRVRAFSSG:
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                                                                EVQLLESGGGVAQPGRSLRLSCVASGFSLRSYGMHWVRQAPGKGLEWV
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                                                                                                                                Conservative
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                                                                                                                                             68.0%;
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                                                                                                                              Score 447.5; DB Pred. No. 1.2e-37.5; Mismatches 2
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                                                                                                                                                         Length
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                                 VAFDIWGRGT 119
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US-08-428-197-1
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                                                                                                                                                                                                                                              Query Match
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Sequence 1, Application US/08428197 Patent No. 5891438
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/
APPLICATION NUMBER: PCT/US93/
EILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: SILVER
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TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOPTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                      CLONE: 18/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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121 VTVSS 125
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California
                                                                                                                                                                                                                                     Similarity
                                                                     ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
                                                                                                                                                       EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
                                        ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCTKGQVLYYGSGSYHWFDPWGQGTL
                                                                                                                            BVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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1880 Century Park East - Suite 500
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                                                                                                                                                                                                                                   67.6%; Score 445; DB 2; 67.2%; Pred. No. 2.2e-37;
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RESULT 6
US-09-202-181-4
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; APPLICANT: REISNER, Yair et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIB
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: REISNER=5
CURRENT APPLICATION NUMBER: US/09/202,181
CURRENT FILING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: 118625
PRIOR FILING DATE: 1996-06-11
PRIOR APPLICATION NUMBER: IL97/00184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-315-574-30
                                                                                                                                                                        Sequence 4, Application US/09202181
Patent No. 6254867
GENERAL INFORMATION:
APPLICANT: REISNER, Yair et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
PRIOR APPLICATION NUMBER: US 08/665,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
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13-JUN-1996
                                                                                                                                                    Yair et al.
HUMAN MONOCLONAL ANTIBODIES TO THE HEPAT ITS B SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.3%; Score 456; DB 4; Length 123
72.0%; Pred. No. 1.7e-38;
Live 14; Mismatches 19; Indels
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; LENGTH: 121
; TYPE: PRT
; ORGANISM: human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: S1egel, Donald L.
APPLICANT: S1egel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT FILLING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 126
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Best Local Similarity 70.4%;
Matches 88; Conservative 13
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                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                      Query Match
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
PEATURE:
OTHER INFORMATION: anti-Rh(D) chain D04
                                                                                                                                                                                                                               Match 68.0%;
Local Similarity 68.3%;
les 86; Conservative 1
121 MVTVSS 126
                                    120 MVTVSS 125
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                                                                                                         61 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATW-RAFDIWGRGT 119
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                                                                           ; Score 447.5; DB 3;
; Pred. No. 1.2e-37;
15; Mismatches 24;
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                                                                                                                                                                                                                                                                        Length 126;
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US-09-240-274-144

Sequence 144, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:

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PATENTIAL OF SEPRENCIAL OF SERVICE

PATENTIAL INFORMATION:
APPLICANT: Siegel, Donald L.
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER FILING DATE: 1999-01-380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-10-11
NUMBER: OF SEQ ID NOS: 224
SOFTWARE: PATENTIAL DATE: 2.0
SEQ ID NO 27
LENGTH: 127
TYPE: PRT
TYPE: PRT
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; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-75
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Best Local
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CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
PILE REFERENCE: P0979
                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                               EVQLLESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQAPGKGLEWVS
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GTTVIVSS 127
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72.7%;
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                                                                                                                                                                                             Score 460; DB 3; Length 127
Pred. No. 7e-39;
L1; Mismatches 23; Indels
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Pred. No. 1.4e-38;
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GENERAL INFORMATION:
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Patent No. 5977322
      GENERAL INFORMATION:
APPLICANT: Marks, Ja
APPLICANT: Schier, R
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                         Sequence 30, Application US/09315574 Patent No. 6512097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 90; Conserva
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APPLICATION NUMBER: US 60/000,250

PILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: HULLER, Tom

REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 02307E-061-

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
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APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el |
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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CITY: San Francisco
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Marks, James D.
Schier, Robert
VENTION: No. 6512097el High Affinity Human
VENTION: Tumor Antigens
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72.0%;
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); Pred. No. 1.7e-38;
14; Mismatches 19; Indels
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Title:
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Sequence:
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Gapop 10.0 , Gapext 0.5
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   EVQLVKSGEGLVKPGGSLRL......AATWRAFDIWGRGTMV VSS
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   GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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US-08-918-148-78
US-08-918-148-75
US-08-918-148-75
US-09-240-274-27
US-08-665-202-30
US-09-315-574-30
US-09-240-274-14
US-09-240-274-15
US-08-428-197-1
US-08-428-197-1
US-08-379-057-32
US-07-934-373C-4
US-08-197-150-62-4
US-08-197-150-62-4
US-08-197-150-62-4
US-08-197-150-62-4
US-08-197-150-63-150-63
US-09-240-274-24
US-09-240-274-24
US-09-240-274-28
US-09-25-769B-38
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D _D	. <i>5</i>	ş 8	문 왕	Query Ma Best Loo Matches	; TYPE: P ; ORGANIS ; PEATURE ; PEATURE ; NAME/KE ; LOCATIO ; OTHER I US-08-918-1	CURRI CURRI NUMBI SEQ II	; APPLICANT ; APPLICANT ; APPLICANT ; TITLE OF ; FILE REFI	<pre>; Patent No. ; GENERAL INF ; APPLICANT: ; APPLICANT:</pre>	RESULT 1 US-08-918-		4 4 4 5 4 3	4 4 4 2 1 0	398	3 3 5 3 6 5	ນ ເມ ເມ 4a ເ	31 32	30 30	28
116 VT		61 AD	1 EV	Match Local Simi	PRT ISM: RB: KEY: ION: INFO	: 80 H	APPLICANT: Carte APPLICANT: Fendl APPLICANT: Gurne TITLE OF INVENTI FILE REFERENCE:	3350	148 78		434 434 55	435.5 435.5	437.5	4 4 4 3 8 8	439.5 439	439.5	9.9	. 6
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		SRDNANN	VKPGGS	04	al unknown	NUMBER: U 1997-08- 3: 79	J. n M. in L. nist	ellia	n us/o		125 1 120 2 124 4	שיביוט	207		- 01 0	000	39	24
		VVYLOMNSLRJ stylomystrj	LRLSCAASGF	; Score 467 ; Pred. No. 11; Mismat	amino acid	US/08/918,148A -25	Antibodies		ion US/08918148A	ALIGNMENTS	909-	US-08-974- US-08-983- US-08-478-	-09	999	99-	-08-13 -08-97	-09-54	-09-42
		ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 	BVQLVKSGBGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY 	re 467.5; DB 4; d. No. 2.7e-39; Mismatches 14;		L48A				MENTS	6-349A-99 8-201-10 5-638A-54	3-607-47 3-039-99)-274-19)-029-10	-125-098-2 -540-018-2	8-148-76 0-274-151	346		-638
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		GRGTM 120	WYIDY 60 : SYIYY 62	Gaps 2							004	. App dga . App		2, Appli 2, Appli 2, Appli			•	•

RESULT 2
US-08-918-148-75
; Sequence 75, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: W.
; APPLICANT: W.
; APPLICANT: Carter, Paul J.

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; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PAtentIn Ver. 2.0
; SEQ ID NO 1937
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1937
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US-09-880-748-1937
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; ORGANISM: Homo sapiens
US-09-880-748-1179
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
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publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
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SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 1179
                                                                                           Matches
                                                                                                               Query Match
Best Local
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CURRENT FILLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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CURRENT FILING DATE: 2001-06-15
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PRIOR FILING DATE: 2000-10-17
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1 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
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                                                                                           93; Conservative
                                                                                                               Similarity
                                                                                                             70.4%;
75.0%;
                                                                                           8; Mismatches
                                                                                        Score 463; DB 11;
Pred. No. 5.1e-36;
B; Mismatches 15;
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Sequence 2040, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-16

PRIOR RILING DATE: 2001-03-21

PRIOR RILING DATE: 2001-03-21

PRIOR RILING DATE: 2001-03-21
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR TILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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US-09-880-748-2019
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US-09-880-748-2040
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SEQ ID NO 2019
LENGTH: 237
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Best Local Similarity 73.6%;
Matches 92; Conservative
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121

GEGILVIVS 129 GRGTMVTVS

124

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APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PD
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION UNMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 270
LENGTH: 126
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
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                                                                                                                                                                                                                                                                                                               APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
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SEQ ID NO 883
LENGTH: 250
TYPE: PRT
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Best Local Similarity 75.8%;
Matches 94; Conservative
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NUMBER OF SEQ ID NOS: 3239
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TYPE: PRT
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PRIOR PELLACATION NUMBER: 60/293,499
PRIOR FILLING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1764
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: homo sapiens US-10-041-860-270
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RESULT 12
US-09-880-748-1179
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Best Local S
Matches 93
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
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Best Local Similarity
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PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/240,816 PRIOR FILING DATE: 2000-10-17
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                                                                                                                                                                                                                                                                                          93; Conservative
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                                                                         WGKGTLVTVSS 124
                                                                                                                                             ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDEYDILTGLLQG---
                                                                                                                                                                                                                   71.0%; Score 467.5; DB 1
74.6%; Pred. No. 9.7e-37;
                                                                                                                                                                                                                                                                                       71.0%; Score 467.5; DB 11; 71.0%; Pred. No. 2e-36; tive 11; Mismatches 14;
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Sequence 1179, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523

CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 13

2002-01-07 377

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APPLICANT: Peng, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 208
LENGTH: 126
TYPE: PRT
US-10-091-300-31
; Sequence 31, Application US/10091300
; Publication No. US20030108545A1
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Best Local S
Matches 95
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Best Local Similarity
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10-041-860-208
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1 Similarity 75.4%;
95; Conservative
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Similarity 75.4%;
95; Conservative
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Pred. No. 4.1e-37;
9; Mismatches 21; Indels 1;
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Pred. No. 4.1e-37;
9; Mismatches 21; Indels 1;
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APPLICATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-06-15
PRIOR REPLICATION NUMBER: 60/240,816
PRIOR REPLICATION NUMBER: 60/276,248
PRIOR REPLICATION NUMBER: 60/276,248
PRIOR REPLICATION NUMBER: 60/276,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PRILING DATE: 2001-03-21
PRIOR PRILING DATE: 2001-03-21
PRIOR PRILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1318
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1318
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Best Local S
Matches 94
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LENGTH: 116
                                                                                                                                                                                                  Query Match 71.4%; Score 469.5; DB 11; Best Local Similarity 72.1%; Pred. No. 1.3e-36; Matches 93; Conservative 11; Mismatches 20;
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CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
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Local Similarity 75.2%;
nes 94; Conservative
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                          ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARD-GTIFGSAATWR----AFDIW 115
                                                                                                                                EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHMVRQTPGKGLEWVSSISSGGNYIDY 60
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ADSVKGRPTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLGSFYDILTALRLENYGMDVW
                                                                                                  EVQLVQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYY
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Pred. No. 4.6e-37;
8; Mismatches 14; Indels 9;
                                                                                                                                                                                                        20; Indels
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RESULT 2
US-10-091-300-24
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Publication No. US20030108545A1
GENERAL INFORMATION:
APPLICANT: ROCKWell, Patricia
APPLICANT: Goldstein, Neil I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/10150475A Publication No. US20030103985A1 GENERAL INFORMATION:
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SEQ ID NO 6
LENGTH: 444
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                     APPLICANT: Adolf, G. et al.

TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates

FILE REFERENCE: 1/1211

CURRENT APPLICATION NUMBER: US/10/150,475A

CURRENT FILING DATE: 2002-05-17

PRIOR APPLICATION NUMBER: US 60/307,451

PRIOR FILING DATE: 2001-07-24

NUMBER OF SEQ ID NOS: 9
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TYPE: PRT
ORGANISM: Human
                                                                                                                                               10-150-475A-6
                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain:
                                                                                    Local
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                                                               l Similarity
92; Conserv
1 EVQLVKSGEGLVKPGGSLRLSCAASGETFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY 60
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                                                                               71.8%;
73.6%;
                                                            Score 472.5; DB 15; Length Pred. No. 1.3e-36; B; Mismatches 14; Indels
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Pred. No. 1.6
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                                                                                                       Length 444;
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SEQ ID NO:
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US-10-041-860-13
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212.210
PRIOR FILING DATE: 2000-06-15
PRIOR PPLICATION NUMBER: 60/240.816
PRIOR FILING DATE: 2000-10-17
PRIOR PRIOR PRIOR DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 913, A Publication No.
                                                                                                                                                                                                                                        Sequence 13, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
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APPLICANT:
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
            APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OP INVENTION: ANTIBODIES DIRECTED TO
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABGENIX.051A
                                                                                                                                                                                                   APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                APPLICANT:
CURRENT APPLICATION NUMBER: US/10/041,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 248
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                                                                                                                                   Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
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b. US20030059937A1
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                                                             PDGFD AND USES
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US09_PUB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US10E_PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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             244
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                US-09-880-748-1362
US-10-13-09-300-24
US-10-150-475A-6
US-09-880-748-913
US-10-041-860-13
US-10-091-300-31
US-10-99-300-748-1318
US-09-880-748-1318
US-09-880-748-1764
US-09-880-748-1779
US-09-880-748-1179
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US-09-880-748-1279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
Sequence 1362 Apple Sequence 24, Appl Sequence 913, Apple Sequence 913, Apple Sequence 31, Apple Sequence 31, Apple Sequence 1318, Apple Sequence 270, Apple Sequence 1764, Apple Sequence 1764, Apple Sequence 1779, Apple Sequence 1179, Apple Sequence 1179, Apple Sequence 1179, Apple Sequence 2019, Apple
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69.2	٩	9	9	9.	٩	9	69.3	69.4	9	69.4	9	69.5	9	9	69.7	69.7	69.7	69.7	69.7	69.7		69.8	69.9	70.0	70.1	•	70.1	70.3	70.3
238	237	237	237	237	237	255	250	254	240	240	237	248	237	240	240	239	237	237	237	237	236	240	127	247	255	249	124	248	240
11	11	11	11	11	11	11	12	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	15	11	11
US-09-880-748-2024	-09-880-748-211	-880-748-	880-748-	-09-880-748-	US-09-880-748-2005	-748-	US-10-120-414-72	-09-	-748-	-748-	-09-880-748-	US-09-880-748-1965	US-09-880-748-2039		-09	-09-880-748-203		US-09-880-748-2036	US-09-880-748-2020	US-09-880-748-2006	-748	US-09-880-748-2025	US-09-848-798-27	US-09-880-748-1703	US-09-880-748-1608	US-09-880-748-1856	US-10-040-244-16	US-09-880-748-1974	US-09-880-748-2007
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence
2024,	2118,	2115,	2111,	2110,	2005,	1819,	72, Ap	1428,	2045,	2029,	2003,	1965,	2039,	2044,	2030,	2034,	•	2036,	2020,	2006,	2010,	2025,	27, Ag	1703,	1608,		16, Ap		2007,
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ALIGNMENTS

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RESULT 1

US-09-880-748-1362

; Sequence 1362, Application US/09880748

publication No. US20030059937A1

; GENERAL IMPONANTION: Antibodies that Immunospecifically Bind BLyS

rITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

rITLE DEFERENCE: PF523

; CURRENT PILING DATE: 2001-06-15

pRIOR APPLICATION NUMBER: 60/212,210

pRIOR PILING DATE: 2000-06-15

pRIOR PILING DATE: 2001-03-16

pRIOR PILING DATE: 2001-03-16

pRIOR PILING DATE: 2001-03-27

pRIOR APPLICATION NUMBER: 60/277,379

pRIOR PILING DATE: 2001-03-22

pRIOR PILING DATE: 2001-03-2
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Search completed: December 30, 2003, 10:54:36 Job time: 41.2945 secs
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                                                                                                                                                                                                                                              Query Match 70.9%; Score 466.5; DB 22; Length 119; Best Local Similarity 70.3%; Pred. No. 1e-35; Matches 90; Conservative 12; Mismatches 13; Indels 13;
                                                                                                                                                                                                                                                                                                                                          The invention relates to producing gene libraries, comprising immunoglobulin light and heavy variable region. The method involves selecting light chain that binds with the heavy chain product to produce a functional conformation, producing a gene library comprising a collection of these light chain variable genes, and combining with gene library of heavy chain variable genes. The method is used for production of gene and antibody libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing gene libraries and antibody libraries, involves selecting a light chain that binds to a heavy chain product to produce a functional formation, and producing a gene library of the light chain variable
                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Examples; p 168-169; 181pp; Japanese.
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N-PSDB; AAH47732.
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2 QGTLVTVS 119
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RESULT 14
ABP4573
ID ABP45
XX ABP45
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XX BLY8;
CHUMAN
XX HIMMAN
XW ELWOU
KW LIMMAN
KW ANTIA
KW ANTIA
KW SYSTE
KW COMMO
XX COMMO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc megakaryocytes. They may also be able to stimulate megakaryocytes to cc immunological or hematopoletic disorders, especially thrombocytopenia. CC Thrombocytopenia - associated bone marrow hypoplasia (e.g. aplastic anemia cc following chemotherapy or bone marrow transplant) may be effectively compounds as well as disorders such as CC disseminated intravascular coagulation (DIC), immune thrombocytopenia (CC treated with the antibody compounds as well as disorders such as CC disseminated intravascular coagulation (DIC), immune thrombocytopenia (CC congenital thrombocytopenia, thrombotic thrombocytopenia and CC congenital thrombotytopenia, and immune cc didopathic aplastic anemia, congenital thrombocytopenia, and immune cc dispathic aplastic anemia, congenital thrombocytopenia, and immune cc used for improving neuromuscular function in a patient, e.g. in muscular cd disposition proving neuromuscular function in a patient, e.g. in muscular contribodies have a longer half-life than the natural ligand for the TPO-R. CC sequences AAY06713-Y06718 represent single chain Fv (scFv) fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New thrombopoietin receptor agonist antibodies - useful treating immunological or hematological disorders
                                                                                                                                                                                    BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemato lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 various antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                          19-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   ABP45753;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP45753 standard; Protein; 247
                                                                                                                                                                                                                                                                                                                Human BLyS binding scFv SEQ ID 1764.
  15-JUN-2001; 2001WO-US19110
                                           10-JAN-2002.
                                                                                                                            Homo sapiens.
                                                                                                                                                                   common variable
                                                                                    WO200202641-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARDR----GST-----GMDVWGRGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLVESGGGLVKPGGSLRLSCAASGFTFSSHNWNWVRQAPGKGLEWVSSISSSSYIYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                   immunodeficiency; acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 467.5; DB 2
Pred. No. 1.8e-35;
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                                                                                                                                                                     immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115
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RESULT 15
AAG65568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TMF) super family and induces B cell the CC proliferation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC antitheumatic and antiAIDS activity and can be used in vaccines to complete the expression and activity of BLyS. The antibodies bind to BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC discould samples and may be used in this way to disgnose disease CC associated with aberrant expression of BLyS. They may also be conditively such as cancer, immune, and autoimmune disorders and CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, cc immunodeficiency (e.g. common variable immunodeficiency (CVID) and cc quired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent confirmed introduces and fragments of the antibodies described in the method confirmed intervention.
UX A X F X B X B X S X B X B
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17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 2507-2508; 3148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-114799/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM,
                                                                                                                                                                                                                  AAG65568 standard; protein; 119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-)
                                                                                                                      Amino acid sequence of protein seq Id No. 93
                                                                                                                                                       30-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CAMB-)
                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention.
                                                                                                                                                                                                                                                                                                                            115
                                                                                         library;
                                                                                                                                                                                                                                                                                                114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
                                                                                                                                                                                                                                                                                              WGKGTLVTVSS 124
                                                                                                                                                                                                                                                                                                                            WGRGTMVTVSS 125
                                                                                                                                                                                                                                                                                                                                                                              ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARD-----GTIFGSAATWRAFDI 114
                                                                                                                                                                                                                                                                                                                                                                                                                        ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDEYDILTGLLQG------MDV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                       (first entry)
                                                                                           immunoglobulin; antibody library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.0%; Score 467.5; DB 2
71.0%; Pred. No. 1.8e-35;
tive 11; Mismatches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 247;
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30-AUG-2001

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RESULT 12
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABB47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                         BLys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                            Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
    Claim
                                                                                                          Ruben
                                                                                                                                       (CAMB-)
                                                                                                                                                                                                                                                                                                        10-JAN-2002
                                                                                                                                                                                                                                                                                                                                     WO200202641-A1
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                              common variable immunodeficiency; acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human BLyS binding scFv SEQ ID 883.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP44872 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the invention.
                                                                                                                                                                                                                                                                       15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116
1; Page 1455-1456; 3148pp; English
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KS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
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                                                                                                                                      HUMAN GENOME SCI INC
CAMBRIDGE ANTIBODY TI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARDLGSFYDILTALRLENYGMDVW
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                                                                                                        Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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72.1%; Pred. No. 1.3e-35;
                                                                                                        Choi GH,
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                                                                                                                                      TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 AA.
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                                                                                                        Vaughan
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                                                                                                        Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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RESULT 13
AAYO6717
ID AAYO6
XX AAYO6
XX AAYO6
XX Agoni
KW Megak
KW bone
KW megak
KW bone
KW meyelo
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agonist antibody; thrombopoletin receptor; TPO-R; thrombopoletin; DIC; megakaryocyte; platelet; immunological; hematopoletic; thrombocytopenia; bone marrow hypoplasia; disseminated intravascular coagulation; anemia; myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MuSK; CDR; neuromuscular; muscular dystrophy; complementarity determining region.
   WPI; 1999-204666/17
                                                                                                                                                                                       25-AUG-1997;
                                                                                                                                                                                                                                                 21-AUG-1998;
                                                                                                                                                                                                                                                                                                              04-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                           WO9910494-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody 12B5 single chain Fv (scFv) fragment.
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                                                                                                                             (GETH ) GENENTECH INC
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                                                                Carter PJ,
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The invention relates to a novel antibody having a first antigen bindi site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells
                                                                                                                                                       New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
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                                                                                                                       Page 74; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AA;
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factor; tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-2000;
17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
  This invention describes novel antibodies that immunospecifically bind B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                       Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
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; 2000US-240816P.
; 2001US-276248P.
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Pred. No. 4.3e-36;
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This invention describes novel antibodies that immunospecifically bind B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLy and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomdulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritts; CVID; AlDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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Pred. No. 1.2e-35;
8; Mismatches 14
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Matches 90
                                                                                                                                      Inhibiting tumor growth in numame in endothelial growth factor receptor a radiation, chemotherapeutic agents,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABB47228 represent the antibodies and fragments of the antibodies described in the method
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                                                                                                                                                                                               WPI; 2002-691738/74.
N-PSDB; AAD46294.
                                                                                                                                                                                                                                                                                                                                                                                                                      Human; tumour; vascular endothelial growth factor receptor; metastasis; epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
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                                                                                                         Example 12; Page 127; 151pp; English.
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                                                                                                                                                                                                                                 ROCKWELL P.
GOLDSTEIN N I.
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                                                                                                                                              tumor growth in humans involves administering vascular
il growth factor receptor antagonists in combination with
chemotherapeutic agents, or epidermal growth factor receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                         heart; EGFR; therapy; invasiveness; heavy chain;
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Pred. No. 7.
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The invention relates to a method of inhibiting tumour growth which involves administering, vascular endothelial growth factor receptor (VEGFR) antagonists in combination with radiation, chemotherspeutic agent, or epidermal growth factor receptor (EGFR) antagonist. The method is useful for inhibiting tumour growth in a human, where the tumour (e.g. tumour of the breast, heart, lung, metall intestine, colon, spleen, bone, kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin, bone marrow, blood, thymus, uterus, testicles, cervix or liver) over

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RRESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIWA8 antibody;
VH; VL; CD44v6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIWA8 antibody heavy chain variable region.
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                                                                                                                                                                                                                 New antibodies specific for an epitope coded by the variant exon CD44 gene, useful for treating cancer, including non-small cell l breast, head and neck, ovarian and lung cancer -
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26-SEP-2001; 2001US-325147P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOEH )
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BOEHR INGER
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Pred. No. 1.5e-36;
7; Mismatches 14
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The present invention relates to novel antibody molecules comprising variable region of the heavy (VH) and/or light chain (VL) of CD44v6 specific humanised antibody called BIWA8 and BIWA4. Sequences of the invention are useful for manufacturing a medicament and for treating

Claim

1; Column 43; 78pp; English.

The present invention relates to novel antibody molecules comprising a variable region of the heavy (VH) and/or light chain (VL) of CD44v6 specific humanised antibody called BIWA8 and BIWA4. Sequences of the invention are useful for manufacturing a medicament and for treating cancer including colorectum, non-small cell lung, breast, head and neck, ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the brain. They are also useful in antibody therapy. The present sequence is BIWAA/8 antibody heavy chain mature protein. This sequence is used in the exemplification of the invention.

Claim 24; Column 44; 78pp;

English

New antibodies specific for an epitope coded by the variant exon of t CD44 gene, useful for treating cancer, including non-small cell lung, breast, head and neck, ovarian and lung cancer

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIWA8 antibody; heavy chain variable region; light chain variable region; VH; VL; CD44v6; medicament; cancer; antibody therapy.
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26-SEP-2001; 2001US-325147P.
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Pred. No. 2.7e-36;
B; Mismatches 14
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Best Local S
Matches 97
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                                                                                                                                                                                      Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; tumour; vascular endothelial growth factor receptor; metastasis; epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC; breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; VH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-2001; 2001US-0798689
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97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                         IMCLONE SYSTEMS INC. ROCKWELL P.
                                                                                                                                                                                                                                                                                                      AAD46290, AAD46292.
                                                                                                                                                                                                                                                                                                                                                                                                            GOLDSTEIN N I.
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Pred. No. 2.2e-36;
6; Mismatches 15
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The invention relates to a method of inhibiting tumour growth which involves administering, vascular endothelial growth factor receptor

Example 9; Page 123; 151pp; English

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RRESULT 5
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ABJ26763
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AC ABJ2
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                                                                                   New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGP) receptor and for a second VEGP receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; antibody; antigen binding site; leukaemia cell; vascular endothelial growth bispecific antigen-binding protein; human.
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                              Claim 15; Page 70-71; 98pp; English
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DB; ABT23325.
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Pred. No. 1.5e
7; Mismatches
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RRESULT 2
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                                                                                                                                                                                                                                                                                                                                                          Voorberg
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This invention describes a novel polynucleotide (I) (and comple hybridizable polynucleotides) comprising a contiguous nucleotic coding for a human antibody with factor VIII specificity which hemostatic activity. (I) is useful a primer or probe for detect
                                                                                                                                                                                     New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
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A3-C1.
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Pred. No. 2.1e-53;
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This invention describes novel antibodies that immunospecifica B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member tumour necrosis factor (TMF) super family and induces B cell proliferation and differentiation. The antibodies of the inven

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Matches 125;
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17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                    Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
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Listing first 45 summaries
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                                                   658
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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Gapop 10.0 , Gapext 0.5
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658
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Human FVIII antibo
Human FVIII antibo
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Human KCR (VEGFR-2
VEGF binding relat
BIWA# antibody hea
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Human BLYS binding
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n	AAU02616	22	127	69.5	457	45
Human BLyS binding	ABP45954	23	248	69.5	457.5	44
Human BLyS binding	ABP46028	23	237	69.5	457.5	43
	AAY32406	21	138	•	458	42
	ABP46033	23	240	•	458.5	
	ABP46019	23	240	69.7	458.5	40
	ABP46023	23	239	69.7	458.5	39
	ABP46103	23	237	69.7	458.5	38
	ABP46025	23	237	69.7	458.5	37
	ABP46009	23	237	69.7	458.5	36
	ABP45995	23	237	69.7		3 5
Human BLyS binding	ABP45999	23	236	69.7		34
Human protein SEQ	AAB99111	22	152	69.7	458.5	33
Amino acid sequenc	AAG62934	22	126	69.7		32
Anti-adipocyte mon	AAU02570	22	118	69.7	458.5	31
Human anti-HBs ant	AAB52191	21	118	•		30
Human BLyS binding	ABP46014	23	240	69.8	459.5	29
	AAG93584	22	127	69.9	460	28
Human BLyS binding	ABP45692	23	247	•	460.5	27
Antibody 5E5 singl	AAY06714	20	245	•	460.5	26
Human BLyS binding	ABP45597	23	255		461	25
Human BLyS binding	ABP45845	23	249	70.1	461.5	
=	ABJ36939	24	177	70.1	461.5	23
	ABP45963	23	248	70.3	462.5	22
	ABP45996	23	240	70.3	462.5	21
BLyS	ABP46029	23	237	70.3	462.5	20
BLyS	ABP46008	23	237	•	462.5	19
BLyS	ABP45926	23	241	•	463	18
BLyS	ABP45168	23	250		an .	17
MUC-1	AAB46007	22	240	•		16
acid	AAG65568	22	119	70.9		15
Human BLyS binding	ABP45753	23	247	•		14
	AAY06717	20	245			13
Human BLyS binding	ABP44872	23	250	71.2	•	12
Human BLyS binding	ABP45307	23	256		469.5	11
VEGF binding relat	ABJ26766	24	116	71.5		10

ALIGNMENTS

XX XX Human FVIII antibody heavy chain variable region B04 protein fragment. XX KW Human; heavy chain; antibody; factor VIII; hemostatic; variable region; XX KW hemophilia A. XX XX MO9958680-A2. XX XX XX XX XX XX XX XX XX	RESULT 1 AAY50969 ID AAY50969 standard; Protein; 125 AA. XX AC AAY50969; XX XX AC AAY50969;
Human; heavy chain; antibody; factor VIII hemophilia A. Homo sapiens. W09958680-A2. 18-NOV-1999. 07-MAY-1999; 99WO-NL00285. 08-MAY-1998; 98EP-0201543. (SANQ-) STICHTING SANQUIN BLOEDVOORZIENIN Voorberg JJ, Van Den Brink EN, Turenhou WFI; 2000-053102/04.	Human FVI
Homo sapiens. W09958680-A2. 18-NOV-1999. 07-MAY-1999; 99WO-NL00285. 08-MAY-1998; 98EP-0201543. (SANQ-) STICHTING SANQUIN BLOEDVOORZIENIN Voorberg JJ, Van Den Brink EN, Turenhou WPI; 2000-053102/04. N-PSDB; AAZ43866.	Human; hea
WO9958680-A2. 18-NOV-1999. 07-WAY-1999; 99WO-NL00285. 08-WAY-1998; 98EP-0201543. (SANQ-) STICHTING SANQUIN BLOEDVOORZIENIN VOORDERG JJ, Van Den Brink EN, Turenhou WPI; 2000-053102/04. N-PSDB; AAZ43866.	Ното варі
18-NOV-1999. 07-MAY-1999; 99WO-NL00285. 08-MAY-1998; 98EP-0201543. (SANQ-) STICHTING SANQUIN BLOEDVOORZIENIN Voorberg JJ, Van Den Brink EN, Turenhou WPI; 2000-053102/04. N-PSDB; AAZ43866.	WO9958680
07-MAY-1999; 99WO-NL00285. 08-MAY-1998; 98EP-0201543. (SANQ-) STICHTING SANQUIN BLOEDVOORZIENIN VOORDERG JJ, Van Den Brink EN, Turenhou WPI; 2000-053102/04. N-PSDB; AAZ43866.	18-NOV-19
08-MAY-1998; 98EP-0201543. (SANQ-) STICHTING SANQUIN BLOEDVOORZIENIN Voorberg JJ, Van Den Brink EN, Turenhouwpi; 2000-053102/04. N-PSDB; AAZ43866.	07-MAY-19
(SANQ-) STICHTING SANQUIN BLOEDVOORZIENIN Voorberg JJ, Van Den Brink EN, Turenhou WPI; 2000-053102/04. N-PSDB; AAZ43866.	08-MAY-19
Voorberg JJ, Van Den Brink EN, Turenhou WPI; 2000-053102/04. N-PSDB; AAZ43866.	(SANQ-) S
WPI; 2000-053102/04. N-PSDB; AAZ43866.	Voorberg .
	WPI; 2000 N-PSDB; AJ

ZFF

New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for

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RESULT 15
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Matches 81
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Q9HCC1;
01-MAR-2001 (TrEMBLrel. 16, C:
01-MAR-2001 (TrEMBLrel. 16, Li
01-MAR-2003 (TrEMBLrel. 23, Li
Single chain Fy (Fragment).
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Q9UL93;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
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Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

"An antibody fragment2A3 specific for native lysozyme :Isolaion from human synthetic phage display library and characterization.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AB049915; BAB16829.1; -.

HSSP; P01772; 2FB4.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                               Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AP035021; AAD56257.1; -.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                         InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney Young D.C., "Myosin-reactive autoantibodies in rheumatic carditis
                                                                                                                                                                                                                                                                                         fetus."
rPro; IPR007110; Ig-like.
rPro; IPR003006; Ig_MHC.
rPro; IPR003596; Ig_v.
; PF00047; ig; 1.
T; SM00406; IGv; 1.
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113
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                 TVSS 125
                                                                         DSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTMV 121
TVSS 116
                                     DSVKGRFTI
                                                                                                                                                       116 116
116 AA; 12434 MW;
                                                                                                                Conservative
                                     ||||||: | :|||||||||| |:|:|| | :
                                                                                                                          62.0%; Score 408; DB 4; Length 116; 65.3%; Pred. No. 1.3e-34;
                                                                                                                13; Mismatches
                                                                                                                                                       ODA0348154DD6061 CRC64;
                                                                                                                   Indels
                                      -GLGYWGQGTLV 112
                                                                                                                  Gaps
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Search completed: December 30, 2003, 11:01:09 Job time: 31.463 Becs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 84
  Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010327; AAH10327.1; -.
MGD; MGI:2144967; AU044919.
InterPro; IPR000345; CytC heme_bind.
InterPro; IPR007110; Ig_like.
InterPro; IPR007106; Ig_wHC.
InterPro; IPR003906; Ig_wHC.
InterPro; IPR003906; Ig_wHC.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UL84 PRELIMINARY; PRT; 122 AA.
Q9UL84;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q91Z05;
                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                 01-DRC-2001 (TrEMBLrel. 19, Created)
01-DRC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 51.9 kDa protein.
AU044919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF035030; AAI
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C., "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998).
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                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADSVKGRFTIFRDNSKNMMDLQMNSLRAEDTAVYYCAKDERGRLVGT----YFDYWGQG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARD--GTIFGSAATWRAFDIWGRG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSALAML
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122
122 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD56266.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122
13579 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.9%; Score 420.5; DB 4
66.1%; Pred. No. 7.1e-36;
tive 17; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36054D41366545B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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RESULT 13
Q920E7
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                                                                                                                                                                                                                     Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;

"Definition of the Idiotope of Pterin-Mimicking Antibodies Expresse
IT in Mammalian Cells.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF307937; AAL09421.1; -.

InterPro; IPR0037110; Ig-like.

InterPro; IPR003096; Ig_MHC.

InterPro; IPR003996; Ig_MHC.

InterPro; IPR003996; Ig_V.

Pfam; PP00047; ig; 1.

SMART; SM00406; IGv; 1.

R PROSITE; PS50835; IG_IIKE; 1.

R PROSITE; PS50835; IG_IIKE; 1.

NON_TER 11 119
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Best Local S
Matches 82
                                                                                                                                                      Query Match
Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q920E7 PRELIMINARY; PRT; 119 AA. Q920E7; Q920E7; Q920E7; Q1-DEC-2001 (TrEMBLrel. 19, Created) Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update) Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update) Pterin-mimicking anti-idiotope heavy chain variable
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00190; CYTOCHROME_C; PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein SEQUENCE 473 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Fragment)
 111
                        117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 TITVSS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 65.1
32; Conservative
                                                                                                   OGTLVIVSA
                                                                   ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDI----WG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATW-RAFDIWGRGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
                         RGTMVIVSS
                                                  PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARHGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAMYYCARE-----LWLRRIDYWGQGT
                                                                                                                                                                                                          119 AA; 13025 MW;
                                                                                                                                                         Conservative
                        125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51946 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.6%;
                                                                                                                                                      63.5%; Score 418; DB 11; 63.6%; Pred. No. 1.2e-35; tive 17; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 418.5; DB 11;
Pred. No. 6.4e-35;
4; Mismatches 21;
                                                                                                                                                                                                             F6E904044381CA7C
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                                                                                                                                                         16;
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                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                Length 119;
                                                                                                                                                         Indels
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                                                                                                                                                         14;
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                                                   YDVGFAYWG
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                                                                                                                                                      Gaps
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RESULT Q9HCC1

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RESULT
Q8N5K4
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Best Local Similarity
Matches 85; Conserv
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ dat
Submitted (JUN-2002); to the EMBL/GenBank/DDBJ dat
EMBL; BC032249; AAH32249.1; -.

InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 4.
SMART; SM00407; Ig; 4.
SMART; SM00409; IG, 1.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS05035; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      099KA4 PRELIMINARY; PRT; 487 AA.
099KA4:
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8N5K4;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                 Hypothetical 52.6 kDa protein.

Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                              EMBL; BC004786; AAH04786.1; HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                              Strausberg
Submitted (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Blood;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TMVTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADSVKGRFTISRDNAKNSLYLQMNSLRVEDTALYYCARDPTKYCSGGSCLGYYMDVWGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARDGTIFGSAATWRAF--DIWGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVOLVESGGGVVRPGGSLRLSCATSGFTFDDSGASWVRQAPGKGLEWVSSINWNGGSTNY
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                                                                                                                                                                                                                              (MAR-2001) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 429; DB 4;
; Pred. No. 5.6e-36;
13; Mismatches 27
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Last sequence update)
Last annotation update)
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RESULT 10
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Best Local S
Matches 83
                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 83
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Q9UL90;
01-MAY-2000
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NON_TER
SEQUENCE
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PROSITE; P800290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 487 AA; 52554 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998). EMBL; AF035024; AAD56260.1; -. HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=98277139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu X., Liu B., Van der Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                      EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
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                                           VIVSS
                                                                                        ADSVKGRFTISRDNSKVTLYLQMNSLRAEDTAVYYCAKD
                                                                                                                                                                                EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYY
  VTVSS 113
                                                                                                                                                                                                                                                                                                                                                                 113
113 AA;
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487 AA; 52554 MW;
                                                                                                                                                                                                                                                                      64.6%; Score 425; DB 4; llarity 66.4%; Pred. No. 2.2e-36; Conservative 13; Mismatches 17
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n der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                    12437 MW;
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Best Local S
Matches 87
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01-MAR-2002 (TrEMBLrel. 20
01-MAR-2002 (TrEMBLrel. 20
01-MAR-2003 (TrEMBLrel. 20
01-MAR-2002 (TrEMBLrel. 20
01-MAR-20
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67296 MW;
                                                                                                                                                                                                                                                                                                                                                                                            OJUL71;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC020240; AAH20240.1; -. InterPro; IPR007110; Ig-11ke. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
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                                                                                               SEQUENCE FROM N.A.

MEDLINE=98277139; PubMed=9614934;

Mu X., Liu B., Van der Merwe P.L.,

Young D.C.;
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UL71
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                                                                  "Myosin-reactive autoantibodies in rheumatic carditis
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                                                                                                                                                                                                                                                                                                                                                                  (Fragment).
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      Immunol.
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      Immunopathol.
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67296 MW; 60C7F5950671B315 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 438.5; DB 4; Pred. No. 7.5e-37;
      87:184-192(1998)
                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                           Kalis
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                                                                                                                        N.N.,
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Best Local S
Matches 88
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Submitted (JAN-2002) to the EMB Submitted (JAN-2002) to the EMB EMBL; BC021276; AAH21276.1; --
InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003096; Ig_v. Pfam; PF00047; Ig; 4.

Pfam; PF00047; Ig; 4.

SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS50835; IG MHC; 2.
Hypothetical protein.
SEQUENCE 573 AA; 62967 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; P850835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8WU38
Q8WU38;
Q1-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF035043; AAD56279.1;
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Tonsil;
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                                         138
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                                         TVIVSS
                                                                                                                                                        ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGS-AATWRAFDIWGRGT 119
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121 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                         143
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                                                                                                                                                                                                                                                                                                                                                                                                                                  66.0%; Score 434.5; DB 4 69.8%; Pred. No. 1.8e-36;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FD072344033AC530 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Best Local S
Matches 92
                                                                                                                                                                                                                                 Q96K68 PRELIMINARY; PRT; 494 AA.
Q96K68;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ14473.
Homo saplens (Hunan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Bukaryota; Metazoa; Primates; Catarrhini; Hominidae
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EMBL; AF035023; AAD56259.1; -.
HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
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Q9UL91;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE=Mammary gland;
Isogai T., Ota T., Hayashi K.,
Nishikawa T., Nagai K., Sugano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fetus.
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                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
118 AA;
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12843 MW; D0633949F2AC149D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.7%; Score 445.5; DB 4; Length 74.2%; Pred. No. 1.7e-38; tive 9; Mismatches 16; Indels
                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
    Sugiyama T., Otsuki T.,
S., Shiratori A., Sudo I
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                                                   Suzuki Y.,
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At Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
At Yamamoto J., Wakamatsu A., Nakamira Y., Najahari K., Masuho Y.,
At Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
BR EMBL; AK027379; BAB55072.1; -.
BR InterPro; IPR003006; Ig_MHC.
BR InterPro; IPR003006; Ig_MHC.
BR InterPro; IPR0030596; Ig_W.
BR InterPro; IPR0030596; Ig_W.
BR InterPro; IPR003596; Ig_W.
BR PROSITE; M00406; IGV; 1.
BR PROSITE; M00406; IGV; 1.
BR PROSITE; PS00835; IG_LIKE; 4.
BROSITE; PS00835; IG_LIKE; 4.
BROSITE; PS00290; IG_MHC; 1.
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Matches
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Best Local Similarity
Matches 83; Conserv
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-v.
Ffam; PP00047; ig; 5.
PFAm; PS00406; IGv; 1.
PROSITE; PS05085; IG-LIKE; 5.
PROSITE; PS05090; IG-MHC; 3.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MM; 4FCA3AD8ECE263D9 CRC64;
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Q968B9; TremBLrel. 19,
01-DEC-2001 (TremBLrel. 19,
01-DEC-2003 (TremBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE 494 AA; 5
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ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
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                                           EVQLLESGGGLVQPGGSLRLSCAASGFSPSSYAMNWVRQAPGKGLEWVSAISGSGGSTYY
                                                            EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
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                                                                                                       66.7%; Score 439; DB 4; 66.4%; Pred. No. 6.5e-37; tive 18; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.1%; Score 441.5; DB 470.4%; Pred. No. 2.8e-37;
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Last annotation update)
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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sp_rodent:*
sp_virus:*
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sp_archeap:*
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sp_mammal:*
sp_mhc:*
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sp_human:*
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 Q8tc77 homo
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47.0	47.6	47.6	47.7	47.7	47.9	48.0	48.3	48.6	49.2	49.9	52.0	53.0	53.2	53.5	54.2	54.3	54.3	54.7	54.8	55.0	55.2	57.6	57.8	58.1	58.2	59.6	61.2	61.8
117	168	613	497	147	481	119	614	473	142	159	125	124	112	104	484	298	124	95	124	521	437	480	469	486	131	479	118	147
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Q9gxe9 mus musculu	Q8vdc9 mus musculu	mus	Q8wy24 homo sapien	ana	Bum	homo	Q96ga6 homo sapien	Q9d8l4 mus musculu	1 mus	Q96qs0 homo sapien	homo	homo	homo	Q9ul87 homo sapien	0	Q9qyf0 mus musculu	Q9n0w6 oryctolagus	Q9ulb6 homo mapien			Q9rla4 mus musculu	Q91xe1 mus musculu	Q8r3v9 mus musculu	Bum	homo	5 mus	homo	Q9y509 homo sapien

ALIGNMENTS

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RESULT
AC DT TAKENDA

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NON TER
SEQUENCE
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Barly P., Huang H., Davis M., Calame K., Hood I
"An immunoglobulin heavy chain variable region
three segments of DNA: VH, D and JH.";
Cell 19:981-992(1980).
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                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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MEDLINE=75065510; PubMed=4530984;
Segal D.M., Padlan B.A., Cohen G.H., Rudikoff S., Potter M.,
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Immunoglobulin V region; Signal; 3D-structure
SIGNAL 1 19
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; 3D-structure.
DOMAIN 1 121 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binding myeloma protein.";
Biochemistry 13:4033-4038(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                             "The three-dimensional structure of a phosphorylcholine-binding modimmunoglobulin Fab and the nature of the antigen binding site.";
Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).
-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rudikoff S., Potter M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=75017346; PubMed=4213527;
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SMART; SM00406; IGv;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Variable region sequence of the heavy chain from a phosphorylcholine
                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains
                                                                                                                                                                                                                                                                                                                                                                                                        BINDS PHOSPHORYLCHOLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
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74.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E826733F1A3CB0F1 CRC64;
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RESULT 15
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PIR; A02067; AVDGGM.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SWART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
DOMAIN
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21-JUL-1986
21-JUL-1986
15-SEP-2003
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SEQUENCE
                                                                                           Wasserman R.L., Capra J.D.;
"Primary structure of the variable regions immunoglobulin heavy chains.";
Biochemistry 16:3160-3168(1977).
                                                                                                                                                                     15-SEP-2003 (Rel. 42, Last a Ig heavy chain V region GOM. Canis familiaris (Dog).
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                                                                                                                                                       Bukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
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                                                                            -!- MISCELLÂNEOUS: THIS CHAIN WAS ISOLATED FROM A MYE!
-!- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                         MEDLINE=77242268; PubMed=407924;
                                                                                                                                 SEQUENCE.
                                                                                                                                                                                                                    CANFA
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                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGN--YI
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                                                                                                                                                                                                                                                                         TMVTVSS 125
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114
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01, Last sequence update)
42, Last annotation updat
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Pred. No. 8.9
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H-BOND WITH THE
  IG-LIKE
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Canis.
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RESULT 12
HV3E HUMAN STANDARD; PRT; 1
DT HV3E HUMAN STANDARD; PRT; 1
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence up
DT 15-SEP-2003 (Rel. 42, Last annotation
DE Ig heavy chain V-III region BRO.
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SEQUENCE.

SECUENCE.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region BUT.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
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HSSP; P01789; IMCP.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR003596; Ig_v.
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k; Pred. No. 2.9e
16; Mismatches
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SMART; SM00406; IGv; 1.

PROSITE; PB50835; IG LIKE; 1

Immunoglobulin V region.

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                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
EMBL; J00236; AAA53516.1; -.
EMBL; M35415; AAA58735.1; -.
PIR; A02047; H3HU26.
PDB; 1HOU; 23-DEC-99.
Genew; HGNC:5545; IGHV@.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0003825; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matthyssens G., Rabbitts T.H.;

"Structure and multiplicity of genes for the human immunoglobulin "structure and multiplicity of genes for the human immunoglobulin matrix variable region.";

Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).

-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; |
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region VH26 precursor.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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InterPro; IPKUUJA,
InterPro; IPKUUJA,
IFFAM; 19; 1.
PRAM; PF00047; 1g; 1.
PROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic
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SEQUENCE
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MEDLINE-83289131; PubMed-6884994;

Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;

Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;

"Three-dimensional structure determination of antibodies.

structure of crystallized monoclonal immunoglobulin IgG1 K

Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MAMMATTAXID=9606;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marquart M., Deisenhofer J., Huber R., Palm W.; "Crystallographic refinement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=81072295; PubMed=7441755;
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; 2IG2; 12-JUL-89.
; 0:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity; NAS.
GO:0006955; P:immune response; NAS.
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ADSVKGRETISRDNSKNTLFLQMDSLRPEDTGVYFCARDGGHGFCSSASCFGPDYWGQGT
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RESULT 11
HV3F_HUMAN
ID HV3F_HUMAN
AC P01767;
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HV3U_HC
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Best Local S
Matches 79
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SMART; SM00406; IGv; l.

PROSITE; PS08035; IG LIKE; l

Immunoglobulin V region.

DOMAIN 1 112

NON TER 120 120

SEQÜENCE 120 AA; 13440 MM
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-!- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN DISULFIDE BONDS.

-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=80020921; PubMed=114209;
Steiner L.A., Garcia Pardo A., Margolies M.N.;
"Amino acid sequence of the heavy-chain variable region
crystallizable human myeloma protein Dob.";
Biochemistry 18:4068-4080(1979).
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
77 heavy chain V-III region DOB.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HSSP; P01772; 2FB4.
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Homo sapiens (Human)
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21-JUL-1986
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                                                                                                                                                                                                         ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
                                                                                                                                                                                                                                                    EVQLVESGGDLVQPGRSLRLSCAASGFNFHEYNMHWLRQGPGKGPEWVSTITWNGGSVLY
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13440 MW;
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STANDARD;

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Best Local
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P01762;
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NON_TER
SEQUENCE
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Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
--- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN
--- SIMILARITY: Contains 1 immunoglobulin-like domain.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updating heavy chain V-III region TRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), II. The amino acid sequence of the H-chain, alpha-type, subgroup III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE (MYELOMA PROTEIN TRO)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=76023781; PubMed=809331;
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                   ADSVKGRFTISRDNAQKSLYLZMBSLRTZBTAVYYCAATBBF----BWSTFSLBYWGZG
                                                                                            ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAF--DIWGRG
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13566 MW;
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SMART; SM00406; IGv; 1.
PROSITE; P850835; IG LIKE; 1
Immunoglobulin V region.
DOMAIN
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P01781;
21-JUL-1986
21-JUL-1986
15-SEP-2003
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"The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mtype), subgroup H III. Architecture of the complete IgM-molecule.";
Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region KOL.
Homo sapiens (Human).
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Submitted (JUN-1975) to
-!- MISCELLANEOUS: THIS
MACROSLOBULIN.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=75059123; PubMed=4803843;
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GG; GG:0005576; C:extracellular; NAS.
GG; GG:0003823; F:antigen binding activity;
GG; GG:0003823; F:immune response; NAS.
InterPro; IPRO03006; Ig_MIC.
InterPro; IPRO03006; Ig_MIC.
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                                                                                                                                                   HV3K_HUMAN
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12730 MW;
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Best Local S
Matches 81
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DISULFID
NON_TER
                     Goni F., Frangione B.;

"Amino acid sequence of the Pv region of a human monoclonal (protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33.";

Proc. Natl. Acad. Sci. U.S.A. 80:4837-4881(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
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Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                  SEQUENCE
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119 AA;
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P01771;
21-JUL-1986
Pfam; PF00047; 1g; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Pyrrolidone carboxylic acid.

DOMAIN

1 12 IG-LIKE.

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GO; GO:0005276; C:extracellular; NAS.
GO; GO:0003827; F:antigen binding activity;
GO; GO:0003827; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_V.
                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 immunoglobulin-like domain PIR; A02054; GHUHL.
HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                "Amino acid sequence of the VH reg
cryoimmunoglobulin IgG Hil.";
Biochemistry 18:533-560(1979).
-!- MISCELLANEOUS: THIS CHAIN WAS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Chiu Y.-Y.H., Lopez de Castro J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Immunoglobulin V region; Pyrr.
DOMAIN 1 112
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR, A02046; M3HUWE.
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SMART; SM00406; IGv; 1.
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114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                   ISOLATED FROM
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on of human myeloma
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SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG Sign
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SEQUENCE
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MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wall modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V region MOPC 21 precursor (Fragment).
                                                                                                                                                                                                                                                                                          CHAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular analysis of spontaneous somatic mutants.", Nature 265:299-304(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baltimore D.;
"Heavy chain variable region
antibodies: somatic mutation
Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                          interPro;
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                                                                                            Similarity
VIVSS
                      VIVSS 125
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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63.2%;
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                                                                                                                                          ; Score 408.5; ; Pred. No. 2.16 17; Mismatches
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DN -> ND (IN REF. 2).

W -> H (IN REF. 2).

Y -> W (IN REF. 2).
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(See http://www.isb-sib.ch/announce/
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RESULT 3
HV3H_HUMAN
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003096; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic DOMAIN
1 112 IG-LIKE.
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P01770;
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 02, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V-III region GA.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Florent G., Lehman D., Putnam F.W.; "The switch point in mu heavy chains of human IgM Biochemistry 13:2482-2498(1974).
                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
15-SEP-2003 (Rel. 42, Last ann
1g heavy chain V-III region NI
Homo sapiens (Human)
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A02052; M3HUGA.
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                 SEQUENCE.
MEDLINE=77070269; PubMed=826475;
  Ponstingl H., Hilschmann N.;
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122 AA;
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61.6%; Pred. No. 2.9e-35;
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RESULT 15
C36005
Ig heavy chain V region (30p1) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C;Accession: C36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: C36005
A;Status: preliminary
A;Molecule type: mANA
A;Residues: 1-19 <SCH>
A;Cross-references: GB:M18513
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology <IMM>
Search completed: December 30, 2003, 11:03:19 Job time: 11.9821 secs
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F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                    Query Match 67.6%; Score 445; DB 2; Length 119; Best Local Similarity 69.8%; Pred. No. 1.9e-34; Matches 88; Conservative 11; Mismatches 19; Indels
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C.Speciés: Homo sapiens (man)
C.Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C.Accession: S31116
R.Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S3116
A;Accession: S3116
A;Kolecule type: mRNA
A;Residues: 1-18 «RAA»
A;Residues: 1-18 «RAA»
A;Cross-references: EMBL:X62966
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Bubmitted to the EMBL Data Library, October 1992
A.Reference number: S30520
A.Accession: S30532
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-123 cMAR>
A.Cross-references: EMBL: Z18318
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                            Ig heavy chain V region - human
(;Speciles: Homo sapiens (man)
(;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
(;Accession: $30532
R;Mariette, X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.0%; Score 447.5; DB 2 72.0%; Pred. No. 1.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 448; DB 2
Pred. No. 1e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
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A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                        C;Accession: G36005

R;Schroeder Jr., H.W.; Wang, J.Y.

R;Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A;Title: Preferential utilization of conserved immunoglobulin heavy

A;Reference number: A36005; MUID:90349571; PMID:2117273

A;Accession: G36005

A;Residues: preliminary

A;Residues: 1-121 <SCH>
                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W. Eur. J. Immunol. 22, 241-245, 1992

Bur. J. Immunol. 22, 241-245, 1992

A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam A;Reference number: S26786; MUID:92111632; PMID:1730251

A;Accession: S26786
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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                                                                           A; Gene: GDB: IGH@; IGHDY1
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A;Molecule type: mRNA
A;Residues: 1-128 <MOR>
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                                                                                                                         A;Cross-references: GB:M34031
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Best Local S
Matches 91
                                                                                                 ;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 67.9%; Score 446.5;
Similarity 69.5%; Pred. No. 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSSSYTNY
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Ig heavy chain (subclass IgM) - human (fragment)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Pate: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C.Accession: S31104
R.Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.
Eur. J. Immunol. 22, 247-251, 1992
A.Title: Restricted utilization of germ-line V(H)3 genes and short diverse the content of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X63081; NID:g32648; PIDN:CAA44803.1; PID:g32649
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, Eur. J. Immunol. 22, 247-251, 1992

A;Title: Restricted utilization of germ-line V(H)3 genes A;Reference number: S31104; MUID:92111633; PMID:1730252

A;Accession: S31105
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A;Residues: 1-118 <RAA>
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: S31105
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Pred. No. 7.4e-35;
9; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                              26-May-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 125;
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A;Cross-references: EMBL:X62956
A;Note: the nucleotide sequence was submitted to C;Superfamily: immunoglobulin V region; immunoglo C;Keywords: heterotetramer; immunoglobulin
                                                                                  A;Status: preliminary; nucleic acid
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
                                                                                                                                             C;Accession: S31108

R;Raaphorst, F.M.; Timmers, B.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.;

Eur. J. Immunol. 22, 247-551, 1992

A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse thir

A;Reference number: S31104; MUID:92111633; PMID:1730252

A;Accession: S31108
                                                                                                                                                                                                                                                                                                                                        RESULT 10
S31108
                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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31595
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z14171; NID:g31007; PIDN:CAA78540.1; PID:g31008 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;23-106/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate
                                                                                                                                                                                                                                                                                                                     Ig heavy chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-128 <CUI>
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R; Cuisinier, A.M.;
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Best Local S
Matches 90
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Similarity 72.8%;
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Pred. No. 8.4e-35;
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                                                                                                                            sequence not shown; translation not
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                     nitted to the EMBL Data Library, October 1991 immunoglobulin homology
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Ig heavy chain V region - human (fragment)
C;Species: Homo Bapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S11239
R;Felgenhauer, M.; Kohl, J.; Rueker, F.
Nucleic Acids Res. 18, 4927, 1990
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and A;Reference number: S11239; MUID:90370490; PMID:1697678
A;Accession: S11239; MUID:90370490; PMID:1697678
A;Cross-references: EMBL:X53613; NID:g23865; PIDN:CAA37675.1; PID:g762936 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-145 <FEL>
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A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23624
A;Status: preliminary A;Molecule type: DNA
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
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F;15-98/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 73.6%;
Matches 95; Conservative
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Pred. No. 1.7e-36;
9; Mismatches 20
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submitted to the EMBL Data Library, October 1
A;Reference number: $30520
A;Accession: $30531
A;Status: preliminary
A;Molecule type: mENA
A;Residues: 1-125 < mARA
A;Residues: 1-125 < mARA
C;Residues: 1-125 < maraily: immunoglobulin V region; immun
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < TMM>
                                                                                                                                                                                     Ig heavy chain V region - hum C;Species: Homo Bapiens (man) C;Date: 06-Jan-1995 #sequence C;Accession: S30531 #R;Mariette, X.
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S30531
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A; Residues: 1-117 <MAR>
A; Cross-references: EMBL: Z18324
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-95/Domain: immunoglobulin homology < IMM>
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S34012; S30538
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Bur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidic sequence analysis of the variable domains of four human A;Reference number: S34001; MUID:93209281; PMID:7681398
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;; Pred. No. 4.8e-35;
11; Mismatches 24;
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Pred. No. 4.3e-35;
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ALIGNMENTS

RESULT

Ig heavy chain V region - human (fragment)

Ig heavy chain V region - human (fragment)

() Species: Homo sapiens (man)

() Species: Homo sapiens (man)

() Species: Species: Homo sapiens (man)

() Accession: S31669

R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A; Description: Mechanisms that generate human immunoglobulin diversity oper:

immunoglobulin diversity operate from the

A; Reference number: S31585 A; Accession: S31669 A; Status: preliminary

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 «MOR»
A;Cross-references: EMBL:X61013; NID:g32798; PIDN:CAA43347.1; PID:g1335128
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W. Eur. J. Immunol. 22, 241-245, 1992

Bur. J. Immunol. 22, 241-245, 1992

A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene A;Reference number: S26786; MUID:92111632; PMID:1730251

A;Accession: S26790
                                                                                                                                                                                                                          RESULT 2

226790

1g heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change

C;Accession: S26790
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A,Residues: 1-141 <CUI>
A,Residues: 1-141 <CUI>
A,Crose-references: EMBL:Z14212; NID:g30959; PIDN:CAA78581.1; PID:g30960
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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Search completed: December 30, 2003, 11:05:35 Job time : 12.2685 Becs

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Sequence 22, Application US/09240274

PATENT NO. 6253455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: CATION FOR PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: CORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-42U2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver: 2.0
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Best Local
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Patent No. 6255455
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ORGANISM: Homo sapiens
FEATURE:
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Similarity 74.2%; Pred. No. 2.3e-40;
95; Conservative 10; Mismatches 12;
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LENGTH: 125
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                                                                                                                                                                                                                     Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTMARE: Patentin Ver. 2.0
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CURRENT FILLING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILLING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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121
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                              116 VIVSS 120
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95; Conserva
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                                                                                      ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNI-----AEALWGQGTL
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125
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73.6%;
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                                                                                                                                                                                                                 t; Score 473.5; DB 3;
t; Pred. No. 5.6e-40;
11; Mismatches 17;
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INFORMATION:

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APPLICANT: McCafferty, John G
APPLICANT: Conroy, Louise A
APPLICANT: Tempest, Philip R
TITLE OF INVENTION: Specific binding members for
FILE REFERENCE: 2811/35620A
CURRENT APPLICATION NUMBER: US/09/560,198A
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/131,983
PRIOR APPLICATION NUMBER: US 60/131,983
PRIOR FILING DATE: 1999-04-30
INUMBER OF SEQ ID NOS: 25
SOFTWARE: PALENTIN VEY: 2.1
SEQ ID NO 4
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                                                                                                                                                                                                SOFTWARE: Patentin
SEQ ID NO 10
                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/560,198A CURRENT FILING DATE: 2000-04-28 PRIOR APPLICATION NUMBER: US 60/131,983 PRIOR FILING DATE: 1999-04-30 PRIOR SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                               APPLICANT: Du Fou, Sarah L
APPLICANT: McCafferty, John G
APPLICANT: Conroy, Louise A
APPLICANT: Tempest, Philip R
TITLE OF INVENTION: Specific binding members for TGFbetal
FILE REFERENCE: 2811/35620A
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Thompson, Julia B
APPLICANT: Lennard, Simon N
APPLICANT: Wilton, Alison J
APPLICANT: Braddock, Peta SH
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                                                                                                                                                                     TYPE: PRT
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TYPE: PRT
ORGANISM: Homo sapiens
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1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
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Similarity 78.0%;
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96; Conserv
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Lennard, Simon N
Wilton, Alison J
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78.0%;
                                                        Score 477.5; DB 4;
Pred. No. 2.2e-40;
5; Mismatches 19;
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Pred. No. 1.8e-40;
5; Mismatches 19
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SOPTWARE: Patentin Ver.
SEQ ID NO 20
LENGTH: 125
TYPE: PRT
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TITLE OF INVENTION: Rh(D)-BIDDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-10-11
NUMBER: 07 SEQ ID NOS: 224
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 8
LENGTH: 125
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TITLE OF INVENTION: Rh (D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-42U2

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1996-04-10

EARLIER FILING DATE: 1996-10-11

NUMBER: 09/028,550

EARLIER FILING DATE: 1996-10-11

NUMBER: 09 SEQ ID NOS: 224
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Patent No. 6255455
GENERAL INFORMATION:
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TYPE: PRT
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US 07/596,289

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                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-198A-2
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LENGTH: 123
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Best Local Similarity
                                                                            Matches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Bllen Lauver
NAME: Weber, Bllen Lauver
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
                                                                                                Best Local
                                                                                                                Query Match
                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/560,198A CURRENT FILING DATE: 2000-04-28 PRIOR APPLICATION NUMBER: US 60/131,983 PRIOR FILING DATE: 1999-04-30 NUMBER OF SEQ ID NOS: 25 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: McCafferty, John G
APPLICANT: Conroy, Louise A
APPLICANT: Tempest, Philip R
TITLE OF INVENTION: Specific binding members for TGFbetal
FILE REFERENCE: 2811/35620A
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thompson, Julia APPLICANT: Lennard, Simon APPLICANT: Wilton, Alison
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tent No. 6492497
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
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TOPOLOGY: 111
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96; Conservative
                                                                                            h 78.1%;
Similarity 78.0%;
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McCafferty, John G
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78.3%;
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56Pl'CL VH region"
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                                                                          Score 485.5; DB 4;
Pred. No. 3.6e-41;
7; Mismatches 17;
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                                                                          Gaps
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US-09-560-198A-4

Sequence 4, Application US/09560198A Patent No. 6492497

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US-09-025-769B-24
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                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                          Matches
                                                                                                                                                                                                                                                                  TELEPAX: (212)596-9090
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
TUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
PILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Relase #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
PILING DATE: 18-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                      TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALUNKUSEEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                NAME: James F. Haley, Jr. REGISTRATION NUMBER: 27, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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 61
                           61 ADSVKGRPAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS 120
                                                            96; Conservative
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USA
                                                                                                                                                                                                                                                                                                                (212) 596-9090
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                                                                                                                                                                                                                                                                                                                                  (212) 596-9000
                                                                                                                                                                                                      protein
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                                                                                                                                           77.9%;
                                                                                                                                                                                                                                                                                                     24:
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                                                                                                                            4; Mismatches
                                                                                                                                           Score 484.5; DB 4; Pred. No. 4.2e-41;
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                                                                                                                                                          DB 4;
                                                                                                                                                          Length 117;
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RESULT 5
US-08-759-804A-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                       COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
STRANDEDNESS:
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-0CT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Tumor-Specific Antibody Fragments, TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                 APPLICATION NUMBER: US/08/759,804A FILING DATE: 03-DEC-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 78.2%;
Local Similarity 78.3%;
nes 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAMB/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"
                                                                                                                                                                                                                                                                                                                                            STREET: Two Embarcac
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/767,331 FILING DATE: 30-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARRSARTYYFD-YWGQGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                             California
                                                                                                                                                                                                                                                                                                                                                                         B: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46:
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Pred. No. 2.7e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6287562
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
PILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
PILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAX: (415) 576-03: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: P
APPLICANT: B
APPLICANT: P
APPLICANT: J
APPLICANT: J
                                                                                                                                                                                                                                                                                                   STREET: Steum-
CITY: San Francisco
STATE: California
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LENGTH: 119 amino acide
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REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 015280-126140US
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
               PILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LEB, Byungkook
TITLB OF INVENTION: HUMANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein LOCATION: 1..119 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ADSVKGRFTISRDNSKNTLYLOMNSLRABDTAVYYCARRSARTYYFD-YWGQGTLVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLIESNIAEALWGOGTLVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
                                                                                                                                                                                                                                                                                                                                                                3E: Townsend and Townsend Khourie and Crew Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09227693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BENHAR, Itai
PADLAN, Eduardo A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Human fetal immunoglobulin
56P1'CL Variable Heavy chain (V-H)"
                                                                                                                                                                  Release #1.0, Version
US 07/767,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 119;
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RESULT 5
US-08-652-816A-6
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                                                                                                                          Sequence 6, Application US/08652816A Patent No. 5872215
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206372.6

FILING DATE: 23-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9525004.9

FILING DATE: 07-DEC-1995
                                                                                     GENERAL INFORMATION:
APPLICANT: Osbouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 312-474-6300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GE
FILING DATE: 02-DEC-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GE
FILING DATE: 02-DEC-19
 APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 23-MAY-199
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 02-DEC-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE: 23-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: David W. Clough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/244,597 FILING DATE: 01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                        121
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                                                                                                                                                                                                                                                                                                                                                                                  QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNSPINWLRQAPGQGLEWMGSIIPSFGTANY 60
                                                                                                                                                                                                                                      VSS 123
                                                                                                                                                                                                                                                                                                             AQKFQGRLTITADESTSTAYMELSSLRSEDTAVYYCAGRSHNYELYYYYMDVWGQGTMVT 120
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                                                                    Allen, DJ
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23-MAY-1996
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02-DEC-1991
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Pred. No. 1.2e-43;
8; Mismatches 8;
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RESULT 6
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INFORMATION FOR SEQ ID NO:
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APPLICATION UNMBER: GB 9206

PILING DATE: 23-SEP-1000

PRIOR ADDRE: 23-SEP-1000
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APPLICATION NUMBER: US/0
FILING DATE: 23-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILING DATE: 02-DEC-1992 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: David W. Clough REGISTRATION NUMBER:
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                                                                  121 VSS 123
                                                                                                 112 VSS 114
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                                                                                                                                                 61 AQKPQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWPY--IWGQGTMVT 111
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                                                                                                                                                                                                                                                           l Similarity 79.7
98; Conservative
                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                               AQKFQGRLTITADESTSTAYMELSSLRSEDTAVYYCAGCSHNYBLYYYYMDVWGQGTMVT 120
                                                                                                                                                                                           QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNSPINWLRQAPGQGLEWMGSIIPSFGTANY
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Pred. No. 1.2e-43;
8; Mismatches 8;
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Sequence 8, Application US/08652816A Patent No. 5872215 GENERAL INFORMATION:

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PRIOR APPLICATION NUMBER: GB 912
PILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 912
PRIOR APPLICATION NUMBER: GB 912
PRIOR APPLICATION NUMBER: GB 912
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 920
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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TITLE OF INVENTION: Specific
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER:
FILING DATE: 01-JUN-
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 96
FILING DATE: 23-MAY-1996
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NAME: David W. Clough
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APPLICATION NUMBER:
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STATE: Illinois
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121
                                 112 VSS 114
                                                                 61 AQKFQGRLTITADESTSTAYMELSSLRSEDTAVYYCARHNHNYELYYYYMDVWGQGTMVT 120
                                                                                                  61 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWFY--IWGQGTMVT 111
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VSS 123
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6300 Sears Tower, 233
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02-DEC-1991
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                                                                                                                                                                                                                     Score 492.5; DB 2;
Pred. No. 1.2e-43;
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                                                                                                                                                                                                       Mismatches
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South Wacker Drive
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RESULT 7
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Patent No. 5
                                                                                                           Matches
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Best Local S
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APPLICANT: OBSOUR
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APPLICATION NUMBER: GB 9
FILING DATE: 02-DEC-1991
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APPLICATION NUMBER:
FILING DATE: 02-DEC-
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acide
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08
PILTUR DATE:
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APPLICATION NUMBER

APPLICATION NUMBER

FILING TO
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                           Local Similarity
                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
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61 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----
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                                              David W. Clough
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                                                                                                            Conservative
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23-SEP-1992
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                                                                                                           Score 492.5; DB 2;
Pred. No. 1.2e-43;
8; Mismatches 8;
                                                                                                                                                                                                                                                                                                 28111/33308
                                                                                                                                        Length 123;
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    ELDWFY--IWGQGTMVT
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APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/210,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/270,349
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
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Search completed: December 30, 2003, 11:45:25 Job time : 24.4484 secs
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1509
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1509
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Best Local Similarity 85.8%;
Matches 103; Conservative
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                 107 GTMVTVSS 114
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APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
SEQ ID NO 191
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US-10-308-817-191
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-49
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GENERAL INFORMATION:
APPLICANT: OLLNER, JONATHAN D.
APPLICANT: OLLNER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 49
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Publication No. US20030219861A1 
GENERAL INFORMATION:
Sequence 19, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
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Best Local Similarity
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ORGANISM: human
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84.9%;
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Pred. No. 1.7e-43;
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Pred. No. 1.9e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12;
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; ORGANISM: Homo US-10-269-805-19
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; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-025-687-1
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US-10-025-687-1
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 121
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                                                                                                                                          Sequence 1, Application US/10125687 Publication No. US20030054407A1 GENERAL INFORMATION:
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Best Local Similarity
APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 1
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CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
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TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION
FILE REFERENCE: 26050-705
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TYPE: PRT
ORGANISM: Artificial Sequence
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Pred. No. 6.6e-43;
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RESULT 7

US-10-269-805-35

US-10-269-805-35

Sequence 35, Application US/10269805

Publication No. US20030124129A1

GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.

TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722

CURRENT APPLICATION NUMBER: US/10/269,805

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 60/328,604

PRIOR FILING DATE: 2001-10-11

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin version 3.1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-9
                                                                                                                RESULT 8
                                            Sequence 2, Application US/09976118
Patent No. US20020058033A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR PILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
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Best Local Similarity 86.0
Matches 104; Conservative
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Best Local
APPLICANT: Raisch, Kevin Paul
APPLICANT: Curiel, David T.
APPLICANT: Bonner, James Alle
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ORGANISM: Homo
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                                                                                                                                                                                                                                                               61 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCE------LDWFYIWGQGTM 109
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 James Allen
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Pred. No. 1e-43;
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Sequence 3, Application US/10269805

FNEDICATION NO. US20030124129A1

GENERAL INFORMATION:
APPLICANT: OLLNER, JONATHAN D.
TITLE OF INVENTION ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR APPLICATION UMBER: US 60/328,604
PRIOR APPLICATION SECULO-11
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-10-269-805-3
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US-10-269-805-3
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LENGTH: 270
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CURRENT APPLICATION NUMBER: US/09/976,118
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,353
PRIOR PILING DATE: 2000-10-13
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121
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SSA
                                                                                                      AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDW---FYIWGQGTMVT 111
                                                                                                                                                               OVOLVOSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
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123
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Pred. No. 1.5e-43;
4; Mismatches 7;
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RESULT 10 US-10-269-805-49

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US-10-300-675-12

Sequence 12, Application US/10300675

Publication No. US20030198638A1

GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519

CURRENT APPLICATION NUMBER: US/10/300,675

CURRENT APPLICATION NUMBER: US/10/300,675

CURRENT FILING DATE: 2002-11-19

PRIOR APPLICATION NUMBER: US 09/989,901

PRIOR FILING DATE: 2001-11-19

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12

SEQ ID NO 12
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TITLE OF INVENTION: Tumor Specific Monoclona
FILE REFERENCE: P-IX 5519
CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
PRIOR REPLICATION NUMBER: US 09/989,901
PRIOR FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PastSEQ for Windows Version 4.0
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US-10-300-675-14
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                                                    Sequence 14, Application US/10300675
Publication No. US20030198638A1
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
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85.6%;
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Pred. No. 4.2e-44;
6; Mismatches 7;
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Pred. No. 4.2e-44;
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US-10-269-805-9
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Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANY: OLLNER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
         Sequence 9, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC
FILE REFERENCE: A-722
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SEQ ID NO 25
LENGTH: 124
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Best Local Similarity
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CURRENT FILING DATE: 2002-11-19
CURRENT APPLICATION NUMBER: US/10/269,805
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ORGANISM: Homo
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Pred. No. 4.4e-44;
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Pred. No. 4.2e-44;
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Perfect score:
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1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

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6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/US10B_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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RESULT 2
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S-quence 10, Application US/10300675
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CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 09/989,901
PRIOR FILING DATE: 2001-11-19
NUMBER OP SEQ ID NOS: 59
SOFTWARE: FABSTEQ for Windows Version 4.0
SEQ ID NO 6
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Publication No. US20030198638A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
GENERAL INFORMATION:
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Best Local Similarity
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85.6%;
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Pred. No. 4.2e-44;
6; Mismatches 7;
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                                                                                                                               Query Match
Best Local S
Matches 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel method for the construction of a library of recombinant antibodies. The novel method comprises clustering variable regions of a collection of antibodies having known 3D structures into at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Constructing a library of recombinant antibodies useful as source of antibody candidates for screening antigens comprises clustering variable regions of antibodies having known 3-dimensional structures
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85.8%;
                                                                                                                                                                                                                                                                                                     Score 508; DB 24;
Pred. No. 3.9e-37;
                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                 Length 120;
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RESULT 12
AAB67618
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Best Local :
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AAB67617-23 represent single chain antibody (scFv) fragments which are specific for human leukocyte antigen (HLA)-CW6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoglobulin fragments specific
                                                                                                   Claim 3; Fig 1; 23pp; English.
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                                                                                                                                                                                                                                                                                                           26-AUG-1999;
                                                                                                                                                                                                                                                                                                                                            28-AUG-2000;
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                                                                                                                                 isolated human immunoglobulin or functional immunoglobulin ent specific for human leukocyte antigen Cw6, useful for tromans and for human leukocyte antigen phenotyping -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukocyte antigen-Cw6
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Pred. No. 6.5e-37;
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RESULT 13
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Best Local &
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Best Local
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                                                                                                                                                                                Sequence
                                                                                                                                                                                                                          The present sequence is the human antibody heavy variable region synthetic sequence VHIA, used in a human derived antibody gene library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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                                                                                                                                                                                                                                                                                                                      Example
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                                                                                                                                                                                                                                                                                                                                                              sequences, for highly
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Pred. No. 3
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Pred. No. 7.1e-37;
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1.9e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunomodulatory human NHC class II antigen-binding protein; HLA; human leukocyte antigen; immune system; immunesuppression; antibody; major histocompatibility complex; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antithybetic; antipsoriatic; immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis; thyromimetic; hepatotropic; immune response suppressor; narcolepsy; rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulitis; Grave's disease; insulin-dependent diabetes; Hashimoto's disease; systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis; transplant rejection; graft versus host disease; pemphigus vulgaris; glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis; irritable bowel disease; Stocrem's avortrome
                The present invention describes a composition (I), comprising a polypeptide comprising an antibody-based antigen-binding domain of human composition with binding specificity for an antigen expressed on the surface of a cell, where treating cells expressing the antigen with the polypeptides leads to suppression of an immune response, and the IC50 for the suppression of immune response and the IC50 for antirheumatic, antispristic, neuroprotective, antiinflammatory, antidiabetic, antisportatic, immunosuppressive, dermacological, antithyroid, nephrotropic, thyromimetic and hepatotropic activities, and can be used as suppressor of immune response. (I) is useful for suppressing activation or proliferation of a cell of the immune system with another cell, immunosuppressing a patient and for immune system with another cell, immunosuppressing a patient and for the immune system with another cell, immunosuppressing a patient and for the immune system with another cell, immunosuppressing a patient and for the immune system with another cell, immunosuppressing the interaction of a cell of the immunosuppressing a patient and for the immune system with another cell, immunosuppressing the interaction of a cell of the immunosuppressing the immune system with another cell, immunosuppressing the system with another cell, immunosuppressing the system with another cell, immunosuppressing the system with another cell with a system with another cell with a system with a syst
                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition for suppressing immune response, treating diseases immune system, has polypeptide comprising antibody-based antigen-binding domain of human composition, which binds antige expressed on a cell surface
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                                                                                                                                                                                                                                                                                                                                                                                     Example;
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06-OCT-2000;
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Claim

Page

153;

English

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cancer 228pp;

The invention relates to a novel purified preparation of a human antibody, which binds to a tissue inhibitor of metalloprotease-l and neutralises a matrix metalloprotease (MMP)-inhibiting activity

activity

0£

(TIMP-1)

New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate

N-PSDB;

2003-129114/12.

ABZ74781.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on the surface of the cell, where neither cytotoxic entities nor immunological mechanisms are needed to cause or lead to the killing. (I) (optionally linked to cytotoxic or immunogenic agent) is useful for preparing a pharmaceutical preparation for the treatment of rheumatoid arthritis, juvenile arthritis, multiple sclerosis, Grave's disease, insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus erythematosus, ankylosing spondylitis, transplant rejection, graft versus host disease, Hashimoto's disease, myssthenia gravis, pemphigus vulgaris, glomerulonephritis, thyroiditis, pancreatitis, insulitis, primary biliary cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
                                                                                                                                                                                                                                                                                                                                                                                                   Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human anti-TIMP-1 antibody heavy chain #8.
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(MORP-)
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                                                                                                                                                                                                                                                                                                                                                                                        idiopathic pulmonary fibrosis; benign prostate
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Best Local S
Matches 101
The invention relates to a novel purified preparation of a human antibody, which binds to a tissue inhibitor of metalloprotesse-1 (TIMP-1) and neutralises a matrix metalloprotesse (MMP)-inhibiting activity of TMP-1. The antibody comprises a variable heavy chain (VMC)DR3 region and a variable light chain (VLC)DR3 region. An antibody preparation of the invention has hepatotropic, cytostatic, nephrotropic and cardiant activity. The human antibody is useful for decreasing an MMP-inhibiting activity of a TIMP-1. It is especially useful for ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus nephritis, glomerulosclerotic renal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nehotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer; idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or amellorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                   cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.3%;
                                                                                                                                                                                                                                                                                                                                                           English.
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Pred. No. 1.7e-37;
5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hirth-dietrich C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₿
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heavy
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RESULT 9
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                         are specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoglobulin fragments specific for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping.
                                                                                                                                                                                                                                 fragment s
of humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pulmonary fibrosis, benign prostate hypertrophy, lung cancer or cancer. The antibody is also useful for detecting a TIMP-1 in a t preparation, or in diagnosing a disorder in which a TIMP-1 level elevated. The sequences shown in ABR01502-ABR01545 represent the chain regions of a human anti-TIMP-1 antibody of the invention.
                                                                                                                                                                                                                                            Novel isolated human immunoglobulin or functional immunoglobulin fragment specific for human leukocyte antigen Cw6, useful for tre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                       AAB67617-23 represent single chain antibody (scrv) fragments which
                                                                                                                                                                                                     Claim 3;
                                                                                                                                                                                                                                                                                                                     Kretzschmar T,
                                                                                                                                                                                                                                                                                                                                                                                26-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-2000; 2000WO-EP08388
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200114558-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         miscarriage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB67617;
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                                                                                                                                                                                                  Fig 1; 23pp;
                                                                                                                                                                                                                                specific for husan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELDWFYI--WGQGTWVTVSS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIFILGTGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        etandard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARQEWYMDYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        abortion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                99EP-0116691
                                                                                                                                                                                                                                                                                                                       Tesar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen-Cw6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
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87.1%;
                                                                                                                                                                                                  English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         psoriasis; antibody;
                                                                                                                                                                                                                                 leukocyte
                                                                                                                                                                                                                                                                                                                     Marget
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Pred. No. 4.7e
5; Mismatches
                                                                                                                                                                                                                                                                                                                       Z,
                                                                                                                                                                                                                              antigen
                                                                                                                                                                                                                                                                                                                     Kroenke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 24;
.7e-37;
                                                                                                                                                                                                                                phenotyping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phenotyping;
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                                                                                                                                                                                                                                               treatment
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Query Match Best Local S Matches 102

Similarity

85 87

.34;

Score 509.5; DB Pred. No. 5.8e-37 5; Mismatches

DB 22;

Length

245; ω ••

Gaps

2

102;

Sequence

245

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The IgG1, in its nascent form, bears no sialy1-Lex side chains. inventors designed a molecule including several such sites for attachment of sialy1-Lex side chains (see AAR2442, FT). The additional N-linked glycosylation sites are introduced at locati which impair complement fixing and Fc receptor binding ability. Antibodies bearing multiple sialy1-Lex determinants are useful fisrupting undesirable interactions between cells or proteins. Disrupting this interaction has therapeutic applications, for a protein and the simple sialy1-lex determinants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
02-JAN-1992
                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR24442 standard;

    used in treating
psoriasis, etc.

                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                 18-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                   11-JUN-1992.
                                                                                                                                                                                                                                                                                   WO9209293-A1
                 example,
                                                                                                             Disclosure; Fig 1; 46pp;
                                                                                                                                                 Inhibition of cell
                                                                                                                                                                                                              (GEHO)
                                                                                                                                                                                                                                23-NOV-1990;
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                                                                                                                                                                            1992-216789/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                    AAQ25443
                                                                                                                                                                                                               GEN HOSPITAL
                                                                                                                                                                                              Walz G;
          ဓ္ဌ
         in minimising inflammation on 25-MAR-2003 to correct F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (updated)
(first en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                         adhesion mediated through ELAM-1 chronic inflammation, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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          following tissue PN field.)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
        The invention relates to a novel purified preparation of a human antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1) and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and a variable light chain (VHC)DR3 region. An antibody preparation of the invention has hapatotropic, cytostatic, nephrotropic and cardiant activity. The human antibody is useful for decreasing an MMP-inhibiting activity of a TIMP-1. It is especially useful for ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic myndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variable light chain; cytostatic; nephrotropic; cardiant; liver fib-
alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
lupus nephritis; glomerulosclerotic renal disease; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-2002; 2002WO-US12801
                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human anti-TIMP-1
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                                                                                                                                                                                                   New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a disoin which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung cancer
                                                                                                                                                                                                                                                                      N-PSDB; ABZ74783.
                                                                                                                                                                                                                                                                                                               Pan
                                                                                                                                                                                                                                                                                                                                         (FARB )
(MORP-)
                                                                                                                                                                                                                                                                                                                                                                                 24-APR-2001; 2001US-285683P
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200286085-A2
                                                                                                                                                                         Claim 20; Page 154; 228pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer
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                                                                                                                                                                                                                                                                                    2003-129114/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;
metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;
le light chain; cytostatic; nephrotropic; cardiant; liver fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,..
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                                                                                                                                                                                                                                                                                                                                         MORPHOSYS
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                                                                                                                                                                                                                                                                                                               Knorr AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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  fibrosis,
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Pred. No. 3.4e
3; Mismatches
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  idiopathic or colon
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                                                                                            The present sequence is the heavy chain variable region of a human cumur-specific monoclonal antibody. Neoplastic cells selectively express antigens which are not present on normal cells. Thus monoclonal can be produced that are specifically directed against tumour-specific antigens. The antibodies can be conjugated to cytotoxic or cytostatic agents and used to selectively target cancer cells for the climination of tumours. They can also be linked to diagnostic moieties that allow the imaging of neoplastic cells. Nucleic acids encoding human tumour-specific monoclonal antibodies can be used to express the cantibodies and can be recombinantly engineered to produced modified antibodies with higher affinity or higher selectivity for tumour cells. Tumour-specific antibodies were produced by hybridomas that were generated by in vitro immunisation of human spleen cell cultures with the produced from the hybridoma by RT-PCR. The present sequence was then isolated from the hybridoma by RT-PCR. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis of cancer, ermining region -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor-specific human monoclonal antibody, useful for the treatment diagnosis of cancer, comprises at least one complementarity
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DB; AAA48411.
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cytotoxic;
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  Score
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  Length 118
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                                                                                                                                                                                                    The present invention relates to human anti-epidermal growth factor receptor single-chain antibodies (anti-EGFR-eGFVs) Solated from a human IgM phage display library using EGFR as antigen. Two isolates with different amino acid sequences were identified. The anti-EGFR-eGFVs are useful for treating cancer, and for the diagnostic location and assessment of tumour growth, where the anti-EGFR-eGFV is radiolabelled. The present sequence represents human anti-EGFR single-chain antibody isolated from clone pSEX81-63.
                                                                                                                                                                                                                                                                                                                                             treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; anti-epidermal growth
anti-EGPR-scFv; IgM; cancer;
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                     Claim 3; Fig 2; 51pp;
                                                                                                                                                                                                                                                                                                                                                                      Novel human anti-epidermal
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for diagnostic location and
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                                                                                                                                           Similarity
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                                                                                            QVQLVQSGAEVKKPGSSVKVSCKASGGTPSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
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     MVTVSS 114
                                                                             QVQLVQSGAEVKKPGSSVKVSCKASGTFSSYAISWVRQAPGQGLEWMGGIIFIFGTANY
                                                                                                                                                                                                                                                                                                                                               cancer
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tumour growth; clone pSEX81-63; cytostatic
                                                                                                                                           Score 516; DB 23;
Pred. No. 1.7e-37;
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                                                                                                                                                                                                                                                                                                                                                        factor receptor single-chain antibody assessment of tumour growth, and in
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                                                                                                                                                                                                                                 WPI;
hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents a human
                                                                                                                                    Example 9; Fig 11A; 61pp; English.
                                                                                                                                                                                   New polynucleotide, polypeptide and presence of neutralizing antibodies
                                                                                                                                                                                                                                                              Voorberg
                                                                                                                                                                                                                                                                                                                            08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                         07-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention describes a novel polynucleotide
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nilarity 100.0%;
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CC acceptor tyrosine kinase family), or modulating formation of cells into capillary-like structures by contacting the cells with a composition comprising (1). The method is useful modulating formation of cells into comprising (1). The method is useful modulating angiogenesis at a site (C (preferably, within a human) or modulating the formation of cells (c (indothelial cells of human origin) into capillary-like structure. The CC (in is useful for preventing, treating or ameliorating a medical c condition e.g., cancer, metastasis, diabetic retinopathy, macular CC degeneration, cardiovascular disease, wound, pregnancy, or a clinical condition involving angiogenesis in the reproductive system, including CC condition involving angiogenesis in the reproductive system, including c regulation of placental vascularization in an individual. The variant CC protein is supplied to the individual as a source of polymucleotide conding the protein and expressing the protein in vivo. (I) is used CC useful for modulating angiogenesis at a site. Polymucleotides are useful for modulating angiogenesis at a site. Polymucleotides encoding the useful in gene therapy technique for treating above mentioned CC medical conditions. The present sequence represents the scFv lb4 antibody
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in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Examples; Page 79-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modulating angiogenesis at a site, for treating or preventing metastasis, diabetic retinopathy, cardiovascular disease, wour supplying composition comprising variant Ryk protein to the si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAY-2001; 2001WO-US15043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         supplying composition
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; ophthalmological; cardiant; vulnerary; antiangiogenic;
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                   1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                           SIDSI gcgdata/geneseq/geneseqp-embl/AA1980.DAT:

SIDSI gcgdata/geneseq/geneseqp-embl/AA1981.DAT:

SIDSI gcgdata/geneseq/geneseqp-embl/AA1982.DAT:

SIDSI gcgdata/geneseq/geneseqp-embl/AA1983.DAT:

SIDSI gcgdata/geneseq/geneseqp-embl/AA1983.DAT:

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Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.
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                                Human FVIII heavy
Human FVIII antibod
scFv 1b4 antibody
Human LH13 monoclo
Human anti-EGFR si
Sequence of antibo
Human anti-TIMP-1
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                Human
anti-TIMP-1
leukocyte an
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248	246	256	222	222	245	223	222	257	248	248	253	248	231	248	248	248	249	254	222	248	248	244	223	219	125	248	248	229	253	120	120	120	245	225	115
23	23	23	22	22	24	22	22	23	23	23	23	23	24	23	23	23	21	23	24	23	23	23	24	24	22	23	23	24	23	24	24	18	22	24	23
ABP45706	ABP46051	ABP45589	AAU04976	AAU04974	ABP60521	AAU04973	AAU04972	ABP45542	571	ABP45716	ABP45869	ABP45730	ABR01524	ABP45726	72	70	AAB36083	ABP45855	ABR01531	ABP45868	ABP45707	ABP45870	ABR01535	ABR01523	AAU02555	ABP45723	ABP45722	ABR01518	ABP45498	ABJ18718	ABJ18672	AAW27550	AAB67618	ABR01510	ABB57559
Human BLyS binding		Human BLyS binding	9	Synthetic antibody	Q.	Synthetic antibody	Synthetic antibody				BLys	BLyS					binant	Human BLyS binding	anti	BLyS		BLyS	anti-	anti-	adipoc	BLyS		Human anti-TIMP-1	Human BLyS binding	Antibody library r	Antibody library r	Human Ab heavy cha	Human leukocyte an	Human anti-TIMP-1	HLA-DR-specific pr

ALIGNMENTS

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RESULT 1
AAY50974
  New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for
                                                                                                                                                                                                                                  \operatorname{Human}_i heavy chain; antibody; factor VIII; hemostatic; variable region; hemophilia A.
                                                                                                                                                                                                                                                                   Human FVIII heavy chain variable region protein fragment
                                                                                                                                                                                                                                                                                                                    AAY50974;
                                                                                                                                                                                                                                                                                                                                        AAY50974 standard; Protein; 114 AA
                                 WPI; 2000-053102/04.
N-PSDB; AAZ43867.
                                                                   Voorberg JJ,
                                                                                                                  08-MAY-1998;
                                                                                                                                        07-MAY-1999;
                                                                                                                                                                                      WO9958680-A2
                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                            23-MAR-2000
                                                                                          (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                                                               18-NOV-1999
                                                                                                                                                                                                                                                                                            (first entry)
                                                                    Van Den Brink EN,
                                                                                                                 98EP-0201543.
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                                                                      Turenhout EAM
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Result
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Maximum DB seq length: 200000000
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Perfect score:
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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         US-09-674-752-51
597
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         Issued Patents AA:*
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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         GenCore version 5.1.6 (c) 1993 - 2003 Compu
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US-09-025-769B-57
US-09-652-816A-1
US-08-652-816A-9
US-08-652-816A-9
US-08-652-816A-9
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US-08-308-655-63
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Sequence 35, Appl Sequence 21, Appl Sequence 1, Appli Sequence 8, Appli Sequence 9, Appli Sequence 9, Appli Sequence 10, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 63, Appli Sequence 63, Appli Sequence 63, Appli Sequence 63, Appli Sequence 55, Appli Sequence 63, Appli Sequence 64, Appli Sequence 64, Appli Sequence 65, Appli Sequence 65, Appli Sequence 64, Appli Sequence 65, Appli Sequence 65, Appli Sequence 64, Appli Sequence 65, Appli 
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45	44	43	42	41	40	39	38	37	36	35	34	£.	32	31	30	29	28
431.5	431.5	431.5	431.5	432	432	432.5	432.5	432.5	432.5	435.5	441.5	441.5	441.5	449.5	452	452	452
72.3	72.3	72.3	72.3	72.4	72.4	72.4	72.4	72.4	72.4	72.9	74.0	74.0	74.0	75.3	75.7	75.7	75.7
117	117	117	117	118	118	449	235	222	119	122	129	129	129	125	128	128	128
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US-08-487-200-105	US-08-474-040-105	US-08-477-728-105	US-07-634-278-105	US-07-987-264-60	US-08-428-257A-78	US-08-458-516-13	US-08-458-516-23	US-08-458-516-22	US-08-458-516-10	PCT-US95-00067-2	PCT-US95-01219-45	US-08-525-539A-77	US-08-561-521-45	US-09-199-149-3	US-08-635-109-3	US-08-964-690-22	US-08-202-047-22
Sequence 105, App	Sequence 105, App	Sequence 105, App	Sequence 105, App	Sequence 60, Appl	Sequence 78, Appl	Sequence 13, Appl	23	Sequence 22, Appl	Sequence 10, Appl	Sequence 2, Appli	Sequence 45, Appl	Sequence 77, Appl	Sequence 45, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 22, Appl	Sequence 22, Appl

ALIGNMENTS

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ZIP: 10021

COMPUTER READABLE PORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/025,7698
PILING DATE: 10-FEB-1990
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
PILING DATE: 10-AUG-1995
ATTORNEY/ACENT IMPORMATION:
APPLICATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-09-025-769B-35
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                                                                                 TELEPHONE: (212)596-900
TELEPAX: (212)596-9000
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NC. STATE: NC. USA COUNTRY: USA 10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
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Pack, Peter
Ilag, Vic
                                                                                    120 amino acids
                         linear
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Query Match Best Local Similarity Matches 103; Conserv

Conservative

85.1%; 85.8%;

Score 508; DB 4; Length 120, Pred. No. 2.8e-45; 3; Mismatches 8; Indels

6; Gaps

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RESULT 2
US-09-025-769B-57
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; MOLECULE TYPE: protein
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Sequence 21, Application US/09025769B Patent No. 6300064
                                                                                                                                                                                                                                                               Matches 103; Conservative
                                                                                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INPORMATION:
NAME: James F. Haley, Jr., Bsq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSES: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Knappik, Achim APPLICANT: Pack, Peter
                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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                                                                                                                                                                                       QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIPGTANY
                                                                                                           AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARWGGDGFYAMDYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                 120 amino acids
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Ilag, Vic
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                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                              Score 508; DB 4; Length 120; Pred. No. 2.8e-45;
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RESULT 4
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APPLICANT: Knappik
APPLICANT: Pack, R
APPLICANT: 11ag, V
APPLICANT: Ge, Lim.
APPLICANT: Moroney
APPLICANT: Plueckti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/025,769B
PRIOR APPLICATION DATE: 19-FBB-1998
PRIOR APPLICATION UNMBER: EP 95 11 3021.0
PILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAMB: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCEJ DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                    sequence 1, Application US/08652816A
Patent No. 5872215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                    GENERAL INFORMATION:
APPLICANT: Obbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                   NUMBER OF SEQUENCES: 5. CORRESPONDENCE ADDRESS:
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Local Similarity 84.9%;
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               CITY: Chicago
STATE: Illinois
                                                      STREET:
                                                                      ADDRESSE:
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1251 Avenue of the Americas
                                                B: Marshall, O'Toole,
6300 Sears Tower, 233
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United States of America
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Pred. No. 8.1e-45;
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South Wacker Drive
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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AAY50971
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Human FVIII heavy
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Human anti-TIMP-1
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ALIGNMENTS

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RESULT 1
AAY50974
WPI; 2000-053102/04.
N-PSDB; AAZ43867.
                                                                                                  07-MAY-1999;
                                                                                                                   18-NOV-1999.
                                                                                                                                  WO9958680-A2
                                                                                                                                                                 Human; heavy chain; antibody; factor VIII; hemostatic; variable region; hemophilia {\tt A.}
                                                                                                                                                                                           Human FVIII heavy chain variable region protein fragment
                                                                                                                                                                                                            23-MAR-2000
                                                Voorberg JJ, Van Den Brink EN,
                                                                                  08-MAY-1998;
                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                             AAY50974;
                                                                                                                                                                                                                                              AAY50974 standard; Protein; 114
                                                                (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                                                                                                            (first entry)
                                                                                  98EP-0201543.
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                                                 Turenhout EAM
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New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for

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RESULT 4
AAY99558
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Best Local :
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                                     tumour-specific antigens. The antibodies can be conjugated to cytotoxic or cytostatic agents and used to selectively target cancer cells for the elimination of tumours. They can also be linked to diagnostic moieties that allow the imaging of neoplastic cells. Nucleic acids encoding human tumour-specific monoclonal antibodies can be used to express the antibodies and can be recombinantly engineered to produced modified antibodies with higher affinity or higher selectivity for tumour cells. Tumour-specific antibodies were produced by hybridomas that were generated by in vitro immunisation of human spleen cell cultures with breast carcinoma cells. The nucleic acid encoding the monoclonal antibody was then isolated from the hybridoma by RT-PCR. The present sequence
                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA48411.
                                                                                                                                                                                                                                                                                                                                                                                                                           Watkins JD, Huse WD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; LH13 cytostatic;
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                                                                                                                                                                                                                                                                                    Claim 10; Page 82-83; 84pp;
                                                                                                                                                                                                                                                                                                                  determining region -
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                                                                                                                                                                                                         tumour-specific monoclonal antibody. Neoplastic cells selectively express antigens which are not present on normal cells. Thus monoclonal antibodies can be produced that are specifically directed against
                                                                                                                                                                                                                                        The present sequence is the heavy chain variable region of a human tumour-specific monoclonal antibody. Neoplastic cells selectively (
                                                                                                                                                                                                                                                                                                                                 and diagnosis of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IXSY-) IXSYS INC
                             was produced by LH13 hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                               tumor-specific human
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milarity 87.2%;
Conservative
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cytotoxic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody; hybridoma;
heavy chain variable
                                                                                                                                                                                                                                                                                                                              monoclonal antibody, useful for the treatment comprises at least one complementarity
                                                                                                                                                                                                                                                                                    English.
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                              cell line
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Query Match

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YX 12-C
YX 11-C
YX 1
                                                                                                                                                                                                    Query Match
Best Local Sim:
Matches 103;
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                                                                                                                                                                                                                                                                                                                                                        The present invention relates to human anti-epidermal growth factor receptor single-chain antibodies (anti-EGFR-eCFVs) isolated from a human IgM phage display library using EGFR as antigen. Two isolates with different amino acid sequences were identified. The anti-EGFR-scFvs are useful for treating cancer, and for the diagnostic location and assessment of tumour growth, where the anti-EGFR-scFv is radiolabelled. The present sequence represents human anti-EGFR single-chain antibody isolated from clone pSEX81-63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human anti-epidermal growth factor receptor single-chain antibody useful for diagnostic location and assessment of tumour growth, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human anti-EGFR single-chain antibody isolated from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU97198 standard; protein;
                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; anti-epidermal
anti-EGFR-scFv; IgM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 2; 51pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
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                                                                                                   QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer
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AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELD------
                                                                                                                                                                                                                                                                                                                270 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RES FOUND
                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                  86.4%;
81.7%;
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                                                                                                                                                                                                                                  Score 516; DB 23;
Pred. No. 1.7e-37;
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clone pSEX81-0
                                                                                                                                                                                                                                                          Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pSEX81-63;
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Best Local :
                            The invention relates to a novel purified preparation of a human antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1) and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and a variable light chain (VLC)DR3 region. An antibody preparation of the invention has hepatotropic, cytostatic, nephrotropic and cardiant activity. The human antibody is useful for decreasing an MMP-inhibiting activity of a TIMP-1. It is especially useful for ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer. The antibody is also useful for detecting a TIMP-1 in a t preparation, or in diagnosing a disorder in which a TIMP-1 level preparation. The sequences shown in ABRO1502-ABRO1545 represent the chain regions of a human anti-TIMP-1 antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                               Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                upus nephritis; glomerulosclerotic renal disease; lung cancer;
idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer
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DB; ABZ74809.
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87.1%;
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Pred. No. 1.7e-37;
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Query Match Best Local Sim Matches 102;

Similarity

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                                               AAB67617-23 represent single chain antibody (scFv) fragments which are specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinuclectides. The specification describes a human immunoglobulin fragments specific for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobuli fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pulmonary fibrosis, benign prostate hypertrophy, lung cancer or cancer. The antibody is also useful for detecting a TIMP-1 in a t preparation, or in diagnosing a disorder in which a TIMP-1 level elevated. The sequences shown in ABR01502-ABR01545 represent the chain regions of a human anti-TIMP-1 antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated human immunoglobulin or functional immunoglobulin fragment specific for human leukocyte antigen Cw6, useful for troof humans and for human leukocyte antigen phenotyping -
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Pred.
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sis; antibody; HLA phenotyping; ss.
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AAB67617-23 represent single chain antibody (scPv) fragments which are specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoclobulin frameworks.
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                                                                                                                                                                                                           Fig 1; 23pp;
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Pred. No. 6.5e-37;
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                                                                                                                                                                                                                                                                                                                                                 The present sequence is the human antibody heavy chain variable region synthetic sequence VHIA, used in the present the property of the present of the prese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparation of human consensus sequences, framework for highly
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Pred. No. 7.1e-37;
4; Mismatches 8;
                                                                                                                                         Score 508; DB 18; Pred. No. 3.9e-37;
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1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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12 US-10-300-675-12
12 US-10-300-675-12
12 US-10-300-675-14
15 US-10-269-805-25
15 US-10-269-805-3
9 US-09-976-118-2
15 US-10-269-805-3
15 US-10-308-817-191
15 US-10-025-687-1
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Sequence 6, Appli
Sequence 10, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 25, Appl
Sequence 9, Appli
Sequence 35, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 49, Appl
Sequence 191, App
Sequence 191, Appl
Sequence 1, Appli
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ALIGNMENTS

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Sequence 6, Application US/10300675
; Publication No. US20030198638A1
; CENERAL INFORMATION:
APPLICANT: Matkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
CURRENT APPLICATION NUMBER: US/10/300,675
; CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 09/989,901
PRIOR PILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 59
SOFTMARE: PastSEQ for Windows Version 4.0
SEQ ID NO 6
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-675-6
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Best Local &
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61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREDSSGWYHYWGQGTLVTVSS 118
                          61 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELD-----WFYIWGQGTMVTVSS 114
                                                                              Similarity 85.6%;
                                                                                                                                                            Score 520; DB 12; Length 118; Pred. No. 4.2e-44; 6; Mismatches 7; Indels
                                                                                                                                                              Indels 4;
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RESULT 2 US-10-300-675-10

; Sequence 10, Application US/10300675; Publication No. US20030198638A1; GENERAL INFORMATION:

2002-10-10

60/328,604

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US-10-269-805-35

/ Sequence 35, Application US/10269805

/ Publication No. US20030124129A1

/ GENERAL INFORMATION:

/ APPLICANT: OLINER, JONATHAN D.

/ TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS

/ FILE REFERENCE: A-722

/ CURRENT APPLICATION NUMBER: US/10/269,805

/ CURRENT FILING DATE: 2002-10-10

/ PRIOR APPLICATION NUMBER: US 60/328,604

/ PRIOR FILING DATE: 2001-10-11

/ NUMBER OF SEQ ID NOS: 76

/ SOUTWARE: Patentin version 3.1

/ SEQ ID NO 35

LENGTH: 125

/ Type: Date: 125
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PRIOR APPLICATION NUMBER: US 60/;
PRIOR FILING DATE: 2001-10-11;
NUMBER OF SEQ ID NOS: 76;
SOFTWARE: Patentin version 3.1;
SEQ ID NO 9;
LENGTH: 121
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                                                                                            RESULT 8
US-09-976-118-2
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Sequence 2, Application US/0976118
PATENT NO. US/20/20058033A1
GENERAL INFORMATION:
APPLICANT: Raisch, Kevin Paul
APPLICANT: Curiel, David T.
APPLICANT: Bonner, James Allen
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Best Local S
Matches 104
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Local Similarity 83.2%;
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Local Similarity 86.0%;
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Pred. No. le-43;
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Pred. No. 7.7e-44;
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US-10-269-805-3
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Best Local Simi
Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A.722
FILE REFERENCE: A.722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2
LENGTH: 270
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Best Local Similarity
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CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTMARE: Patentin version 3.1
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,353
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor TITLE OF INVENTION: Single-Chain Antibodies FILB REFERENCE: D6355
                                                                                                                                                                                                                                                                                            LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: artificial sequence
PEATURE:
OTHER INFORMATION: amino acid sequence of anti-EGFR scFV
OTHER INFORMATION: clone pSEX81-63
                                112 VSS 114
121
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                                                                                                                                                                                                                        Similarity
                                                                                      AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDW---FYIWGQGTMVT 111
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                                                                  AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGVVGDFDWLSFFDYWGQGTLVT
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123
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83.7%;
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81.7%;
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Pred. No. 1.5e-43;
4; Mismatches 7;
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Pred. No. 2.6e-43;
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RESULT 10 US-10-269-805-49

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Sequence 1509, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/216,216

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/273,499

PRIOR FILING DATE: 2001-03-21

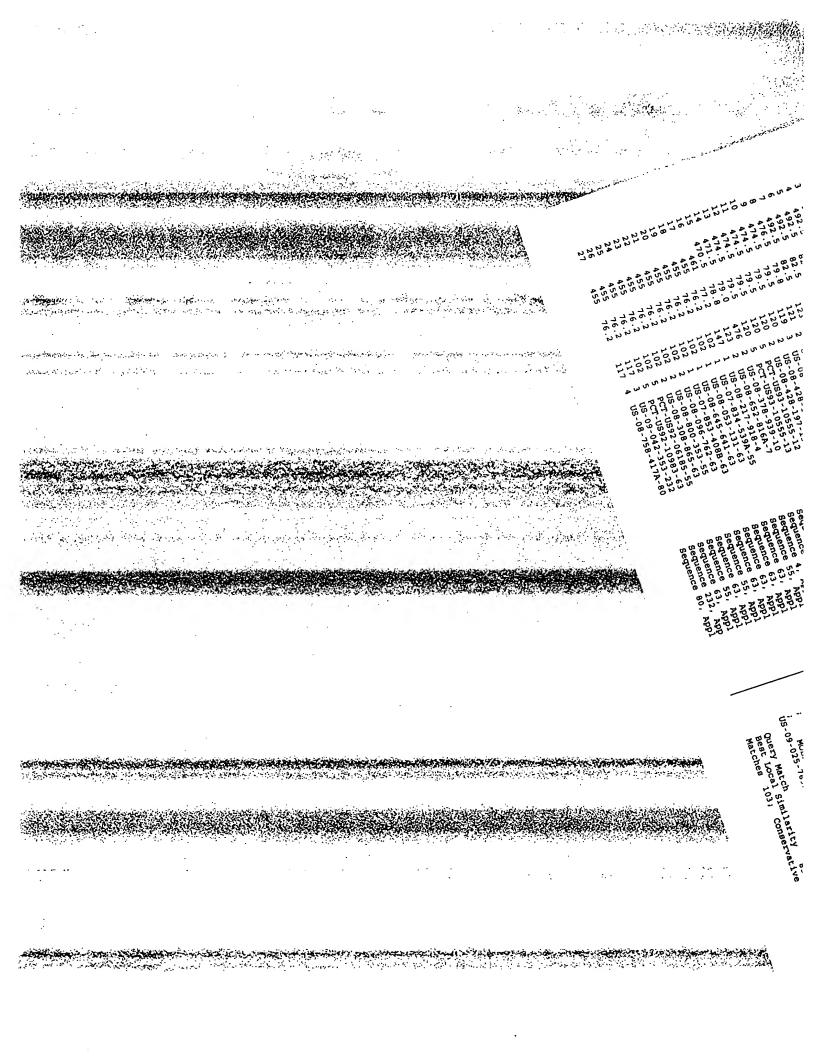
PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTAL SECUENCE SECUENC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ঠ
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Search completed: December 30, 2003, 11:45:25
Job time : 24.4484 secs
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US-09-880-748-1509
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US-09-880-748-1509
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Best Local Simi
Matches 102;
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Best Local Simi
Matches 103;
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Local Similarity 79.7%; Pred. No. 1.9e-42;
heb 102; Conservative 4; Mismatches 8; Indels 1
                                                                                                                              107 GTMVTVSS 114
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121 GTMVTVSS 128
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                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC------ELDWFYIWGQ 106
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85.8%; Pred. No. 6.6e-43;
tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels 14;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                     Score
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length: 2000000000
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//ggn2_6/ptodata/1/iaa/5B_COMB.pep:*
//ggn2_6/ptodata/1/iaa/6B_COMB.pep:*
//ggn2_6/ptodata/1/iaa/6B_COMB.pep:*
//ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
//ggn2_6/ptodata/1/iaa/backfiles1.pep:*
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642
1 EVQLVESGGDLVQPGGSLRL......GYKYYGMDVMGQGTTVTVSS 122
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        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
        Gapext 0.5
US-09-025-769B-38
US-09-025-769B-63
US-09-025-769B-78
US-09-025-769B-78
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US-08-137-642B-21
US-08-137-642B-21
US-08-138-607-32
US-09-069-821-3
US-08-148-99-6
US-08-148-99-6
US-08-148-37-6348-4
US-08-148-2066-4
US-08-148-2066-4
US-08-983-607-47
US-08-983-607-47
US-08-983-607-51
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  Sequence 38, Appl Sequence 178, Appl Sequence 53, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 32, Appli Sequence 3, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 9, Appli Sequence 4, Appli Sequence 47, Appli Sequence 47, Appli Sequence 47, Appli Sequence 48, Appli Sequence 48, Appli Sequence 47, Appli Sequence 48, Appli Sequence 48, Appli Sequence 48, Appli Sequence 48, Appli Sequence 51, Appli Sequence 51
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ALIGNMENTS

RESULT 1 US-09-025-769B-38

Sequence 38, Patent No. 6

8, Application US/09025769B 6300064

GENERAL INFORMATION: APPLICANT: APPLICANT: APPLICANT:

Knappik, Achim Pack, Peter Ilag, Vic

APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373

c/o Fish & Neave

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US-09-025-769B-38
                                                                                                                                                                                                              FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
PILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (212)596-9090
INFORMATION FOR SEQ ID NO: 38:
  Best Local Similarity Matches 100; Conserva
                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: LAUL
STREET: New York
CITY: New York
                                                                                                  MOLECULE TYPE:
                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq.
ADDREST: 1251 Avenue of the Americas
                                                                                                                     STRANDEDNESS:
TOPOLOGY: 11
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Conservative
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                  81.8%; Score 525; DB 4; Length 120; 82.0%; Pred. No. 1.9e-43;
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Mismatches
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GENERAL INFORMATI
                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                           Matches
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APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNET/AGENT INFORMATION:
NAME: James F. Haley. Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                         TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1251
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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     121 SS 122
                                                                                                                                                                       tch 81.8%; Score 525; DB 4; Length 120, al Similarity 82.0%; Pred. No. 1.9e-43; 100; Conservative 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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amino acid
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                                                         ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
                                                                                                                          EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY 60
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                                     ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARWGGDG--FYAMDYWGQGTLVTV 118
                                                                                                        EVOLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
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Ilag, Vic
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                                                                                                                                                                                                                                                                                linear
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US-10-039-785-53
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; Sequence 53, Applicat:
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo el
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Patent No.
                                                                                                                                                                                                                                                                                                                           Query Match
81.8%; Score 5/5; Feet No. 4.9e-
Best Local Similarity 82.0%; Pred. No. 4.9e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION: NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Moroney, Šimon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 18-FEB-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/025,769B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 ŚŚ
                                                                                                                                    144 SS 145
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                                                                                                                                                                                                                                                                       EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                Application US/10039785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B: James F. Haley, Jr., Esq.
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knappik, Achim
Pack, Peter
Ilag, Vic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212)596-9000
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                                                                                                                                                                                                                                                                                                                                                       Score 525; DB 4;
Pred. No. 4.9e-43;
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RESULT 5
US-07-934-373C-21
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/07934373C Patent No. 5821337
                                                                                                                                                                                                                                                                                                                                                             Patent No. 5821337
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/309,176 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/323,807 PRIOR FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/327,364 PRIOR FILING DATE: 2001-10-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-11-14
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ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                         APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 249
                 SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                    STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                           COUNTRY:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                ADDRESSEE:
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100; Conser
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80.0%; Pred. No. 4.80
tive 12; Mismatches
                                      (Genentech)
US/07/934,373C
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US-08-437-642B-21
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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APPLICATION NUMBER: US/08/437,642B FILING DATE: 09-May-1995 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/934373 FILING DATE: 21-AUG-1992 PRIOR APPLICATION NUMBER: 08/146206 FILING DATE: 17-MOV-1993 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/US92/05126 APPLICATION NUMBER: PCT/US92/05126 FILING DATE: 15-JUN-1992
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
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ATTORNBY AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE POCKET NUMBER: P070
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Paul J. Ca. APPLICANT: Leonard G. TITLE OF INVENTION: II
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/7:
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4054297
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Pred. No. 9.1e-43;
9; Mismatches 11
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:

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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acide
                 SEQUENCE CHARACTERISTICS:
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APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
Method for Making Humanized Antibodies
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REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                           FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                 SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEPHAX: 650/952-9881
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TYPE: Amino Acid
TOPOLOGY: Linear
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   ENGTH:
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122 amino acids
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82.1%;
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Pred. No. 9.1e-43;
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PCT-US93-07832-21
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                                                 Query Match
Best Local Similarity
Matches 101; Conserv
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                                                                                                                                                                                                                TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 70
REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/934373 FILING DATE: 21-AUG-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Genentech, Inc.
                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US92/05126 FILING DATE: 15-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/7:
FILING DATE: 14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
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                                                     Score 518; DB 5;
Pred. No. 9.1e-43;
9; Mismatches 11
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                                                                                    Length 122
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; LIBRARY: DM414 scFv antibodies obtained from ; LIBRARY: fUSE5 fusion phage construct ; CLONE: V86 ; FEATURE: ; NAME/KEY: heavy chain and linker US-08-983-607-32
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US-08-983-607-32
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Query Match 79.9%; Score 513; DB 3; Length 140; Best Local Similarity 80.2%; Pred. No. 3.2e-42; Matches 101; Conservative 11; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 residues
                                                                                                                                                                                                                                                                 DESCRIPTION:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEPAX: 203-773-1183
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APPLICATION NUMBER: PCT/IB
FILING DATE: June 28, 1996
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APPLICATION NUMBER: US/08/91
FILING DATE: April 27, 1998
CLASSIFICATION: 435
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MEDIUM TYPE: 3.5" 1.44 Mb diskette
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Xiaohong Cai
                                                                                                                                                                                        MMEDIATE SOURCE:
                                                                                                                                                                                                      ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
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OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 0
                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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linear
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                                                                                                                                                                                                                                                                                   polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT/IB96/01032
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                                                                   ; MOLECULE TYPE: US-09-069-821-3
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   Query Match
Best Local Similarity
Matches 101; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 30-APR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
PRIOR APPLICATION NUMBER: US 60/063,074
PILING DATE: 27-OCT-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                 TELEPHONE: (202)371-2600
TELEPAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          FILING DATE: 23-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Palanning
                                                                                                  TYPE: amino acid
STRANDEDNESS: sil
TOPOLOGY: not re
                                                                                                                                                                                                                                                  NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 61 FILING DATE: 23-JUN-1997
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STREET: 1100 NEW YORK AVE.,
                                                                                                                                                ENGTH:
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LEE, LIHSYNG S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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SHORR, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
     Conservative
                                                                                                  SS: single not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                peptide
79.4%; Score 510; DB 4; Length 263; 77.1%; Pred. No. 1.3e-41; tive 11; Mismatches 9; Indels
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US-09-420-592A-6
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US-08-428-197-1
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                                        Sequence 1, Application US/08428197 Patent No. 5891438 GENERAL INFORMATION:
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Best Local S
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APPLICANT:
                                                                                                                                                                                                                                                                                                                Matches
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CURRENT FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: UNSURE LOCATION: (234)
OTHER INFORMATION: NAME/KEY: UNSURE LOCATION: (239)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 283
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: UNSURE
LOCATION: (232)
OTHER INFORMATION: May
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ITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
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                                                                                                                                            WGQGTLVTVSS
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Pred. No. 1.4e-41;
1; Mismatches 9
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; NAME/KEY:
; LOCATION:
US-08-428-197-1
                                                   Sequence 1, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIM
TITLE OF INVENTION: VARIABLE REGION
TITLE OF INVENTION: VACCIDATION WITH
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
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PCT-US93-10555-1
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Best Local
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/
PILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPERENCE/DOCKET NUMBER: FD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONB:
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                                                                                                                                                                                                                                                                                                          GTTVTVSS 122
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1880 Century Park East
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                                                                                           SILVERMAN, GREGG J.
VENTION: METHOD FOR STIMULATING PRODUCTION OP
VENTION: METHOD FOR STIMULATING PRODUCTION OP
VENTION: VARIABLE REGION GENE PANILY RESTRICTED ANTIBODIES THROUGH
VENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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77.3%;
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Pred. No. 1.2e-41;
9; Mismatches 11
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Suite
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          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb f
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                    APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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                                                                                                                                          STREET: 1 DNA Way
CITY: South San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/
FILING DATE: 29-OCT-1993
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                                                                                                                                                                           ADDRESSEE:
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APPLICATION DATA:
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California
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                                                                                                                            California
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77.3%;
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                                                              1.44 Mb floppy disk
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Pred. No. 1.2e-41;
9; Mismatches 11
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US-08-478-039-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5681722
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 99, Application US/08478039 Patent No. 5681722
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                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAW 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
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                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/478,039
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                    ZIP: 22313-1404
COMPUTER READABLE FORM:
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LENGTH: 113 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/0 PILING DATE: 11/27/96 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
           APPLICATION NUMBER: US 0'
FILING DATE: 23-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 113 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 40
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 78.1%;
Local Similarity 78.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/974,899
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                                                                                                                                                                                                                                                                                                                                                                                                                                  699 Prince St.
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                               US 07/856,281
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Pred. No. 3.2e-41;
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APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-2021
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acide
TYPE: amino acide
TYPE: amino acide
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
TOPOLOGY: not relevant
TOPOLOGY: not relevant
CHROMOSOME/SEGMENT: 18/2
US-08-478-039-99
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Search completed: December 30, 2003, 11:05:37 Job time: 13.4716 secs
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                                                                        118 GTLVTVSS 125
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MOLECULE TYPE: protein
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STATE: New York
COUNTRY: USA
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STREET: 125
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                                                                       December 30, 2003, 10:47:45; Search time 11.576 Seconds (without alignments) 416.677 Million cell updates/sec
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                                                                                                                                                    1 QVQLVQSGAEVKKPGSSVKV.....YCELDWFYIWGQGTMVTVSS 114
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Sequence 21,
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/Regrows.comB.pep:*

(cgn2_6/ptodata/1/iaa/Regrows.comB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-025-769B-21
US-08-652-816A-6
US-08-652-816A-9
US-08-652-816A-9
US-08-322-018A-1
US-08-322-018A-1
US-08-323-018A-1
US-08-323-018-41
US-08-428-197-13
PCT-US3-10555-13
US-08-645-641-63
US-08-217-918-4
US-08-217-918-4
US-08-645-641-63
US-08-645-641-63
US-08-645-641-63
US-08-645-641-63
US-08-645-641-63
US-08-645-641-63
US-08-933-40BB-63
US-08-933-40BB-63
US-08-933-40BB-63
US-08-933-40BB-63
US-08-933-40BB-63
US-08-933-40BB-63
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                  328717 segs, 42310858 residues
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                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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Sequence 22,	22		App		Ϊ.	, App	Api	, Ar	, Ap	, Appl	, Ap	, Ap	, App.			5, A	5, App
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US-08-202-047-22	US-08-964-690-22	US-08-635-109-3	US-09-199-149-3	US-08-561-521-45	US-08-525-539A-77	PCT-US95-01219-45	PCT-US95-00067-2	US-08-458-516-10	US-08-458-516-22	US-08-458-516-23	US-08-458-516-13	US-08-428-257A-78	US-07-987-264-60	US-07-634-278-105	US-08-477-728-105	US-08-474-040-105	US-08-487-200-105
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128	128	128	125	129	129	129	122	119	222	235	449	118	118	117	117	117	117
75.7	75.7	75.7	75.3	74.0	74.0	74.0	72.9	72.4	72.4	72.4	72.4	72.4	72.4	72.3	72.3	72.3	72.3
452	452	452	449.5	441.5	441.5	441.5	435.5	432.5	432.5	432.5	432.5	432	432	431.5	431.5	431.5	431.5
28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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GENERAL INFORMATION:
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                         1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY 60
                                                  1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGGGLEWMGGIIPIFGTANY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITAL TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-40G-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                 Sequence 57. Application US/09025769B

Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
APPLICANT: 11ag, Vic

APPLICANT: 11ag, Vic

APPLICANT: 11ag, Vic

APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 508; DB 4;
Pred. No. 2.8e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.81
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New YORK STATE: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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US-09-025-769B-21 ; Sequence 21, Application US/09025769B ; Patent No. 6300064

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1 QVQLVQSGABVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCE----LDWFYIWGQGTMVTVSS 114
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Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: OSPECIATION: JA
APPLICANT: Allen, DJ
APPLICANT: MCCAfferty, JG
TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

SOFTWARE: Petentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

PILING DATE: 18-FBB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

APPLICATION NUMBER: EP 95 11 3021.0

ATTORNEY AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REFERENCE/COCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

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STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                 c/o Fish & Neave
                                                APPLICANT: Ilag, Vic
APPLICANT: G. Liming
APPLICANT: G. Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 84.3%; Score 503.5; DB 4; Best Local Similarity 84.9%; Pred. No. 8.1e-45; Matches 101; Conservative 3; Mismatches 10;
                                                                                                                                                                                                                                            ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abbarrant Sav C. CITY: Glosso STATE: Illinois STATE: United States of America
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Knappik, Achim
Pack, Peter
Ilag, Vic
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61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
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US-10-001-934-39
Sequence 39, Application US/10001934
Sequence 39, Application US/10001934
Sequence 39, Application US/10001934
GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE TITLE OF INVENTION: KILLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS; TITLE OF INVENTION: KILLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS; CURRENT APPLICATION UNUMBER: US/10/001,934
CURRENT FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTING OF CELLS INCLUDING SEQ ID NOS: 63
LENGTH: 118
                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                              DB 12; Length 313;
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80.8%; Score 519; DB 15; Length 118;
Best Local Similarity 81.1%; Pred. No. 1.2e-40;
Matches 99; Conservative 10; Mismatches 9; Indels 4
                                                                                                                                                                                                                                                                                                                              Score 519.5; DB 12; Length
Pred. No. 2.9e-40;
9; Mismatches 11; Indels
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SQOTHARE: FeatSEQ for Windows Version 3.0
SQOTHARE: 1313
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Best Local Similarity 78.9%;
Matches 101; Conservative
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CORGANISM: Homo sapiens
US-10-001-934-39
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                                                                                                                                                                                                                                                          , ORGANISM: Homo sapiene
US-10-291-265-427
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61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTIONS
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              3; Gaps
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Sequence 1974, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Nuben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-01-7

PRIOR FILING DATE: 2000-01-7

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFFWARE: PatentIn Ver. 2.0
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              10; Indels
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Best Local Similarity 78.7%; Pred. No. 2.1e-40;
Matches 96; Conservative 12; Mismatches 14;
              7; Mismatches
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Publication No. US20030232054A1
GENERAL INFORMATION:
           Matches 102; Conservative
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US-09-880-748-1974
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US-10-291-265-427
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Pred, No. 7e-41;
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                                                                                                                                                                                                                                                                                                          APPLICANT: Sharon Erickson
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: MATIBODY-MAYTANSINOID CONJUGATES
FILE REFERENCE: GENERNT. 073A2
CURRENT APPLICATION NUMBER: US/9/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR PILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PastSEC for Windows Version 4.0
SEQ ID NOS: 11
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Publication No. US2030086924A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
FILE REFRENCE: P1467R2P1
CURRENT APPLICATION UNMBER: US/10/268,501
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 69/602,812
PRIOR PILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 6
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Patent No. US20020001587A1
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial sequence
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121 GTMVTVSS 128
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TYPE: PRT
ORGANISM: Homo sapiens
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: ACCEPTED TOWN TOWNER: US/10/039,785

CURRENT FILING DATE: 2002-05-07

PRIOR PILING DATE: 2002-11-20

PRIOR PILING DATE: 2001-11-14

PRIOR PILING DATE: 2001-11-09

PRIOR PILING DATE: 2001-11-09

PRIOR PILING DATE: 2001-10-09

PRIOR PILING DATE: 2001-09-21

PRIOR PILING DATE: 2001-09-21

PRIOR PILING DATE: 2001-09-21

PRIOR PILING DATE: 2001-09-21

PRIOR PILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 53
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Sequence 1605, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERENCE: PFE3
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/210,816
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Best Local Similarity 80.0%; Pred. No. 8e-41;
Matches 100; Conservative 12; Mismatches 10; Indels 3;
                                                                                                                                 Sequence 53, Application US/10039785 Publication No. US20020067646A1
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US-10-039-785-53
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121 VTVSS 125
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61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRG-----RGGYKYYGMDVWGQ 114
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
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81.7%; Score 524.5; DB 11; Length 251;
Best Local Similarity 80.0%; Pred. No. 8.1e-41;
Matches 100; Conservative 11; Mismatches 11; Indels 3;
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PRIOR FILING DATE: 2000-10-1,
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN OFF: 2.0
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; Publication No. US20030059937A1
; GENERAL INFORMATION:
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Best Local Similarity 78.19
Matches 100; Conservative
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; PEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-125-687-4
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Publication No. US20030190685A1
GENERAL INFORMATION:
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                                                                                Query Match
Best Local Similarity 82.0%
Matches 100; Conservative
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LENGTH: 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10025687
Publication No. US20020142255A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT PAPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
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Publication No. US20030054407A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
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US-10-025-687-4
                                                                                                                                        1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
                                                                                                         Gaps
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                                                             DB 10; Length 125;
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82.0%; Pred. No. 3.4e-41;
Live 10; Mismatches 10; Indels
                                                         82.8%; Score 531.5; DB 10; Length 82.5%; Pred. No. 8.8e-42; 1ve 8; Mismatches 9; Indels
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ORGANISM: Artificial Sequence
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Matches 100; Conservative
                                                                              Best Local Similarity 82.5
Matches 104; Conservative
; ORGANISM: Homo sapiens
US-09-840-459-76
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US-10-025-687-4
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LENGTH: 120
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                                                           Query Match
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APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/139,785
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/341,310
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR PILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-07
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Best Local Similarity 80.0%; Pred. No. 8e-41;
Matches 100; Conservative 12; Mismatches 10; Indels 3;
81.8%; Score 525; DB 15; Length 120; 82.0%; Pred. No. 3.4e-41; tive 10; Mismatches 10; Indels ;
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                                                                                1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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                                                   1 EVQLVESGGDLVQPGGSLRLSCAASGPTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
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  6; Сарв
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8; Indels
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APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Refe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: WHERE: U$/09/840,459
CURRENT APPLICATION NUMBER: U$/09/840,459
CURRENT APPLICATION NUMBER: U$/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR PRILING DATE: 1909-07-22
PRIOR FILING DATE: 1909-07-22
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
NUMBER: OF SUG ID NOS: 107
SOSTWARE FESTER FSEEQ FOR WINDOWS VERSION 3.0
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85.5%; Score 549; DB 10;
Best Local Similarity 82.0%; Pred. No. 2.2e-43;
Matches 105; Conservative 9; Mismatches 8;
  9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-79
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Matches 105; Conservative
                                                                                                                                                                                                                                                          115 GTTVTVSS 122
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ORGANISM: Homo sapiens
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Sequence 84, Application US/09840459 Patent No. US20020150576A1 GENERAL INFORMATION:

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61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAK---RGRGGYKYYGMDVWGQGTT 117
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3e-43;
ches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LARGEBAILOR APPLICANT: LARGEBAILOR APPLICANT: APPLICANT: Horvath, Christopher APPLICANT: Newmann, Walter APPLICANT: Newmann, Walter APPLICANT: Newmann, Walter APPLICANT: Newmann, Walter APPLICANT: O'Brien, Siobhan H. TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND TITLE OF INVENTION: HUMANIZED ENGINE THEREFOR TITLE OF INVENTION: METHODS OF USE THEREFOR CURRENT APPLICATION NUMBER: US/09/840,459 CURRENT PILING DATE: 2001-02-02 PRIOR PELING DATE: 2000-02-03 PRIOR APPLICATION NUMBER: 09/497,625 PRIOR APPLICATION NUMBER: 09/497,625 PRIOR PILING DATE: 1999-07-22 PRIOR PILING DATE: 1999-07-23 PRIOR PILING DATE: 1998-07-23 NUMBER OF SEQ ID NOS: 107
                                                                                  APPLICANT: Ornes, S. Tarran
APPLICANT: O'Brien, Siohan H.
APPLICANT: O'Refe, Theresa
APPLICANT: O'Refe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT FILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR PILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1998-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 85.3%; Score 547.5; Best Local Similarity 84.0%; Pred. No. 3e-4 Matches 105; Conservative 8; Mismatches
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Horvath, Christopher
Newman, Walter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 VTVSS 122
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(without alignments)
927.994 Million cell updates/sec
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1 EVQLVESGGDLVQPGGSLRL.....GYKYYGMDVWGQGTTVTVSS 122
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodate/2/pubpaa/PCT MRW PUB.pep:*

3: /cgn2_6/ptodate/2/pubpaa/USO6_NEW PUB.pep:*

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12: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

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15: /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO06_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO06_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               724715 segs, 199017464 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 77, Appl	Sequence 79, Appl	Sequence 84, Appl	Sequence 76, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 53, Appl	Sequence 53, Appl	Sequence 1605, Ap	Sequence 1701, Ap	Sequence 3, Appli	Sequence 6, Appli	Sequence 1974, Ap	Sequence 427, App	Sequence 39, Appl
SUMMARIES	ID	US-09-840-459-77	US-09-840-459-79	US-09-840-459-84	US-09-840-459-76	US-10-025-687-4	US-10-125-687-4	US-10-139-785-53	US-10-039-785-53	US-09-880-748-1605	US-09-880-748-1701	US-09-811-123-3	US-10-268-501-6	US-09-880-748-1974	US-10-291-265-427	US-10-001-934-39
	03	10	10	10	10	14	15	12	13	11	11	9	15	11	12	15
	* Query Match Length DB	128	128	125	125	120	120	249	249	251	254	119	119	248	313	118
	Query Match	85.5	85.5	85.3	82.8	81.8	81.8	81.7	81.7	81.7	81.3	81.2	81.2	81.0	6.08	80.8
	Score	549	549	547.5	531.5	525	525	524.5	524.5	524.5	522	521.5	521.5	520	519.5	519
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US-10-120-414-76 Sequence 76,	1	5 Sequence	Sequence	Sequence 989	Sequence	9	Sequence 4	Sequence 4	Sequence 6	Sequence	1 Sequence	3 Sequence	Sequence	Sequence Sequence	740 Sequence	537 Sequence	739 Sequence	3 Sequence	3 Seguence	Sequence		Sequence	Sequence		82 Sequence	9 Sequence		3 Sequence
12 US	10 US	_				11 US						11 U		11 U				10 U	_			12 U			_	10 U	_	12 US
253	124	124	224	253	248	251	136	367	119	128	252	248	248	248	251	252	254	263	263	283	283	244	251	121	123	124	124	245
80.7	80.5	80.4	80.3	80.3	80.2	80.2	80.1	80.1	80.0	79.6	79.6	79.5	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.2	79.2	79.1	79.1	79.1
518	517	516	515.5	515.5	515	515	514	514	513.5	511	511	510.5	510	510	510	510	510	510	510	510	510	509.5	509.5	508.5	508.5	508	508	508
16	11	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44

ALIGNMENTS

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Length 128;
                      Sequence 77, Application US/09840459
Sequence 77, Application US/09840459
Patent No. US2002015057641
GENERAL INFORMATION:
APPLICANT: LARGEA, Gregory J.
APPLICANT: Newman, Walter
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Refe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: DO1-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
PRIOR PRIOR PRIOR PRIORS TO NOS: 107
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Pred. No. 2.2e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.5%;
82.0%;
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ORGANISM: Homo sapiens
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Best Local Similarity
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JS-09-840-459-77
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us-09-674-752-53.rag

This invention relates to a novel humanised, chimeric or human monoclonal antibody or its antigen binding portion that specifically binds to insulin-like growth factor I receptor (IGF-IR). The antibodies of the invention can act as an inhibitor of binding of IGF-IR or IGF-II with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine phosphorylation. The antibodies of the invention are useful for disgnosing the presence or location of an IGF-IR-expressing tumour in a subject. The antibody or its antisen-binding portion is also useful for neoplastic, anti-tumour, anti-analygen-binding portion is also useful for the antibodies may also be useful for increasing IGF-IR activity and thus restoring IGF-IR activity in a condition characterised by low IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the patient, and to treat non-cancerous states or disease, e.g. acromegaly, grantism, psoriasis and atheroselerosis. Fully human anti-IGF-IR antibodies minimise the immunogenic and alleggic responses intrinsic to mouse or mouse-derivatised monoclonal antibodies and thus increase the efficacy and safety of the administered antibodies and thus increase the immediate in a patient, and to be administered antibodies and thus increase the efficacy and safety of the administered antibodies and thus increase the immediate in a patient sequence of the administered antibodies and thus increase the immediate.

124 AA; Sequence

DSVKGRFTISRDNSKNTVYLEMNSLRAEDTALYYCAKR---GRGGYKYYGMDVWGQGTTV 118 2 VQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFYA 61 3; Gaps 81.5%; Score 523.5; DB 23; Length 124; 80.6%; Pred. No. 1.7e-41; tive 9; Mismatches 12; Indels 3; Best Local Similarity 80.6 Matches 100; Conservative **TVSS 122** 121 TVSS 124 62 61 119 පු δ ઠ ઠે

ABP56504 standard; Protein; 121 AA. 20-MAR-2003 ABP56504; RESULT 19

(first entry)

Autoantibody; Fc-epsilon-R1 receptor alpha-chain; immunosuppressive; alleggic disease; urticaria; late phase allergic reaction; malignancy; intrinsic asthma; drug intolerance; food intolerance; immunoglobulin Econditional autoimmunity; IgE mediated disease. Human anti-Pc-epsilon-R1 alpha autoantibody heavy chain LTM-alpha-15.

sapiens Synthetic

40200282085-A2

17-0CT-2002

03-APR-2002; 2002WO-EP03660.

04-APR-2001; 2001US-281024P.

(ZLBB-) ZLB BIOPLASMA AG

Miescher S;

WPI; 2003-103348/09.

Identifying and obtaining inhibitor of a pathological process for treating e.g. autoimmunity comprises determining if a compound is capable of modulating the binding of the Fc-epsilon-R1 receptor and an autoantibody against its alpha-chain -

Claim 20; Page 22; 29pp;

The present invention describes a method for identifying and obtaining an inhibitor of a pathological process. The method comprises determining if a compound is capable of modulating the binding of the Fc-epsilon-R1 receptor alpha-chain and an autoantibody against its alpha-chain. Also described: (1) use of the autoantibody against the Fc-epsilon-R1 receptor alpha-chain for identifying and obtaining an inhibitor of a pathological process; (2) use of the identified inhibitor for inhibiting activity of the autoantibody against the Fc-epsilon-R1 receptor alpha-chain; and activate the receptor; and (4) a polypeptide capable of specific binding to the Fc-epsilon-R1 receptor alpha-chain. The method is useful for obtaining an inhibitor of a pathological process e.g. imbalance between cell-bound and free IgE e.g. allergic disease (urticaria, late phase allergic reactions, intrinsic asthma, drug intolerance and food intolerance). IgE mediated disease or malignancy. The compound is useful cutoimmunity. The present sequence represents a human recombinant the present invention the present invention

121 AA; Sequence

1; Gaps DB 24; Length 121; Query Match 81.4%; Score 522.5; DB 24; Length Best Local Similarity 82.8%; Pred. No. 2.1e-41; Matches 101; Conservative 10; Mismatches 10; Indels

1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWYSAISGSGGSTYY 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY ઠે 셤

120 ADSVKGRFT1 SRDNSKNTVYLEMNSLRAEDTA1YYCAKRGRGGYKYYGMDVWGQGTTVTV 셤 ઠ

SS 122 121 ઠ

SS 121

completed: December 30, 2003, 10:54:38 Job time : 40.3295 secs Search

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9 85

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
                                                                                                                                                                                                                                                        1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
                                                                                                                                                                                                             2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome
           The present sequence is the consensus single chain fragment VH3·V-kappa-2. VH3·V-kappa-2, which comprises the human antibody heavy and light chain variable region consensus sequences VH3 and V-kappa-2, was used in the preparation of a human derived antibody gene library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                 DB 18; Length 281;
                                                                                                                                Match 81.8%; Score 525; DB 18; Length 2 Local Similarity 82.0%; Pred. No. 3e-41; les 100; Conservative 10; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human BLyS binding acFv SEQ ID 1605.
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                                                                                                                                                                                                                                                                                                                                                                                                                            ABP45594 standard; Protein; 251
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2001US-276248P.
2001US-277379P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-114799/15.
                                                                                                     281 AA;
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                                                                                                                                                                                                                                                                                                                     121
                                                                                                        Sequence
                                                                                                                                   Query Match
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Matches
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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRSYDILTGYYTYGMDVWGKGTM 120
                                                                                                                                                                                                                                                                                                                                                                                                                            61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTALYYCAKRGRG---GYKYYGMDVWGQGTT 117
cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABPA 3990-ABPA 7728 represent the antibodies and fragments of the antibodies described in the method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to insulin-like growth factor I (IGF-1) receptor useful for inhibiting binding of IGF-I or IGF-II to receptor and for treating cancer in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel humanized, chimeric monoclonal antibody that specifically binds
                                                                                                                                                                                                                                                                                                                                                                         1 BVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGQEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                                                                                     EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallo
                                                                                                                                                                                                                                                                                                                     3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insulin-like growth factor I receptor; antibody; human; cytostatic; osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
                                                                                                                                                                                                                                                                                   Score 524.5; DB 23; Length 251; Pred. No. 3e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corvalan JR,
                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                   11, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miller PE, Moyer JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG77138 standard; Protein; 124 AA.
                                                                                                                                                                                                                                                                                      81.7%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-2001; 2001WO-US51113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JAN-2001; 2001US-259927P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.09
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-575410/61.
N-PSDB; ABS62700.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 VTVSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 VTVSS 125
                                                                                                                                                                                                                                                      251 AA;
                                                                                                                                                                                                                   of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200253596-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUL-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG77138;
                                                                                                                                                                                                                                                       Sequence
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Claim 13; Page 127; 172pp; English

Sequence

8XCCCXXXX777X8

Query Match Local

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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARWGGDG--FYAMDYWGQGTLVTV 118
artificial antibodies in silico which provides a structurally diverse and yet functionally more relevant source of antibody candidates which can then be screened for binding a wide variety of target molecules, including small molecules, and biomacromolecules such as proteins, peptides and nucleic acids. The libraries constructed are useful as source of antibody candidates for further screening for novel antibodies with high affinity against a wide range of antigens and having no or minimum immunogenecity to human subjects treated with antibody therapeutics. This sequence represents a protein region of an antibody relating to the novel antibody library construction method of the
                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV
                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, antibody; preparation; library; VH3; variable region; light chain; heavy chain; V-kappa-2; single chain; consensus
                                                                                                                                                                                                                                                                                                          Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plueckthun
                                                                                                                                                                                                                                                                                                                                                    10; Indels
                                                                                                                                                                                                                                                                                                       81.8%; Score 525; DB 24;
82.0%; Pred. No. 1.2e-41;
ive 10; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pack P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus single chain fragment VH3-V-kappa-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ge L, Ilag V, Knappik A, Moroney S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW27560 standard; Protein; 281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 8; 436pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95EP-0113021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                    Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-179277/16.
                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT87958.
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                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                            invention.
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                                                                                                                                                                                                                                                                                                              Query Match
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        88888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for the construction of a library of recombinant antibodies. The novel method comprises clustering variable regions of a collection of antibodies having known 3D structures into at least two families of structural ensembles, each comprising at least two different antibody sequences but with substantially identical main chain conformations. The method is useful for constructing a library of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAVYYCARWGGDG--FYAMDYWGQTLVTV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody library related heavy variable chain protein region SEQ ID No 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                      61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV
                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library; recombinant antibody; clustering variable region; in silico; immunogenecity; antibody therapeutic.
                                            Preparation of human derived antibody gene library - using synthetic consensus sequences, and signal consensus antibody gene as universal framework for highly diverse antibody libraries
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Constructing a library of recombinant antibodies useful as source of antibody candidates for screening antigens comprises clustering variable regions of antibodies having known 3-dimensional structures
                                                                                                                                                                      The present sequence is the human antibody heavy chain variable region synthetic sequence VH3, used in the preparation of a human derived antibody gene library.
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                                                                                                                                                                                                                                                                                                          Length 120;
                                                                                                                                                                                                                                                                                                                                                      10; Indels
                                                                                                                                                                                                                                                                                                       81.8%; Score 525; DB 18;
82.0%; Pred. No. 1.2e-41;
ive 10; Mismatches 10;
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                                                                                                                                   Example 1; Pig 5D; 436pp; English
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                                                                                                                                                                                                                                                                                                                                                  Matches 100; Conservative
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                                                                                                                                                                                                                                                                 120 AA
    N-PSDB; AAT87951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS 122
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Unidentified.

24-OCT-2002

Luo P;

06-MAR-2003

ABJ1867

121 119

120

9 9

Gaps

us-09-674-752-53.rag

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a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting c leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmuse disorders such as rheumatoid arthitis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or disposis, and in the manufacture of a medicament for treating CR2-2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and ISB2. C mediated allergic reaction, shock, stenosis, allograft rejection, incurred in mummed deficiency syndrome (AIDS), restenosis, allograft rejection, incurred syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, and inhibiting neointimal hyperplasia of the present sequence is human heavy chain variable (VH) region, 038064.
          8X8888888888888888888
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125 AA; Sequence

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116
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                                                                                                                     1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAK----RGRGGYKYYGMDVWGQGT
                                                                                            1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
                                                  Gaps
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82.8%; Score 531.5; DB 22; Length 125; 82.5%; Pred. No. 3.1e-42; ive 8; Mismatches 9; Indels 5;
                           Best Local Similarity 82.5
Matches 104; Conservative
                         Local Similarity
                                                                                                                                                                                                                                                                         117 TVTVSS 122
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    Query Match
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ABG77157 standard; Protein; 470 AA. 24-OCT-2002 (first entry) ABG77157; RESULT 9

Insulin-like growth factor I receptor; antibody; human; cytostatic; osteopathic; antiatherosclerotic; antiposciatic; IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis; acromegaly; gigantism; psoriasis; Amino acid sequence of anti-IGP-1R antibody 2.13.2 Vh domain. atherosclerosis

Homo gapiens

WO200253596-A2. 11-JUL-2002

20-DEC-2001; 2001WO-US51113

05-JAN-2001; 2001US-259927P (ABGE-) ABGENIX INC. (PFIZ) PFIZER INC

Corvalan JR, Moyer JD, Cohen BD, Beebe J, Miller PE, WPI; 2002-575410/61 Novel humanized, chimeric monoclonal antibody that specifically binds to insulin-like growth factor I (IGF-1) receptor useful for inhibiting binding of IGF-I or IGF-II to receptor and for treating cancer in

WPI; 1997-179277/16

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This invention relates to a novel humanised, chimeric or human monoclonal antibody or its antigen binding portion that specifically binds to insulin-like growth factor I receptor (IGF-IR). The antibodies of the invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine phosphorylation. The antibodies of the invention are useful for diagnosing the presence or location of an IGF-IR-expressing tumour in a subject. The antibody or its antigen-binding portion is also useful for treating cancer in a human. The method for this further involves an antinoplastic, anti-tumour, anti-anglogenic or chemotherapeutic agent. The antibodies may also be useful for increasing IGF-IR activity and chuse restoring IGF-IR activity in a condition characterised by low IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the invention is also useful for inducing apoptosis of specific cells in a invention is also useful for inducing apoptosis of specific cells in a patibodies minimise the immunogenic and allergic responses intrinsic to mouse or mouse-derivatised monoclonal antibodies and thus increase the efficacy and safety of the administered antibodies and thus increase the represents an anti-insulin-like growth factor I receptor antibody of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 ADSVKGRFTISRDNSRTTLYLQMNSLRAEDTAVYYCAKDLGWSDSYYYYXGMDVWGQGTT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 BVQLLESGGGLVQPGGSLRLSCTASGFTFSSYAMNWRQAPGKGLEWVSAISGSGGTTFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKR---GRGGYKYYGMDVWGQGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 82.3%; Score 528.5; DB 23; Length 470; Best Local Similarity 80.8%; Pred. No. 2.5e-41; Matches 101; Conservative 9; Mismatches 12; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, antibody, preparation, library, VH3, variable region,
heavy chain, consensus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Ab heavy chain variable region VH3 consensus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moroney S,
                                  Claim 16; Figure 19B; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW27553 standard; Protein; 120 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 VTVSS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               470 AA;
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  humans
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                                                                                                            61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAK-RGRGG--YKYYGMDVWGQGTT 117
                                                                                                                          The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (BSTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                         9
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                                                                      EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTPY
                                 Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [solated polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                                                                                                               Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
tomato; monkey; dog; sea urchin; expressed sequence tag; BST;
diagnostics; forensic test; gene mapping; genetic disorder;
biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen R, Asundi V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 384;
    DB 23; Length 125;
 Score 539.5; DB 23; Length
Pred. No. 5.5e-43;
8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.7%; Score 537.5; DB 22; Length 78.2%; Pred. No. 2.9e-42; Live 9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ou P, Qian XB, Wang Z, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                    Human EST encoded protein SEQ ID NO: 1626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 1102-1103; 1275pp; English.
                                                                                                                                                                                                                                                                  AAM24101 standard; Protein; 384 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibodies and research use -
 84.0%;
84.0%;
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17-JUL-2000; 2000US-0617746.
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15-SEP-2000; 2000US-0663870
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                                                                                                                                                                                                                                                                                                                         (first entry)
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                            105; Conservative
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              Local Similarity
                                                                                                                                                                    VTVSS 122
                                                                                                                                                                                             VIVSS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAH98760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200154477-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                               AAM24101;
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                                                                                                                                                                    118
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Query Match
Best Local S
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Conservative

Local Similarity

Best Local Sim Matches 104;

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---YYGM 109
                 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSGIGGSGSSTYY 79
                                                                                                                                                                                                                                                                                                                                                                                 Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; relativation immunodeficiency virus; relativation; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis, atherogensis, atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody; necintimal hyperplasia; VH; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'Brien S,
                                                                ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKR
                                                                                                                                                                                                                                                                                                                                                       Human heavy chain variable (VH) region, 038064.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 168; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                      AAE07013 standard; Protein; 125 AA.
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/label= CDR2
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/label= CDR3
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/label= CDR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-FEB-2000; 2000US-0497625.
                                                                                                                                  DVWGQGTTVTVSS 122
                                                                                                                                                                  DVWGQGTTVTVSS 152
                                                                                                                                                                                                                                                                                                                      (first entry)
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Germline protein sequence of anti-IGF-1R antibody DP-47(3-23)/D6-19/JH6.
                                                                                                                                                                                                                                                                                                                   Novel humanized, chimeric monoclonal antibody that specifically binds to insulin-like growth factor I (IGF-1) receptor useful for inhibiting binding of IGF-I or IGF-II to receptor and for treating cancer in
                                                                                                                                                                                                                                                                             Gallo M;
                                                                                        cytostatic; osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
                                                                                                                                                                                                                                                                             Moyer JD, Corvalan JR,
                                                                               Insulin-like growth factor I receptor; antibody; human;
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Figure 19B; 172pp; English
ABG77158 standard; Protein; 470 AA
                                                                                                                                                                                                                                                                             Cohen BD, Beebe J, Miller PE,
                                                                                                                                                                                                       20-DEC-2001; 2001WO-US51113
                                                                                                                                                                                                                            05-JAN-2001; 2001US-259927P
                                         (first entry)
                                                                                                                                                                                                                                              (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                 WPI; 2002-575410/61
                                                                                                                        atherosclerosis.
                                                                                                                                                               WO200253596-A2.
                                                                                                                                            Homo sapiens
                                        24-OCT-2002
                                                                                                                                                                                   11-JUL-2002.
                     ABG77158;
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This invention relates to a novel humanised, chimeric or human monoclonal antibody or its antigen binding portion that specifically binds to insulin-like growth factor I receptor (IGF-IR). The antibodies of the invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine phosphorylation. The antibodies of the invention are useful for diagnosing the presence or location of an IGF-IR-expressing tumour in a subject. The antibody or its antigen-binding portion is also useful for treating cancer in a human. The method for this further involves an antinephotosis may also be useful for increasing IGF-IR activity and thus restoring IGF-IR activity in a condition characterised by low IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the contribution is also useful for inducing apoptions, and the in a condition characterised by low the interpretation is also useful for inducing apoptions of specific cells in a condition and the interpretation is also useful for inducing apoptions. efficacy and safety of the administered antibodies. The present sequence represents an anti-insulin-like growth factor I receptor antibody of the patient, and to treat non-cancerous states or disease, e.g. acromegaly, gigantism, psortiasis and atheroseclerosis. Pully human anti-IFF-IR antibodies minimise the immunogenic and allergic responses intrinsic to mouse or mouse-derivatised monoclonal antibodies and thus increase the invention

470 AA; Sequence

This invention relates to a novel humanised, chimeric or human monoclonal antibody or its antigen binding portion that specifically binds to insulin-like growth factor I receptor (IGF-IR). The antibodies of the invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-IR and can inhibit in vivo tummour growth and IGF-IR tyrosine phosphorylation. The antibodies of the invention are useful for diagnosing the presence or location of an IGF-IR expressing tummour in a subject. The antibody or its antignambing portion is also useful for treating cancer in a human. The method for this further involves an antimaphastic, anti-tummour, anti-angiogenic or chemotherapeutic agent. The antibodies may also be useful for increasing IGF-IR activity and thus restoring IGF-IR activity in a condition characterised by low IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the intention is also useful for inducing apoptosis of specific cells in a patient, and to treat non-cancerous states or disease, e.g. acromegaly, gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR activitatised monoclonal antibodies and thus increase the mouse or mouse edrivatised monoclonal antibodies and thus increase the immunogents and altering responses intrinsic to mouse or mouse derivatised monoclonal antibodies and thus increase the immunosents an antibodies and thus increase the immunosents. The present sequence increase the immunosents and alteriated antibodies and thus increase the immunosents.

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                                                                                          1 EVQLVESGGDLVQPGGSLRLSCAASGPTPSNPAMSWVRQAPGKGLEWVAAIGGRSGTTPY
                                    3; Gaps
84.8%; Score 544.5; DB 23; Length
83.2%; Pred. No. 8e-43;
.ive 9; Mismatches 9; Indels
                  Best Local Similarity 83.2
Matches 104; Conservative
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 Query Match
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DB 23; Length 470;

125 AA;

Sequence

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80 ADSVKGRPTISRDNSKOYTLYLQMNSLRAEDTAVYYCAKGYSSGWYYYYYYGMDVWGQGTT 139
61 ADSVKGRPTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGG---YKYYGMDVWGQGTT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel humanized, chimeric monoclonal antibody that specifically binds to insulin-like growth factor I (IGF-1) receptor useful for inhibiting binding of IGF-I or IGF-II to receptor and for treating cancer in
                                                                                                                                                                                                                                                                                                                                                                                                         Gallo M;
                                                                                                                                                                                Anti-IGF-IR antibody (4.9.2) variable region heavy chain protein.
                                                                                                                                                                                                   Insulin-like growth factor I receptor; antibody; human; cytostatic; osteopathic; antiatherosciarotic; antiposciatic; IGP-IR; tumour; anti-nooplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                          Corvalan JR,
                                                                                                                                                                                                                                                                                                                                                                                                          Moyer JD,
                                                                                                                 ABG77142 standard; Protein; 125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 130; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           Miller PE,
                                                                                                                                                                                                                                                                                                                                   20-DEC-2001; 2001WO-US51113.
                                                                                                                                                                                                                                                                                                                                                       05-JAN-2001; 2001US-259927P.
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           Beebe J,
                                                                                                                                                                                                                                                                                                                                                                           (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC.
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                                          118 VTVSS 122
                                                               140 VTVSS 144
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                                                                                                                                                                                                                                                 atherosclerosis
                                                                                                                                                                                                                                                                                         WO200253596-A2.
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                                                                                                                                                            24-OCT-2002
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                                                                                                                                       ABG77142;
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                                                                                             RESULT 6
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Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                               Disclosure; Page 168; 183pp; English.
WPI; 2001-488888/53
                                                                                                                                                                                                                          Sequence
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fregment, having binding specificity for CC-chemokine receptor 2
(CC2), comprising an antigen binding region of non-human origin. The and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating CR2. They are useful for inhibiting or treating infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple salerosis, atherogenesis and atheroscelerosis, and for inhibiting restenosis. They are useful in therapy or disgnosis, and for inhibiting restenosis. They are useful in therapy or disgnosis, and for inhibiting restenosis. They are allowed a lact of a medicament for treating cCR2- mediated and in the manufacture of a medicament for treating allery, anaphylaxis, malignancy, chronic and acute inflammation, histamine and ISE- mediated allergic reaction, shock, stenosis, allograft rejection, fincluding angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention.

The present sequence is human heavy chain variable (VH) region, 038062. The patent discloses a humanised antibody or its antigen-binding

128 AA;

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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRRNYDFWSGXYYYYGMDVWGQ 120
                                                                                                                                                      61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGR-----GGYKYYGMDVWGQ 114
                                                                                                1 BVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
                                          Gaps
                                            9
  85.5%; Score 549; DB 22; Length 128; 82.0%; Pred. No. 7.3e-44; ive 9; Mismatches 8; Indels
Query Match
Best Local Similarity 82.0
Matches 105; Conservative
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AAE07021 standard; Protein; 125 AA (first entry) 16-OCT-2001 AAE07021; RESULT 4

Human heavy chain variable (VH) region, 4G12.

Human; humanised antibody, CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyce trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angloplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody; neointimal hyperplasia; VH; heavy chain variable region.

Ното варіепв

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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating thy infection. The proteins of the invention are useful for inhibiting or treating cell that the season of a cell expressing CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR2-mediated diagnosis, and in the manufacture of a medicament for treating allery, anaphylaxis, and in the manufacture of a medicament for treating allery, anaphylaxis, fibrotic disease, asthma, inflammatory glomerulopathies, acquired inmune deficiency syndrome (AIDS), restenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting neointimal hyperplasia of a useful for inhibiting neointimal hyperplasia of the comment of a vessel in a mammal, and inhibiting neointimal hyperplasia of the comment of a vessel in a mammal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a vessel in a mammal, preferably associated with vascular intervention. The present sequence is human heavy chain variable (VH) region, 4G12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 BVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAK---RGRGGYKYYGMDVWGQGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 O'Keefe T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٠,
ص
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 547.5; DB 22; Length 125;
Pred. No. 9.9e-44;
8; Mismatches 9; Indels 3;
                                                                       50..66
/label= CDR2
/note= "Complementarity determining region 2"
                                                                                                                                                                               /note= "Complementarity determining region 3"
                                                        "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                               O'Brien S,
                                                                                                                                                                                                                                                                                                                                                                                                                               Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 171; 183pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.3%;
                                                                                                                                      99..114
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                       31..35
/label= CDR1
                                                                                                                                                                                                                                                                                                       02-FEB-2001; 2001WO-US03537
                                                                                                                                                                                                                                                                                                                                             03-FEB-2000; 2000US-0497625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 84.0
nes 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Horvath C,
                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488888/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 VTVSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 125 AA;
                                                                                                                                                                                                                       WO200157226-A1.
                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                           Larова GJ,
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Key
Region
                                                                              Region
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Gaps

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61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
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presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents a fragment of the human factor VIII antibody heavy chain variable region protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody; neointimal hyperplasia; VH; heavy chain variable region.
                                                                                                                                                                                                                                                                                    EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
                                                                                                                                                                                                                                                                                                         1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Complementarity determining region 3"
                                                                                                                                                                                            Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Complementarity determining region 99..117 /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'Brien S,
                                                                                                                                                                                                                                         Indels
                                                                                   of the human factor VIII antibody heavy chain varia DP-47 which is used in the method of the invention.
                                                                                                                                                                                            100.0%; Score 642; DB 21;
100.0%; Pred. No. 1.4e-52;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain variable (VH) region, 038062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newman W, Jones ST,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
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/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31..35
/label= CDR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (first entry)
                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                       122 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE07014;
                                                                                                                                                          Sequence
                                                                                                                                                                                                   Query Match
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                                                                                   hybridizable polynucieotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has presented activity. (1) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents a human factor VIII antibody A2 specific scFv protein DP-47 which is used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ADSVKGRPTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGKGGYKYYGMDVWGQGTTVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; heavy chain; antibody; factor VIII; hemostatic; variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human FVIII heavy chain variable region DP-47 protein fragment.
                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 642; DB 21; Length 122; Best Local Similarity 100.0%; Pred. No. 1.4e-52; Matches 122; Conservative 0; Mismatches 0; Indels 0
                                                                      This invention describes a novel polynucleotide (I) (and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Turenhout EAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY50975 standard; Protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3xample 9; Fig 11c; 61pp; English.
                             Example 9; Fig 11A; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Den Brink EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-NL00285
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                                                                                                                                                                                                                                                                                                               122 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hemophilia A
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Sequence

O'Keefe T;

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Human heavy chain
Germline protein s
Anti-IGF-IR antibo
Human EST encoded
Human heavy chain
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Human FVIII heavy
Human heavy chain
Human heavy chain
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                                                                                                                                                  December 30, 2003, 10:42:39; Search time 39.2461 Seconds (without alignments) 493.415 Million cell updates/sec
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(SIDS1) gcgdata/geneseq_geneseq_pembl/AA1981.DAT: *

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(SIDS1) gcgdata/geneseq_geneseq_pembl/AA1984.DAT: *

(SIDS1) gcgdata/geneseq_geneseq_pembl/AA1984.DAT: *

(SIDS1) gcgdata/geneseq_geneseq_pembl/AA1989.DAT: *

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(SIDS1) gcgdata/geneseq_geneseq_geneseq_pembl/AA2
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642
1 EVQLVESGGDLVQPGGSLRL......GYKYYGMDVWGQGTTVTVSS 122
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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AAE07014
AAE07021
ABG77158
ABG77142
AAM24101
AAE07013
                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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AAW27553 ABJ18675 AAW27560 ABP45594 ABG77138	ABP56504 ABP56506 ABP12061 AAB62088 AAB60401 AAB61586	AAU74541 ABR01515 ABR01515 AAU14320 AAU83803 ABB57561	AAE07018 ABD56507 ABJ3639 ABR01534 ABP45978 ABP45954 ABP55473 ABP55473	AAE28151 AAB67620 AAW06242 AAW13524 AAR30773 AAE07015 ABP45420
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120 120 281 251 124	121 121 254 117 119 119	222 248 313 118 253	124 121 177 221 253 248 251 136	119 245 128 140 122 128 128 121
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## ALIGNMENTS

Human FVIII antibody A2 BcFv heavy chain protein DP-47 #2. Human; heavy chain; antibody; factor VIII; hemostatic; hemophilia A; scFv; A2. Turenhout BAM (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING AAY50973 standard; Protein; 122 AA Joorberg JJ, Van Den Brink EN, 98EP-0201543. 99WO-NL00285. (first entry) WO9958680-A2. 07-MAY-1999; 08-MAY-1998; Homo sapiens 23-MAR-2000 18-NOV-1999. AAY50973; AAY50973 

New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -

WPI; 2000-053102/04.

us-09-674-752-53.rspt

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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.6 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC013656; AAH13656.1;
InterPro; IPR00710; Ig-like.
R InterPro; IPR003006; Ig-MHC.
R InterPro; IPR003006; Ig-W.
R Fam; PF00047; Ig: 4.
R PROSITE; PS00835; IG-V: 1.
R PROSITE; PS00835; IG-LIKE; 4.
R PROSITE; PS00290; IG-MHC; 2.
R Hypothetical protein.
SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004786; AAN04786.1; -.
HSPP; PO1810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR03006; Ig-MHC.
InterPro; IPR03306; Ig-V.
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SMART; SM04406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS0290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;
                                                                                                                                                            01-DEC-2001 (TYEMBLrel. 19, Created)
01-DEC-2001 (TYEMBLrel. 19, Last sequence update)
01-DRC-2003 (TYEMBLrel. 23, Last annotation update)
Hypothetical 51.6 kba protein.
Mus musculus (Mouse).
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Local Similarity 74.69
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Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

"An antibody fragment2A3 specific for native lysozyme :Isolaion from a human synthetic phage display library and characterization.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB049915; BAB16829.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
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                                                                                                                                                                                                                              QBNSK4;
QBNSK4;
QBNSK4;
QBNSK4;
QBNSK4.
QBNSK2.2002 (TYEMBLrel. 22, Last sequence update)
O1-OCT-2003 (TYEMBLrel. 23, Last annotation update)
Hypochetical protein.
Hypochetical protein.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
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O1HAR-2001 (TEMBLrel. 16, Created)
O1-MAR-2001 (TEMBLrel. 16, Last sequence update)
O1-MAR-2003 (TEMBLrel. 13, Last annotation update)
O1-MAR-2003 (TEMBLrel. 23, Last annotation update)
Single chain Pv (Fragment).
Home sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Straubborg R.;
L Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO3249; AAJ3249.1; -.
R InterPro; IPR003599; Ig. -.
R InterPro; IPR003599; Ig.-Iike.
R InterPro; IPR003596; Ig-dl.
R InterPro; IPR003066; Ig-MHC.
R InterPro; IPR003066; Ig-MHC.
R InterPro; IPR003066; Ig-MHC.
R SWART; SM00407; IG; 4.
R SWART; SM00407; IG; 4.
R SWART; SM00406; IG, 1.
R SWART; SW00406; IG, 1.
R SWART; SW0406; IG, 1.
R SWART; SW00406; IG, 1.
R SWAR
                                                                                                                                                                                                            499 AA
                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 GQGTTVTVSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                         116
              116 8
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0885K4
AC 0885KA
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DT 01-0C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARR-----RYALDYWGQGTLV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVESGGGGVVRPGGSLRISCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGY
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                                                                                                                                                                                                                                                                                                                                                Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";

Clin. Immunol. Immunopathol. 87:184-192(1998).

EMBL; AF035030; AAD5266.1; -
HSSP; P0172; ZEP4.

InterPro: IPR007110; 19-1ike.

InterPro: IPR00306; Ig_MHC.

InterPro: IPR003596; Ig_W.

SMART; SM00406; IGy.

SMART; SM00406; IGy.

PROSITE; PS50835; IG_LIKE; 1.
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SEQUENCE FROM N.A.
WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                Ouery Match 71.0%; Score 456; DB 4; Length 112; Best Local Similarity 72.0%; Pred. No. 4.5e-38; Matches 85; Conservative 14; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.6%; Score 453; DB 4; Length 122; 74.6%; Pred. No. 1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QUUD84;
01-MXY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER 1 1 12 112
NON_TER 112 112
SEQÜENCE 112 AA; 12243 MM; 24F1A45EC3B84788 CRC64;
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Best Local Similarity 71.4
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Q9Y509;
Q1-NOV-1999
O1-NOV-1999
O1-MAR-2003
VH3 protein
VH3.
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MEDLINE=96071149; PubMed=7475288;
Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C
Lichtenstein A.K., Berenson J.R.;
"A CD10-positive subset of malignant cells is identified in
                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S80860; AAD14339.1; -. HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myeloma using PCR with patient-specific immunoglobulin Leukemia 9:1948-1953\,(1995).
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                                                                  MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                           Young D.C.;
                                               "Myosin-reactive autoantibodies in rheumatic carditis
                                                                                            SEQUENCE FROM N.A.
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Immunol. Immunopathol. 87:184-192(1998)
AF035024; AAD56260.1; -.
P01772; 2FB4.
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                                                                                                                                                                                                                                                                                                                   TVTVSS 122
                                                                                                                                                                                                                                                                                                                                                      ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGR----GGYKYYGMDVWGQGT
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71.4%;
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Last sequence update)
Last annotation update)
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Pred. No. 2e-38;
9; Mismatches
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                                                                      Kalis N.N.,
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primers.";
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Best Local S
Matches 92
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Best Local S
Matches 90
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

NON_TER 113 113

NON_TER 113 113

SEQUENCE 113 AA; 12437 MW;
                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 1.
SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON TER
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116 116
SEQUENCE 116 AA; 12434 MW;
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Q9UL93;
Q1-MAY-2000
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MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=P.L.,
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InterPro;
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Mammalia; Eutheria; E
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EMBL; AP035021; AAD56257.1; -.
HSSP; P01772; 2FB4.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
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                                                                        DSVKGRPTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVMGQGTTVTVS 121
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IPR003596; Ig_v.
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Pred. No. 2.1e-38;
9; Mismatches 14
                                                                                                                                                                                                                                        Score 459.5; DB 4;
Pred. No. 2.1e-38;
8; Mismatches 16;
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EMBL; BC020240; AAH20240.1; -.

InterPro; IPR003106; Ig MIC.

InterPro; IPR003006; Ig MC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 5.

SMART; SM00406; IGv; 1.

PROSITE; PS00035; IG_MIC; 3.

Hypothetical protein.

SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;
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Q8WUK1;
O1-MAR-2002 (TrEMBLrel. 2:
01-MAR-2002 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 2:
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Q9UL91;
01-MAY-2000
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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Homo mapiens (Human)
Eukaryota, Metazoa, Chordata,
Mammalia; Eutheria, Primates;
   InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
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HSSP; P01772; 2FB4.
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; Pred. No. 6e-38;
11; Mismatches 19
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Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REQUENCE FROM N.A.

RE SEQUENCE FROM N.A.

RE TISSUB-Mammary gland;

RA IEOGRI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA IEOGRI T., Ota T., Hayashi K., Shiratori A., Sudo H.,

RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

RA Wagateuma M., Hosoiri T., Kaku Y., Kodalra H., Kondo H., Sugawara M.,

RA Watanabe M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

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RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

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RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

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RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kamai Y., Saito K., Murakami K., Ishii S., Kawai Y., Saito K.,
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Best Local S
Matches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 494 AA; 53088 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96K68;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ14473.
Homo sapiens (Human).
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SEQUENCE
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1 Similarity 73.6%;
89; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                           87;
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   SS
                                                                                                                                                                           ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
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                                                                         SS
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                                                                                                                                 RDSVKGRFTISRDNAKNSLYLQMNSLRVDDTAVYYCARDSCNGAICYGPSPWGQGTLVTV
                                                                                                                                                                                                                                                                      EVQLVESGGGLVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGKGLEWVSSISSRSDYIYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53088 MW;
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71.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 463; DB 4; I
Pred. No. 5.8e-38;
L4; Mismatches 21;
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Pred. No. 9.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D0633949F2AC149D
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; Homo.
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EMBL; BC015760; AAR15760.1; -
InterPro; IPR003006; Ig_-like.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig__v.
Pfam; PP00047; ig; 5.
PFAm; PP00040; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS00935; IG_LIKE; 5.
PROSITE; PS00909; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                             O9UL71;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UL71
                                                                                                    SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.
Young D.C.;
                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                           "Myosin-reactive autoantibodies in rheumatic carditis
                                                                                                                                                                                                                                                                                                                                               (Fragment)
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Immunol. Immunopathol. 87:184-192(1998) AF035043; AAD56279.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTVSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMWWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIVSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.9%; Score 493.5; DB 4; Length ilarity 76.0%; Pred. No. 6.5e-41; Conservative 13; Mismatches 14; Indels
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Last annotation updat
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Best Local S
Matches 93
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 471 AA; 51791 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8TC77;
01-JUN-2002
01-JUN-2002
01-MAR-2003
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024289; AAH24289.1; -.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; P:
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSMSSSSSYIYY
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13154 MW; 2F045CCFA5D50736 CRC64;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                               51791 MW;
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                                                                                                                                                                                                                                                                             73.2%; Score 470; DB 4; 72.1%; Pred. No. 1.1e-38; tive 18; Mismatches 16
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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5: sp_invertebrate

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

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Q8u177 homo
Q8wuk1 homo
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ntnoon on Friers	3	Bum	Bum	Q9ul89 homo sapien	Q924p7 mus musculu	Q9qxe9 mus musculu	Bum	8 mu 8	Q9ul94 homo sapien	Q9brv0 homo sapien	homo	Q9n0w6 oryctolagus	oryc	homo	•	4 mus	homo	•	Q9qyf0 mus musculu	-	mu8	Q8n4y9 homo sapien	Q91z07 mus musculu	homo	Bum	8nm	Q8ncl6 homo sapien	Q91z05 mus musculu	Q9ul72 homo sapien

#### ALIGNMENTS

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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC021276; AAH21276.1; -.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR0030596; Ig_v.

R Pfam; PP00047; 1g; 4.

R Pfam; PP00047; 1g; 4.

R SMART; SM00406; IGv; 1.

R SMART; SM00406; IGv; 1.

R PROSITE; PS02030; IG_MHC; 2.

R PROSITE; PS02030; IG_MHC; 2.

W Hypothetical protein.

Q SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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      ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKHGSGSYIGYYYGMDVWGQGTTV 139
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79.8%;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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SEQUENCE (TEPC 15).
SEQUENCE (TEPC 15).
MEDLINE=7622762; PubMed=819932;
Rudikoff S., Potter M.;
"Size differences among immunoglobulin heavy chains phosphorylcholine-binding proteins.";
phosphorylcholine-binding proteins.";
Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
                                                                                                                                                                                                                                                                                                                                                                                                     P01787;
P01787;
P01787;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
-- heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
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Mus musculus (Mouse)
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Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Robinson E.A., Appella E.;
"Complete amino acid sequence of a mouse immunoglobulin alpha (MOPC 511).",
Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROT BINDS PHOSPHORYLCHOLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
   SEQUENCE FROM N.A. (H107).
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Gearhart P.J., Johnson N.D., Douglas
"IgG antibodies to phosphorylcholine
their IgM counterparts.";
Nature 291:29-34(1991)
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Rudikoff S., Barstad P., Potter M., H
Unpublished results, cited by:
Hood L., Campbell J.H., Elgin S.C.R.;
Annu. Rev. Genet. 9:305-353(1975).
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Early P., Huang H., Davis M., Calame K., Hood L
"An immunoglobulin heavy chain variable region
three segments of DNA: VH, D and JH.";
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HSSP; P01789; 1MCP.
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i- MISCELLANBOUS: THESE CHAINS WELLATED FROM MYE
HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.
-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
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l3; Mismatches 23;
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Best Local
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InterPro; IPRUUJJ.
InterPro; IPRUUJJ.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin region; Pyrrolidone carboxylic acid.
Immunoglobulin 1 112
IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HV3J_HUMAN
P01771;
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GO; GO:0005823; F:antigen binding activ
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ଜ୍ୟୁ ନ୍ଦ୍ର
ଜ୍ୟୁ ନ୍ଦ୍ର
ଜ୍ୟୁ ନ୍ଦ୍ର
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.; Amino acid sequence of the VH region of human myeloma cryoimmunoglobulin IgG Hil."; Biochemistry 18:553-560(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
MEDLINE=79124695; PubMed=420800;
MEDLINE=79124695; PubMed=420800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3MART; SM00406; 10v, 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V regTon; Pyrrolidone carboxylic acid.
Immunoglobulin V regTon; PyrroLIDONE CARBOXYLIC ACID.
DOMAIN
1 112
PYRROLIDONE CARBOXYLIC ACID.
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V-III region HIL.
Homo sapiens (Human)
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                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; P:antigen binding action GO; GO:0006955; P:immune response; NAS
                                                                                                                                                                                                                                                                                                                                                                         PIR; A02054; G1HUHL.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALL WACROGLOBULIN.
SIMILARITY: Contains 1 immunoglobulin-like domain.
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122 AA;
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13166 MW; 74E5B6959E84100A CRC64;
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                                                                                                                                                                                                                                                                                                                         activity; NAS
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Best Local S
Matches 82
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Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                                                                Pfam; PP00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS0835; IG LIKE; 1.

Immunoglobulin v region.

DOMAIN

NON TER 119 119
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READ D.N., Rudikoff S., Krutzsch H., Potter M.;

Rao D.N., Rudikoff S., Krutzsch H., Potter M.;

Rad D.N., Rudikoff S., Potter M.;

Rad D.N., Rudikoff S., Rudi
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V region T601.
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P01810; 2FBJ.
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                                                                                                                                                                                                                                                                                                    SEQUENCE
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              VSS 122
                                                                                                                                                       EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
                                                     TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLG----
                                                                                                                                      EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY
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119
119 AA;
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121 AA;
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13566 MW;
                                                                                                                                                                                                                                                                                                    13169 MW;
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                                                                                                                                                                                                                   65.7%; Score 422; DB 1; Lt 66.7%; Pred. No. 2.1e-36; 66.7%; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 427.5; D
; Pred. No. 6e-37
12; Mismatches
                                                                                                                                                                                                                                                                                                                                              IG-LIKE
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                                                                                                                                                                                                                                                           Length 119,
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116

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RESULT 10
HV3B_HUMAN
ID HV3B_HUMAN
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Best Local S
Matches 87
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region.

I 11 11

NON TER 120 120

SEQUENCE 120 AA; 13227 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capra J.D., Hopper J.E.;

"Comparative studies on monotypic Igm lambda and IgG kappa from an individual patient. III. The complete amino acid sequence of the VI region of the IgM paraprotein.";

Immunochemistry 13:995-999(1976).

-i- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P01766;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region BRO.
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GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; F:antigen binding activity; NAS.

GO; GO:0006555; P:immune response; NAS.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYYNMMVRQVTGKGLEWVSAI-GTAGDQYY
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72.5%;
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Pred. No. 1.7e-37;
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       PRT;
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RESULT 11
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NON_TER
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PIR; A02046; MAHUWE.
HSSP; P01772; 2F84.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding activity; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0005855; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_W.
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Goni F., Frangione B.;
Goni F., Frangione B.;
Pamino acid sequence of the Fv region of a human monoclonal IgM
"Amino acid sequence of the Fv region of a human monoclonal IgM
"Control MEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).

-I- MISCELLANEOUS: THIS CHAIN MAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.
Plorent G., Lehman D., Putnam F.W.;
"The switch point in mu heavy chains
Biochemistry 13:2482-2498(1974).
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                           HV3H HUMAN STANDARD; PRT; 122 AA P01765; P01765; P170L-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 19 heavy chain V-III region GA.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
                                                                     SEQUENCE.
MEDLINE=74175307; PubMed=4208843;
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21-JUL-1986 (Rel.
15-SEP-2003 (Rel.
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114 AA;
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01, Last sequence update)
42, Last annotation updat
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12256 MW; D88294FB418A07B7 CRC64;
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68.9%;
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Pred. No. 2.
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Best Local Similarity
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                                                                                                                                                                                                                  MOD_RES
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), II. The amino acid sequence of the H-chain, alpha-type, subgroup III; structure of the complete IgA-molecule.";
Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
-i- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE (MYELOMA PROTEIN TRO)
MEDLINE=76023781; PubMed=80933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunglobulin V region; Pyrrolidone carboxylic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kratzin H., Altevogt P., Ruban B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A02045; A1HUTR.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                            DOMAIN
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GO:0003823; F:antigen binding activity; NAS
GO:0006955; P:immune response; NAS.
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SS
                                                                    ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
                                                                                                          QVQLVQSGGGLVKPGGSLRLSCVASGFSFRDFYMSWIRZTPGKGLZWVSYIGGSGSTLYY
                          SS 122
                                                    ADSVKGRFTISRDNAQKSLYLZMBSLRTZBTAVYYCAATBBFBWSTFSLBYWGZGBLVTV
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122 AA;
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Pred. No. 6.1e-38;
o. Mismatches 21;
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Pred. No. 1.6e-37;
4; Mismatches 24; Indels
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                                                                                                                                                                                                                     2E21A11DA04D80F9 CRC64;
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1

Immunoglobulin v region; 3D-
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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PDB; 2FB4; 12-JUL-89.
PDB; 2IG2; 12-JUL-89.
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       13718 MW;
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          E4D71B52B16F8776 CRC64;
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RGO; GO:0003823; F:antigen binding activity; NAS.

RGO; GO:0006955; P:immune response; NAS.

R InterPro; IPR003106; Ig_-1ike.

R InterPro; IPR003906; Ig__W.

R InterPro; IPR00396; Ig__W.

R Pfam; PF00047; ig; 1.

R Pfam; PF00047; ig; 1.

R Pfam; PF00047; ig; 1.

R PROSITE; PS50835; IG_V:

Immunoglobulin V region; Pyrrolidone carboxylic acid.

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1 112 IG-LIKE.
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                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
15 heavy chain V-III region BUT.
Homo sapiens (Human)
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Proc. Natl. Acad. Sci. U.S.A. 77:339-3243(1980).
-i- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PATIENT WITH MACROGLOBULINEMIA.
-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Mammalia; Eutheria; Primates;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                  MEDLINE=78137069; PubMed=416441; Torano A., Putnam F.W.;
                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
"The primary structure of a monoclonal IgM-lmmunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain (type), subgroup H III. Architecture of the complete IgM-molecule.' Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
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PROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region.
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To heavy chain V-III region
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GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
  SEQUENCE
                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                  GO; GO:0005576; C:extracellular; NJ
GO; GO:0003823; F:antigen binding a
GO; GO:0006955; P:immune response;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                               PROSITE;
                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                          REVISION TO 28-33.
                                   PROSITE; PS50835; IG LIKE; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 AA;
  116 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                         01, Last sequence update)
42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12379 MW;
  12730 MW;
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Pred. No. 3.3
                          IG-LIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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  2C67CA9AAAAA1282 CRC64;
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                                                                                                                                              NAS
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Matches 84
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"Structure and multiplicity of genes for the human immunoglobulin heavy chain variable region.";
Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V-III region VH26 precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NON TER
SEQUENCE
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003833; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003059; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIEE; 1.
Immunoglobulin V region; Signal; 3D-structure
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21-JUL-1986
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PDB; 1HOU; 23-DEC-99.
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EMBL; M35415; AAA58735.1; -.
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85.7%;
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Score 453; DB 1; 1
Pred. No. 1.4e-39;
9; Mismatches 5;
                                                                                                                                                   IG HEAVY CHAIN V-III REGION VH26. IG-LIKE.
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tches 19;
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                                             Length 117;
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00306; Ig_MHC.
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P01765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Immunoglobulin structure and genetics. Identity between variable regions of a mu and a gamma2 chain.";
J. Biol. Chem. 252:7192-7199(1977)
-i- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo Bapiens (Human).
Bukaryota; Metazoa; Chordata;
Bummalia; Butheria; Primates;
NCBI_TaxID=9606;
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21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region TIL.
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                                  HV3G_HUMAN
P01768;
                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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	Baltimore D;  Baltimore D;  "Heavy chain variable region contribut antibodies somatic mutation evident i Cell 24:625-637(1981).  [2]  REDLINE=77100368; PubMed=401950; MEDLINE=77100368; PubMed=401950; Adetugbo K., Milstein C., Secher D.S.; Molecular analysis of spontaneous som Mature 265:299-304(1977).  This SWISG-PROT entry is copyright. It between the Swiss Institute of Bioinfiche European Bioinformatics Institute, be unon-profit institute in Bioinformatics in the European Bioinformatics in strengent by non-profit institutes as 1 modified and this statement is not rementities requires a license@isb-sib.ch	, i iii ii	113 116 117 119 1119 1110 1111 1111 1111
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R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-942, 1992

A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from the property of the prope
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
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A;Otoss-references: EMBL:X62963
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31114
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A;Molecule type: DNA
A;Residues: 1-143 <OLE>
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A;Residues: 1-123 <RAA>
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Ig heavy chain V region (M43) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: D36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: D36005
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A;Molecule type: mRNA
A;Residues: 1-122 <SCH>
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Ig heavy chain V region - hum
C;Species: Homo sapiens (man)
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(;Superfamily: immunoglobulin V region; immunoglobulin homology C;Kupvords: heterotetramer; immunoglobulin C;Keyvords: heterotetramer; immunoglobulin pomology <IPM>
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A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                   96;
                                                                                                                                                                                                                                                                                                                                                                                 h 77.6%; Score 498.5; Similarity 78.7%; Pred. No. 1.1
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Pred. No. 1.1e-37;
9; Mismatches 18
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Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 331686
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Accession: S31686
A;Accession: S31686
A;Accession: S31686
A;Status: preliminary
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <1MM>
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A; Residues: 1-140 < CUI>
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138 VSS 140
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Similarity 76.8%; Pred. No. 1.4e-37;
96; Conservative 13; Mismatches 11
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78.9%; Pred. No. 3.1e-37;
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Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

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A;Accession: C36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: GB.M18513
A;Cross-references: GB.M18513
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38489
R;Marks, J.D.; Ouvehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a A;Reference number: S38488
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S38489
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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| Species: Homo sapiens (man)
| Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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Pred. No. 7.6e-38;
0; Mismatches
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Pred. No. 1.8e-38;
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C;Accession: B36005

R;Schroeder Jr., H.W.; Wang, J.Y.
R;Schroeder Jr., H.W.; Wang, J.Y.
1990

R;Title: Preferential utilization of conserved imm
A;Reference number: A36005; MUID:90349571; PMID:21
A;Accession: E36005
                                                                                                                                                                           RESULT
E36005
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R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity
                                                                                                               Ig heavy chain V region (M72) - human C;Species: Homo sapiens (man) C;Date: 21-Dec-1990 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-140 < CUI>
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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A;Molecule type: DNA
A;Residues: 1-127 <MAR>
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74.8%;
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Pred. No. 1.1e-37;
1; Mismatches 12
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Pred. No. 8.1e-38;
1; Mismatches 14
                                                                                                                      21-Dec-1990
                      rved immunoglobulin heavy PMID:2117273
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C;Accession: S31666

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate A;Reference number: S31585
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A;Residues: 1-147 <RES>
A;Residues: 1-147 <RES>
A;Crose-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;28-111/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31666
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A;Residues: 1-138 <CUI>
A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964
A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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C;Accession: S31107
R;Raaghorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
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                                                                                    C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31107
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A;Status: preliminary
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ilarity 82.3%;
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81.1%;
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Pred. No. 1.4e-39;
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Pred. No. 4.9e-39;
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A;Cross-references: EMBL:X62955
A;Note: the nucleotide sequence was submitted to the EMBL C;Superfamily: immunoglobulin V region; immunoglobulin hom C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eubmitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Areference number: S48797
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A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-120 < MAH>
A;Residues: 1-120 < MAH>
A;Residues: 1-120 < MAH>
A;Cross-references: EMBL:246382; NID:9562324; PIDN:CAA86521.1; PID:91340167
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
P;15-98/Domain: immunoglobulin homology < MMM>
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C;Accession: S48798
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                                                                                                                                                                                                                                                                        ADSVKGRFTISRDNSKYTLYLOMNSLRAEDTAVYYCAK-DRGFWSGYK----DYWGQGTL 115
                                                                                                                                                                                                                                                                                                       ADSVKGRPTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRG---GYKYYGMDVWGQGTT 117
                                                                                                                                                                                                                                                                                                                                      VIVSS
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82.0%;
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80.8%;
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Pred. No. 9.7e-39;
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Pred. No. 1.3e-38;
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homology
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Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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514.5
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                             Query
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVESGGDLVQPGGSLRL......GYKYYGMDVWGQGTTVTVSS 122
     GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                   Length DB
     1307870
1317870
131666
131107
1311107
131108
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Ig variable region
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DЬ	ঠ	p &	₽ &	Query Best Match	A;Molec A;Resic A;Cross C;Super C;Keywo F;1-19, F;20-10	A;Cross R;Kishi Nucleic A;Title A;Refes A;Acces	A;Refer A;Acces A;Molec A;Resic	Ig neav C;Speci C;Date: C;Accer R;Kishi	സര	4 4 4 b	38 24 20 21 30 31		33 32 33
140 VTVSS 144	118 VTVSS 122	61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTT 	1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY     :	Query Match 85.3%; Score 547.5; DB 2; Length 160; Best Local Similarity 84.0%; Pred. No. 6.5e-42; Matches 105; Conservative 8; Mismatches 9; Indels 3; Gaps	A;Molecule type: mRNA A;Residues: 1-144 <kis2> A;Cross-references: EMBL:X14584 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <sig>F;20-160/Product: Ig heavy chain (fragment) #status predicted <mat>F;34-117/Domain: immunoglobulin homology <imm></imm></mat></sig></kis2>	A;Cross-references: EMBL:X14584 R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M. Nucleic Acids Res. 17, 4385, 1989 A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and A;Reference number: S04601; MUID:89296497; PMID:2500644 A;Accession: S04602		Ig heavy chain precursor - numan (tragment) C;Species: Homo sapiens (man) C;Date: 30-Jun-1992 #sequence_ revision 30-Jun-1992 #text_change 16-Aug-199 C;Accession: S05271; S04602 R;Kishimoto, T.	1	462.5 72.0 121 2 S31106 Ig heavy chain 462.5 72.0 145 2 S11239 Ig heavy chain 461.5 71.9 119 2 F36005 Ig heavy chain	466.5 72.7 121 2 81966 1g neavy chain 465 72.4 139 2 838808 1g heavy chain 464.5 72.4 127 2 819878 1g heavy chain 464 72.3 139 2 831674 1g heavy chain 464 72.3 139 2 831674 1g heavy chain	469 73.1 141 2 831669 Ig heavy chair 467 72.7 108 2 PH1648 Ig heavy chair 467 72.7 128 2 826790 Ig heavy chair 467 72.7 136 1 GIMS21 Ig heavy chair	470.5 73.3 134 2 831679  470 73.2 128 2 831595  469.5 73.1 117 2 878486  469 73.1 140 2 870442  Ig heavy chair
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of.

Ig variable region (VDJ) (clone T20-11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C;Accession: I37780; S25474
R;Demalson, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

RESULT 2 137780

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TOPOLOGY:
US-08-652-816A-7
                                                                                                                                                                                                                                      MEDIUM TYPE: Plapy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 926318.9
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION NUMBER: GB 9525004.9
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-SEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 36.107
REFERENCE/DOCKET NUMBER: 26111/33308
TELECOMMUNICATION INFORMATION:
TELEDHONE: 312-474-6300
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                          Query Match
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                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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Local Similarity
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                                                                                                                           LENGTH: 123 amino acids TYPE: amino acid
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R SEQ ID NO: 7:
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  78.8%;
77.2%;
Score 470.5; DB 2; Length 123; Pred. No. 2.1e-41;
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Search completed: December 30, 2003, 11:05:36 Job time : 11.6593 Becs
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                                                       121
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                                                                                                                                                                                                                 95;
                                                                                                                                                                             1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
                                                       VSS 123
                                                                                 VSS 114
                                                                                                          AQKFQGRLTITADESTSTAYMELSSLRSEDTAVYYCAGANSCNRSYYYYMDVRGQGTMVT 120
                                                                                                                                                              QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNSPINWLRQAPGQGLEWMGSIIPSFGTANY
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                    8; Mismatches
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ATTORNEY/AGENT INFORMATION:

CLASSIFICATION:

NAME: Howells, Stacy L. REGISTRATION NUMBER: 34,842

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RESULT 13
PCT-US93-10555-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
           TELBFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 455-5110 INFORMATION FOR SEQ ID NO:
                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: FD.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/
PILING DATE: 29-OCT-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: pepi IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watch 79.5%;
Local Similarity 79.2%;
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                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
ZIP: 90067
                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OKFOGRVTITTDESTSTAYMEVSSLRSEDTALYYCAREGRRMAINPFDYWGQGTLVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQLVQSGAEVKKPGSSVKVTCKASGDTFSSSAISWVRQAPGQGLEWMGGIIPIFGTPNYA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILVERMAN, GREGG J.

VENTION: METHOD FOR STIMULATING PRODUCTION OF
VENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
VENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                               FD-2630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 474.5; DB Pred. No. 8e-42;
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                                                                                                                                                                                                                                                                                                Version #1.25
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                                                                                                           ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-10
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LOCATION: 1..120
PCT-US93-10555-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10,
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--- rocal Similarity
                                                       Matches
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                                                                                 Query Match
                                                                                                                                                               TELBEAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
PILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS: ADDRESSEE: ROTHWELL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                       92;
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5876961
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555 THIRTEENTH ST. N.W.
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                                                       Conservative
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                                                                    79.0%;
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                                                       11; Mismatches
                                                                                                                                                                                                                                                   1808-118
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                                                                    Score 471.5; DB 2
Pred. No. 8.4e-41;
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Pred. No. 8e-42;
7; Mismatches
                                                                                 DB 2;
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                                                         Indels
                                                                                 Length 476;
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                                                       Gape
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RESULT 11
US-08-428-197-13
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                                                                                                                                                                                                         Sequence 13, Application US/08428197
Patent No. 5891418
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
                                                                                                                                APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: WETHOD FOR
TITLE OF INVENTION: VARIABLE R
TITLE OF INVENTION: VACCINATIO
TITLE OF INVENTION: THEREOF
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ATTORNEY/AGENT INFORMATION:
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STREET: 1850
CITY: Los Angeles
STATE: Callfornia
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                                                                                         NUMBER OF SEQUENCES: 5
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LOCATION:
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CITY: Los Angeles
STATE: California
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                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                              62 QKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWFYIWGQGTMVTVSS 114
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1880 Century Park East - Suite
                                                  E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
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79.2%;
                                                                                                                                WETHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 474.5; DB 2; Length Pred. No. 8e-42; nismatches 11; Indels
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; LOCATION:
US-08-428-197-13
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Best Local S
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/
PILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
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LENGTH: 120 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 455-5100
     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 29-OCT-19
                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
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                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94;
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                                                                                                                                                                               Los Angeles
California
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1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                          SILVERMAN, GREGG J.

SILVERMAN, GREGG J.

VENTION: METHOD FOR STIMULATING PRODUCTION OF
VENTION: VARIABLE REGION GENE FAMILY RESTRICTED
VENTION: VACCINATION WITH A B-CELL SUPERANTIGEN
                                                                                                                                                                USA
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лыык: PCT/US93/10555
29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.5%;
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AND CONJUGATES
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US-08-232-0818-41
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                                                                     US-08-983-607-50
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                 Sequence 50, Application US/08983607 Patent No. 6140470
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 205-8050 INFORMATION FOR SEQ ID NO: 41:
              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COPPUTER: PC-TOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: SVERSSON, LECONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/232,081B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                        121 S
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                                                                                                                                                                                                            61 AQKFQGRVTITADESTNTAYMELRSLRSDDTAMYYCAKEGYGDYGRPFDFWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                94;
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                                                                                                                                                                                                                                AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELDW------FYIWGQGTMVTVS 113
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                                                                                                                                          121
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77.7%;
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                                                                                                                                                                                                                                                                                                                                                      Score 476.5; DB 2;
Pred. No. 5.1e-42;
8; Mismatches 12;
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Sequence 12, Application US/084281
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR

METHOD FOR STIMULATING PRODUCTION OF

Application US/08428197

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RESULT 10
US-08-428-197-12
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                                                                                                                                                                                                                                Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MATY M. KTINSKY
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human J
TITLE OF INVENTION: bodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
DESCRIPTION: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOPTWARE: Word Processing
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: VH antibodies obtained from fUSE5
LIBRARY: fusion phage construct
CLONE: 2-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: June 2 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens (melanoma patient ORGANISM: immunized with autologous tumor cells) INDIVIDUAL ISOLATE: peripheral blood lympho-INDIVIDUAL ISOLATE: cytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/983,607 FILING DATE: April 27, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United ZIP: 06520-8114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Department of Molecular Biophysics ADDRESSEE: and Biochemistry, Yale University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                  68 VTITADESTSTAYMELSTLTSEDTAVYYC----ELDWFYIWGQGTMVTVSS 114
                                                                            68 VTITADKSTSTAYMELSSLRSEDTAVYYCARGGGRYDAFDIWGQGTLVTVSS 119
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                                                                                                                                                                         8 GABYKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNYAQKFQGR 67
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                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                             heavy chain
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N: 435
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                                                                                                                                                                                                                                                  79.5%;
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                                                                                                                                                                                                                              Score 474.5; DB
Pred. No. 8e-42;
4; Mismatches
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                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                  9,
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